In the Name of God,  
Most Gracious,  
Most Merciful.
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The Kingdom of Saudi Arabia possesses a rich and varied wildlife heritage which the government is deeply committed to protect. Although conservation in the Kingdom of Saudi Arabia began about 30 years ago through the efforts of the Ministry of Agriculture and Water and later by the Meteorology and Environmental Protection Administration (MEPA), it effectively started in 1986 with the creation of the National Commission for Wildlife Conservation and Development (NCWCD) by Royal Decree, and the establishment of the National Wildlife Research Centre (NWRC) at Taif. Both organizations have been fully supported since their inception by the government of the Custodian of the Two Holy Mosques and the guidance of His Royal Highness Prince Sultan bin Abdulaziz Al Saud, Chairman of the Board of Directors of NCWCD.

The gazelle taxa of the Arabian peninsula are an important part of this heritage. Admired for centuries by Arab poets for their beauty and grace, and superbly adapted to the arid and semi-arid environments which they inhabit, traditional hunting methods had little impact on gazelle populations. The advent of modern firearms and motorized vehicles radically altered this situation and numbers were decimated by over-hunting, exacerbated in recent years by over-grazing, bringing most taxa to the verge of extinction. Recognizing the need for urgent measures NCWCD began a two-pronged strategy to ensure the conservation of these remarkable animals: the creation of protected areas to preserve wild populations, and the establishment of a captive breeding programme to secure and propagate gazelle taxa in captivity for eventual reintroduction to the wild.

The hard work and dedication of NCWCD staff, including rangers and scientists, is now bearing fruit. The short-term future of both natural and reintroduced populations of gazelle within protected areas in Saudi Arabia looks to be assured. In addition to these efforts NCWCD is therefore conducting public awareness campaigns to attempt to secure a similarly bright future for the remaining unprotected wild populations of gazelle, which still persist in small numbers distributed in isolated pockets in mountainous regions of the Kingdom.

The need for a Symposium on "Establishing Priorities for the Conservation of Gazelle in the Arabian Peninsula" arose from the large body of scientific and practical conservation work on gazelle undertaken by NCWCD, NWRC and King Khalid Wildlife Research Centre (KKWRC - founded in 1987). The Symposium, an important exercise in international co-operation which assembled experts from around the world, was financed and hosted by NCWCD at Riyadh from the 31 October to 3 November 1992. These Proceedings are a documented record of the Symposium.
Introduction

Chris Magin

The presentations given in the Symposium "Establishing Priorities for the Conservation of Gazelle in the Arabian Peninsula" synthesized existing scientific knowledge and addressed many key issues in gazelle conservation and taxonomy. At the close of the Symposium, an Arabian Gazelle Working Group discussed the current situation in the light of the presentations and produced a series of guidelines and recommendations for the future successful conservation of gazelle in the Arabian Peninsula.

Authors were asked to submit written versions of their oral presentations to the editors. After the Symposium these were then peer-reviewed by two independent referees, and revised in the light of referees' comments by the authors themselves before incorporation in these Proceedings. Consequently some articles are slightly different from the presentations actually given at the Symposium: in particular those on "Taxonomic Diversity in Arabian Gazelles: The State of the Art" and "Measures to Conserve the Wildlife of Kuwait". All or parts of several articles have also been published in scientific journals since the Symposium: for example the article on "Bilki's Gazelle in Yemen - Status and Taxonomic Relationships" appeared in its entirety in *Oryx* (1993, Vol. 27(4): 239-244), and a modified version of the article on "Survey of Gazelle Populations in South-West Saudi Arabia and Recommendations for their Conservation" appeared in *Biological Conservation* (1994, Vol. 70: 69-75). In the interest of presenting as complete a record as possible of the Symposium, such articles have been retained.

It should be noted however that despite repeated requests by the editors, written versions of two oral presentations given at the Symposium, on the conservation of gazelle in Bahrain and the United Arab Emirates, were never received and are therefore not included in these Proceedings.

Several major advances in gazelle conservation have occurred since the Symposium. Most notable of these was the release in March 1995 of 100 Arabian sand gazelle *Gazella subgutturosa marica* into the unfenced 'Uruq Bani Ma'arid Reserve (created in 1994) on the fringes of the Rub al-Khali in the south of the Kingdom. Initial studies indicate that as of October 1995 the population was flourishing. In the same month the reintroduced population of sand gazelle in the fenced Mahazat as-Sayd reserve was estimated to number approximately 360 animals, with substantial scope for future growth.

It is worth noting in passing that one problem alluded to by Williamson and Tatwany in their article entitled "Gazelle Distribution and Status in the Arabian Peninsula" also appears to have been resolved. Based on NCWCD rangers' reports, it was initially thought that the enigmatic "afri" or Saudi dorcas gazelle *Gazella dorcas* ssp. might occur in Harrat al-Harrah and Al-Khunfah. However, photographic evidence and direct observation have now confirmed that the suspected "Afri" are in fact "idmi" or mountain gazelle *Gazella gazella* (Tim Wacher, pers. comm.).
1. Recent Developments in Gazelle Conservation and Taxonomy in Saudi Arabia

Arnaud Greth and Douglas Williamson

Abstract: This paper outlines developments in gazelle taxonomy and conservation in Saudi Arabia between 1986 and 1992. The creation of the National Wildlife Research Center and the King Khalid Wildlife Research Center under the auspices of the National Commission for Wildlife Conservation and Development (NCWCD) has strongly stimulated gazelle conservation and research. At these centers captive breeding of native Arabian gazelle species (sand gazelle, Gazella subgutturosa, mountain gazelle, Gazella gazella gazella and Gazella gazella erlangeri, and Saudi dorcas gazelle, Gazella dorcas saudiya) has been successfully implemented. Taxonomic and other research projects and management programmes have been undertaken, all of which have produced significant results.

The creation of well-guarded protected areas (Harrat al-Harrah, Al-Khunfah, Farasan Islands) by the NCWCD has saved important natural gazelle populations in the Kingdom. The reintroduction of mountain gazelle in the Ibex Reserve at Hawtat Bani Tamim and sand gazelle in Mahazat as-Sayd has been successful so far. The establishment of new protected areas and the continuation of the various research projects should greatly contribute to gazelle conservation in the Kingdom of Saudi Arabia.

Keywords: gazelle, conservation, taxonomy, Saudi Arabia

Introduction

This paper outlines the recent important events in gazelle conservation and taxonomy in Saudi Arabia, particularly since the creation of the National Commission for Wildlife Conservation and Development (NCWCD). This Saudi governmental institution has been particularly active in promoting gazelle conservation and research in the Kingdom. The following account provides an overview of this adventure, dedicated to the conservation of biodiversity in the Arabian peninsula, and the results obtained since 1986. This list does not pretend to be exhaustive, but attempts to highlight only the most important steps. The final result of these endeavours is not known, but it is hoped that it will result in the propagation and scientific management of this important group of ungulates in the Kingdom.

- 1968: David Harrison (1968) publishes in "Oryx" a review of the status and conservation needs of the larger mammals of the Arabian peninsula. He stresses the threat of extinction, due to motorized hunting parties, to the three species of gazelles, the sand gazelle or rheem Gazella subgutturosa, the mountain gazelle or idmi Gazella gazella and the dorcas gazelle or afri Gazella dorcas. The dorcas seems the most vulnerable as it inhabits open gravel plains to the east of the Hejaz range.
- 1985: Groves and Lay (1985) describe a new gazelle species called *Gazella bilkis*, increasing the number of gazelles in the Arabian peninsula to four. This species is described on the basis of morphological criteria from five specimens in the Field Museum of Natural History in Chicago. The specimens were collected in 1951 near Ta'izz in Yemen (Sanborn and Hoogstraal, 1953). Since 1951, no data have been collected about this gazelle... a fact which emphasizes the lack of conservation interest in the region and the low level of knowledge of its natural history.

- 1986: New warning in the journal "Oryx" by Habibi (1986), who emphasizes the extinction risk facing ungulate populations in Saudi Arabia, mainly because of hunting and habitat degradation. Green (1986) also stresses the general decline of the fauna in northern Saudi Arabia in the journal "Mammalia".

- 1986: Creation of the NCWCD by Royal Decree of His Majesty King Fahd bin Abdul-Aziz al Saud, Custodian of the Two Holy Mosques. The goal of the Commission is mainly "to maintain the integrity of the biotic heritage of Saudi Arabia in the face of increasing human development pressures and impacts" (Abuzinada, 1987). The Commission is based in Riyadh.

- March, 1986: Creation of the National Wildlife Research Center (NWRC), near Taif, under the management of Jacques Renaud. The primary aims of the NWRC are the captive-breeding of the houbara bustard *Chlamydotis undulata* and the Arabian oryx *Oryx leucoryx*.

- June, 1986: Discovery of tuberculosis infection in the NWRC Arabian oryx herd. The carriers of the bacteria originate from the late King Khalid's farm at Thumamah, near Riyadh. This farm is famous for its collection of Saudi ungulates.

- November, 1986: First population counts of the different captive species at Thumamah. One hundred and seventy mountain gazelles and 220 Arabian sand gazelles *G. s. marica* are found, which is, for both species, the largest known captive population in the world (according to data in the "International Zoo Yearbook"). However, the collection is in a poor state due to overcrowding, poor hygiene and lack of management.

- January, 1987: Creation of the King Khalid Wildlife Research Center (KKWRC). The KKWRC is mainly dedicated to the captive breeding of, and research on, Arabian gazelle species. The first necessary actions are implemented by Hany Tatwany and Khushal Habibi. In October 1987 responsibility for the management of the collection is given to the Zoological Society of London.

- March, 1987: Gift from the Emir of Najran of a small dark gazelle to the NWRC. This gazelle obviously raises a taxonomic problem for biologists; it has been called successively *G. g. muscatensis, G. bilkis*, and now *G. g. erlangeri*...

- 1987: An area in the north-west of the Kingdom, called Harrat al-Harrah, 13,775 km² in size, is declared protected by the Board of Directors of the NCWCD (Child and Grainger, 1990b). This reserve gives legal protection to the first populations of rheem and idmi in Saudi Arabia.
- April, 1988: Survey of the Farasan Islands (Flamand et al., 1988). The survey confirms the existence of a healthy population of at least 500 mountain gazelles, the largest population known in Saudi Arabia. The Farasan Islands are later declared a "protected area" by the Board of Directors of the NCWCD in 1989.

- 1988: Establishment of a genetic laboratory at the NWRC. One of the aims of this research laboratory is to contribute to the knowledge of gazelle taxonomy in the Arabian peninsula, by the use of cytogenetic and electrophoretic techniques.

- 1988: Approval by the Board of Directors of the NCWCD (Child and Grainger, 1990b) of Al-Khunfah, 20,450 km² in size, as a protected area. The largest concentration of rheem known in Saudi Arabia is thus protected.

- January, 1989: Beginning of the tuberculosis eradication programme in a population of several hundred ungulates of various species at Thumamah. The strategy includes isolation of the gazelles in small groups, regular serological tests, euthanasia of reactive animals and hand-rearing of some of the calves.

- March, 1989: The "Protected Areas Planning Unit" of the NCWCD conducts a survey in the Makshush area, situated beside the Red Sea, 350 km south of Jeddah. Five mountain gazelles are seen. Numerous tracks of other animals, dung middens and bedding sites are also seen. The population is estimated to number about 50 animals. It is facing immediate risk of extinction due to poaching. Most of the gazelle populations in the south-west of Saudi Arabia face a similar situation. Immediate action is needed to save these populations.

- May, 1989: By means of aerial and ground counts, the rheem population of Al-Khunfah is estimated as between 250 and 450 individuals by Thouless, Tatwany and Habibi.

- August, 1989: About 400 rheem are counted in Qassim farm. The management of this private collection, located in the north of the country, has been given to the NCWCD and, in practice, will be conducted by KKWRC staff.

- 1989-1990-1991: Local people write to the NCWCD to indicate the existence of relict gazelle populations, mainly in the south-west of the Kingdom, facing great danger of extinction.

- January, 1990: Meeting of international experts on tuberculosis held at KKWRC to discuss the release of gazelles from Thumamah. A tuberculosis testing protocol is agreed upon, which has subsequently been used to produce animals with a clean bill of health.

- February, 1990: Four (2.2) Saudi dorcas are given to KKWRC by Al Areen Wildlife Sanctuary (Bahrain) to start a captive breeding programme. The dorcas gazelle is believed to be extinct in Saudi Arabia. This programme is intended to be the beginning of the return to the wild of the dorcas in the Kingdom. A group of rheem is translocated from KKWRC to pre-release enclosures.
at Mahazat as-Sayd, a 2,244 km² fenced reserve consisting of open desert steppe, located 150 km north-east of Taif.

- **March, 1990:** Publication of a system plan for protected areas by Child and Grainger (1990a). This system plan proposes the creation of a network of 56 terrestrial reserves and 52 marine reserves to conserve biodiversity in Saudi Arabia and to implement sustainable rural development schemes. The proposed reserves account for 8.1% of the Kingdom's total land area (Thouless, 1991). A draft policy document stating the strategy for the conservation of all three gazelle species in Saudi Arabia is also produced (Child and Grainger, 1990b).

- **October, 1990:** Last case of death due to tuberculosis in the KKWRC gazelle population. The eradication programme is believed to be progressing well. Monitoring of the infection will continue through the use of regular serological tests during the following years.

- **1990:** Examination of the karyotypes of rheem from KKWRC reveals a Robertsonian translocation (Granjon et al., 1991). This chromosomal polymorphism has already been described in *G. s. marica* from Jordan by Kingswood and Kumamoto (1988) and raises the problem of the presence of hybrids between the two subspecies, *marica* and *subgutturosa*, in the KKWRC collection.

- **December, 1990:** First release of a group of 20 mountain gazelles in the Special Ibex Reserve at Hawtat Bani Tamim (Lindsay, 1991). This reserve, located south of Riyadh, covers 2,200 km² of a limestone escarpment and plateau with deeply incised canyons running through it. More than 50 animals have now been moved to the reserve. They are monitored by radio-tracking by Kevin Dunham, a KKWRC biologist. More than 30 births in the wild and a good survival rate attest to the promising beginning of the reintroduction.

- **1991:** Rebholz *et al.* (1991) publish the karyotypes of the presumed Saudi dorcas kept at Thumamah. The high chromosome number found (*2n=47* in female, *2n=50/51* in males) refutes the assumption that these gazelles could be a subspecies of the African dorcas gazelle (30 and 31 chromosomes).

- **1991:** Managements of both NWRC and KKWRC agree on a co-operative programme for gazelles and Arabian oryx. Gazelle captive breeding will be under the full responsibility of KKWRC, oryx under the responsibility of NWRC. Both Centers will co-operate to obtain new founders of the different species. Co-operation replaces competition.

- **1991:** Description of the Farasan gazelle, *G. g. farasani*, as a valid subspecies of the mountain gazelle, by Thouless and Al Bassri (1991) in the *Journal of Zoology, London*. This paper revives the debate on the importance of gazelle subspecies and raises the question of the future management of this small population.
- **May, 1991:** Capture of rheem from Qassim and translocation of 30 individuals to pre-release pens at Mahazat as-Sayd, and ten individuals to KKWRC to increase the genetic variability of these two populations. The chromosomal polymorphism is also found in most of the rheem from Qassim (Vassart et al., 1993).

- **May, 1991:** First release of a group of 35 rheem from KKWRC in Mahazat as-Sayd (Haque and Schwede, 1992). The gazelles are monitored by visual sightings and radio-tracking by Mohammed Haque, an NWRC biologist. The animals seem to cope well with their new environment.

- **August, 1991:** Commissioning of a genetic laboratory in KKWRC. This laboratory will focus on gazelle karyology.

- **1991:** A study by Groves et al. (in press), based on skin descriptions and skull measurements, allows the identification of the small, dark gazelle kept at the NWRC and seen in many private collections of the Kingdom. This taxon represents a south-western subspecies of *G. gazella*, to be called *G. g. erlangeri*.

- **November, 1991:** Poachers kill three rheem in Al-Khunfah, raising the problem of the acceptance of protected areas by local people. Gazelles were traditionally hunted as a major source of protein in the Arabian peninsula. With the recovery of certain populations, it may be possible to start a hunting season of gazelles under strict regulations and quotas.

- **December, 1991:** Four so-called Saudi Dorcas (2.2) are brought to KKWRC from Al Ain Zoo (Abu Dhabi) in exchange for four rheem from Thumamah.

- **1991-1992:** Rangers bring five rheem captured in the wild (old, injured or neonates) in Al-Khunfah to KKWRC to test their karyotypes. Three other rheem, captured as infants in the north of the Kingdom and hand-reared, are also karyotyped. The Robertsonian translocation is found in four wild-caught females (2n=31) and in two males (2n=31; 2n=32), confirming that this polymorphism probably occurs naturally. The decision to reintroduce animals with different numbers of chromosomes is taken.

- **March, 1992:** Visit to Al Wabra estate in Qatar reveals the existence of a group of animals which are also believed to be afri, the Saudi dorcas gazelle, but which are very different to the ones from Al Areen and Al Ain. The karyotypes of these animals are identical to those of the Sudanese dorcas. The afri in the collection of His Excellency Sheikh Khalid Bin Mohammed Al Thani, owner of Al Wabra, were obtained in the spring of 1984 from Bedouin at a place called Tareeq Afif on the old road from Taif to Riyadh. What is the Saudi dorcas?

- **1992:** Release of the second herd of 37 rheem in Mahazat as-Sayd in March (Haque and Schwede, 1992). In September, 21 other animals are released. More than 110 rheem are now in the reserve. The location of nine fawns born in the wild during two reproductive seasons, confirms the successful start of this reintroduction programme (Haque, pers. comm.).
- **1992**: Establishment of a captive population of the new gazelle taxon, *G. g. erlangeri*. Sixteen males and 14 females have been collected at the NWRC and will constitute the founder nucleus of a captive breeding programme. The KKWRC will propagate and ensure the survival of the captive population. No information is available on the distribution and status in the wild of this new subspecies of mountain gazelle. Some populations may occur in North Yemen.

- **July, 1992**: Start of a taxonomic study of various gazelle species at NWRC and KKWRC in collaboration with David Woodruff, from the University of California in San Diego. The aim of the study is to compare gazelle type specimens held in museums with live specimens. Several institutions, such as the Field Museum of Natural History in Chicago, the British Museum of Natural History in London, the Muséum National d'Histoire Naturelle in Paris, and the Berlin Zoological Museum, have agreed to co-operate and sample their specimens. Hairs from many live specimens are also included in the study. Extraction of mitochondrial DNA has so far been successful from the hairs sampled from live specimens. It seems difficult to obtain DNA in sufficient amounts for analysis from museum specimen hairs. Preliminary results will hopefully soon be available.

- **Second half of 1992**: Survey of gazelle populations by Chris Magin, an NWRC biologist, and NCWCD staff in the south-west of Saudi Arabia. Many reports and publications have stressed the critical status of small isolated populations of gazelles, believed to be the mountain gazelle *G. g. cora*, in the Asir/Sarawat mountains and in the Tihama coastal plain (Thouless et al., 1991). No protected areas have yet been established for this subspecies and it is at risk of extinction in the near future, mainly because of hunting pressure. The objectives of the survey are to locate as many gazelle populations as possible in this region, and hopefully to collect data about *G. g. erlangeri* and possibly the enigmatic Bilkis gazelle. The viability of each population identified will be estimated, using the guessestimates of local people and field workers. Proposals for immediate *in situ* conservation actions will be made to the NCWCD.

- **October-November, 1992**: A workshop called "Establishing priorities for gazelle conservation in the Arabian peninsula" is organized in Riyadh by the NCWCD under the auspices of Prof. A. Abuzinada, Secretary General. The aim of this workshop is to discuss taxonomic issues concerning the Arabian gazelle species and to produce guidelines and recommendations for the following years for effective research and conservation of gazelles in Saudi Arabia.

**Acknowledgements**

It is not possible to list here the names of all the actors in this story from NCWCD, KKWRC and NWRC. *Gazella gazella, Gazella subgutturosa* and *Gazella dorcas* would like to deeply thank all of them for their commitment and work for conservation in Saudi Arabia. We would particularly like to acknowledge H.R.H. Prince Saud Al Faisal, who has initiated all these efforts, and Prof. Abdulaziz Abuzinada, Secretary-General of the NCWCD, who manages the day-to-day activities of this organization. Jean Francois Asmodé, Kevin Dunham, Khushal Habibi, Nick Lindsay, Chris Magin, Frank Rietkerk, Georg Schwede, Hany Tatwany, Chris Thouless and Marc Vassart helped us to gather the information.
References


Abstract: The discovery that the type of Gazella arabica does not correspond to any of the known and authenticated taxa of Arabian gazelles ushered in an era of unfortunate instability in Arabian gazelle taxonomy. This was further compounded by the description of Gazella bilkis.

Morphologically, Gazella dorcas - a largely African species - seems closest not to G. saudia (which has generally been regarded as its Arabian representative) but to G. gazella cora and G. g. muscatensis. G. g. gazella is surely correctly regarded as conspecific with these last two, but at the same time shows approaches to G. bilkis, thus completing a confusing ring-species effect.

A further complication is the recent resurrection from synonymy with cora of G. g. erlangeri, a small dark straight-horned subspecies from the south-west of the Arabian peninsula.

There are a few problems with G. subgutturosa as well: is the Bahrain population different from mainland G. s. marica? And are Syrian and Iraqi populations of the species different yet again?

Skull, horn and pelage characters have commonly been used to differentiate gazelle species and subspecies. In my presentation, I will pay attention to these characters and in addition to certain features of body proportion.

Keywords: gazelle, taxonomy, Arabian peninsula

Introduction

- Arabian gazelles: The first description of an Arabian gazelle was that of Buffon (1764), who placed at the head of his thirteen species or varieties of "antilopes" one called simply "the gazelle, found in Syria, Mesopotamia and other provinces of the Levant, as well as in Barbary, and in all the northern parts of Africa". The description specified horns "about a foot in length" (approximately 300 mm), with 12-13 rings; and it was contrasted with a second species, "the kevel", said to be from Senegal, which was smaller, with less rounded, more compressed horns with 14-18 rings. A certain Dr Russel was quoted as saying that in the neighbourhood of Aleppo there were actually two kinds of gazelles, the mountain gazelle, of a deep brown colour, and the gazelle of the plains, much paler and "not so nimble, nor so handsome as the first" (the idmi and the rheem are easily recognizable from these descriptions). Two years later Pallas (1766) gave the name Antilope gazella to Buffon's "gazelle", and Neumann (1906) restricted the name, probably correctly in the main (although it was actually somewhat of a composite), to the Palestine mountain gazelle, nowadays generally called Gazella gazella gazella.

Lichtenstein (1827) gave the name Antilope arabica to some gazelles collected by Hemprich & Ehrenberg: a male from the Farasan Islands and a female and young from Sinai. Brooke (1873) used this name (in the combination Gazella arabica) for South Arabian gazelles, and Neumann (1906) restricted the name to the Farasan male; from that date it was customarily used, in the form Gazella arabica or Gazella gazella arabica, for the common gazelle (idmi) of the Arabian peninsula,
until Groves (1983) re-examined the specimen concerned and showed that it was unlike any other specimen known from that region.

Smith (in Cuvier, 1827) described a new gazelle, *Antilope cora*, based on a pair formerly living in the Tower of London menagerie, "said to have been brought from India, or more properly from the Persian Gulph" (vol. 4), or more definitively from "the shores of the Persian Gulf, eastern Arabia" (vol. 5). Groves (1983) argued that this should be regarded as the earliest name for the idmi of Arabia, which would therefore be known as *Gazella gazella cora*.

Brooke (1873) recognized two species in Arabia: *Gazella dorcas* in the north and *Gazella arabica* in the south. By "North Arabia", however, he meant Sinai, which he called Arabia Petraea; and as far as one can deduce his South Arabian specimens appear to have been restricted to the Farasan specimen in Berlin, and a skull from Mocha in Yemen (now referred to *G. bilkis*), which was the only Arabian peninsular specimen registered in the Natural History Museum, London, by that date. A year later (Brooke, 1874) he added *Gazella muscatensis*, from the Batinah Coast of Oman, to the list; this was based on a pair living in the London Zoo, and his comparative sample of *G. arabica* appears to have been the same as in his earlier paper: this should be borne in mind when reading, for example, his contrasting of the lyrate horns of his new species with the straight horns of *arabica*.

Thomas (1897) described the Arabian sand gazelle, or rheem, as *Gazella marica*. Although Ellerman & Morrison-Scott (1951) associated this with the Saharan *G. leptoceros*, it was later shown (Groves & Harrison, 1967) that its true affinities are with the Central and Western Asian *G. subgutturosa*.

In 1905, Neumann clarified the status of Pallas's *gazella*, as noted above, and observed that the Farasan and Sinai specimens which formed the basis of Lichtenstein's *arabica* were not in fact of the same taxon. Restricting the name *arabica* to Farasan, he described the Sinai specimens as *Gazella arabica rueppelli* (later shown to be synonymous with *G. dorcas isabella* by Groves, 1983), and described a further new subspecies, *G. arabica erlangeri*, from Aden (based on living specimens in the London Zoo).

It was not until well into the present century that the Arabian peninsular *afri* was described, under the name *Gazella gazella saudiya*, by Carruthers & Schwarz (1935). It was briefly raised to specific rank by Morrison-Scott (1939), then assigned to the African *Gazella dorcas* as an Arabian subspecies by Ellerman & Morrison-Scott (1951).

It was Ellerman and Morrison-Scott (1951) who first brought some semblance of order into the by now rather complicated taxonomy of Arabian gazelles, recognizing three species in the Arabian peninsula: *G. dorcas saudiya* Carruthers and Schwarz, *G. gazella arabica* Hemprich and Ehrenberg (recte Lichtenstein), and *G. leptoceros marica* Thomas. Groves and Harrison (1967) followed this scheme, at least in outline; but they referred the taxon *marica* to the Central Asian *G. subgutturosa* instead of to the Saharan *G. leptoceros*, and revived the name *muscatensis* for the subspecies of *G. gazella* living along the Batinah coast of Oman. Groves (1969) added the Indo-Iranian *bennetti* (and its subspecies) to *G. dorcas*, noting its resemblance to *saudiya*: this was perhaps the ultimate in taxonomic oversimplification applied to the genus.

Since that time, the picture has once more become complicated. Groves (1983) found that the type of *Antilope arabica* Hemprich and Ehrenberg, from the Farasan Islands, is quite unlike the form of *G. gazella* which is widespread in the Arabian peninsula, which therefore takes the next available name, *cora* Smith. The gazelle from the Yemen highlands, placed with some misgivings in
G. gazella as a possible undescribed subspecies by Groves and Harrison (1967), was described as a new species, G. bilkis, by Groves and Lay (1985). Groves (1985, 1988) re-established G. bennetti as a separate species; he expressed more and more doubt whether the taxon saudiyaw could really be included in G. dorcas, and Rebholz et al. (1991) confirmed that its karyotype is indeed totally distinct. Thouless and Al Bassri (1991) examined recently taken specimens from the Farasan archipelago, and could not find anything resembling the type of arabica; they described the present-day Farasan population as a new subspecies, and thereby left a big question-mark over the whole arabica problem. Finally Groves, Thouless and Vassar (in press) recognized yet another subspecies of G. gazella on the mainland, for which they revived Neumann’s name erlangeri.

Table 2.1 Putatively recognized gazelle taxa in the Arabian peninsula.

<table>
<thead>
<tr>
<th>Species</th>
<th>Arabian subspecies</th>
</tr>
</thead>
<tbody>
<tr>
<td>G. dorcas Linnaeus</td>
<td>isabella Gray</td>
</tr>
<tr>
<td>G. saudiyaw Carruthers and Schwarz</td>
<td>gazella Pallas</td>
</tr>
<tr>
<td>G. gazella Pallas</td>
<td>cora Smith</td>
</tr>
<tr>
<td></td>
<td>erlangeri Neumann</td>
</tr>
<tr>
<td>G. bilkis Groves and Lay</td>
<td>farasani Thouless and Al Bassri</td>
</tr>
<tr>
<td>G. arabica Hemprich and Ehrenberg</td>
<td>muscatensis Brooke</td>
</tr>
<tr>
<td>G. subgutturosa Güildenstäd</td>
<td>marica Thomas</td>
</tr>
</tbody>
</table>

The result of all this is that the putatively recognizable taxa in Arabia are as given in Table 2.1. In this listing, G. dorcas isabella, G. gazella gazella, G. g. muscatensis and G. bilkis are not confirmed for Saudi Arabia; all the others - six in all, if the enigmatic G. arabica is counted - are known to exist, or have existed until recently, within the borders of the Kingdom.

This paper will examine the interrelationships among these taxa, and outline their differences and recognition features.

The meaning of taxonomic statements

Before reviewing the taxonomy of Arabian gazelles, it is necessary to be explicit about the nature of taxonomic statements: what exactly are species, subspecies, and taxa in general?

Most practising taxonomists, working with what until recently was the only material available for taxonomic study, and is still the most accessible (namely, museum skins and skulls), "know" what species and subspecies are. The working definitions were put succinctly by Deraniyagala (1955):

- A species is a community of similar individuals in which each is distinguishable from another of any other community.
- A subspecies is one of several populations within a species which differ from one another as a whole but possess types of individuals that are common to some or all of these populations.
Figure 2.1c

Figure 2.1 Arabian gazelles formerly in Chester Zoo, U.K. (Adult males): a, b) Gazella gazella cora, from Manwakh, Hadhramaut; c) Gazella bilkis, from Yemen. Photos: Ken Green.

As a general rule, these characterizations have served as implicit guidelines for museum taxonomists since at least the middle of the century, and probably before (see, for example, Miller, 1934, who classes numerous taxa of colobid monkeys as distinct species, however slight their differences, because "among the 72 specimens... I have found no one that is intermediate or of doubtful status..."). Deraniyagala's description of a species leaves little room for manoeuvre, but how much difference "as a whole" might mean in that of a subspecies is wide open. When it is made explicit, a taxonomist has usually proved to be working with the "Coefficient of Difference" of Mayr et al. (1953): when two samples are compared for a given quantitative character, this is the difference between the means divided by the sum of the standard deviations, and a C.D. of >1.27 (joint non-overlap of 90%) is commonly used as rule-of-thumb to indicate subspecies difference.

Historically, the most generally used definition of a species is that of Ernst Mayr (see, for example, Mayr et al., 1953):

A species is a group of actually or potentially interbreeding natural populations which are reproductively isolated from other such groups.

This is commonly known as the Biological Species Concept (BSC for short). The link with the museum taxonomist's working definition (above), though rarely made explicit, is as follows: reproductive isolation equals genetic discontinuity which in its turn implies absolute morphological separability.
Dissatisfaction with the BSC over the past ten years or so has taken various forms. Most are endoheresies (objections from within), and have to do with the meaning and maintenance of reproductive isolation, or the need to fit nonsexually reproducing organisms into it; but we have now to reckon with an exoheresy, the Phylogenetic Species Concept, which maintains that what species are "about" is not reproductive isolation at all, but something quite different (see below). As Vane-Wright (1992) and Endler (1989) note, species are both the basis for cataloguing the living world and an attempt to describe evolutionary relationships. While "...a lack of certainty should be accepted as inherent to the subject" (Vane-Wright, 1992), especially considering that we are dealing with a dynamic, evolving system not an all-or-nothing static one, there is a practical consideration: species are required by conservation workers, who need the concept to calculate species richness, analyze centres of endemism, communicate to the public about "endangered species" and convince legislators of the need for their protection, and plan protected areas to cover the maximum species diversity (Rojas, 1992). How may all these different interests and concerns best be served?

**Biological Species Concepts**

Paterson in particular has objected to defining a species in terms of its external relationships, which as he has argued are a by-product of its species status, not its essence. For him a species is "that most inclusive population of biparental organisms which share a common fertilization system" (Paterson, 1986); this is the Recognition Concept of species. Lack of interbreeding is not part of this definition. The logical domain of this concept, as Templeton (1989) argues, is as unclear as is that of the traditional BSC: not only are nonsexual organisms excluded, but population subdivision (by geographic barriers, for example) and isolation by distance immediately bring their whole basis into question. He proposes instead the Cohesion Concept: the species is "the most inclusive population of individuals having the potential for phenotypic cohesion through intrinsic cohesion mechanisms", these being either genetic (interbreeding and so on) or demographic (evolutionary or ecological). Endler (1989) points out, however, that Templeton's new concept is just as hard to make operational as is Paterson's. This drawback to both these new concepts, even though they do manage to a degree to improve on the old BSC, suggests that for sexually reproducing species at least we should return to Reproductive Isolation as a purely practical measure, even though we must continue to enquire into biological mechanisms.

What, then, does Reproductive Isolation of a species imply? Does it mean that the entity under consideration cannot, under any circumstances, interbreed with any other such entity? (Or, if it does, would the resulting hybrids necessarily be sterile?). Or does it mean that it normally does not but may be persuaded to do so under altered circumstances? Or is a certain - even, a considerable - amount of interbreeding permissible, as long as gene-flow from one species to another does not occur? These problems are reviewed by Groves (1989), who notes that in a dynamic, evolving biosphere all stages in the development of reproductive isolation should be expected, and the taxonomist must simply make the strategic decision most appropriate to the occasion.

Endler (1989) and Templeton (1991) suggest that the botanical concept of Sygameon ("the most inclusive unit of interbreeding in a hybridizing species group"), may be relevant to the species concept in mammals. A good example, in the context of this volume, would be that of *Antilope cervicapra* and *Gazella* spp.: all capable of interbreeding, they would form a syngameon, and within it there are subunits which do not form a natural continuum, some at least of which would be species.
Van Valen (1988), indeed, would see species as "fuzzy sets" - sets (as in mathematics) in which for each potential member there is a number which expresses the degree to which it is a member of that set. This is the logical opposite to the essentialist "species as individuals" proposition (Ghiselin, 1974), and hardly more helpful in systematic practice!

**Phylogenetic Species Concepts**

Nixon & Wheeler (1990) point out that museum taxonomists can observe only pattern, not process: and this of course applies to molecular systematists as well, and even to field biologists in the main (in order to prove that two species do not interbreed, one must see them not interbreeding, which is rather hard to do, though I suppose in principle not impossible). Why not, then, make species definitions depend on observable pattern, and not on this or that hypothesis of how species come to be or are maintained?

The fullest explanation of the Phylogenetic Species Concept (PSC) is that by Cracraft (1989). It emphasizes differentiation; some of this differentiation results in reproductive isolation, some does not. Put simply, populations to qualify as species should be 100% diagnosable - although Cracraft qualifies this by saying that the diagnostic characters may actually be expressed only by one sex or one ontogenetic stage, or indeed they may be obscured by individual variation. The diagnostic character or characters can be morphological, behavioural, chemical - anything, provided a genetic basis can be plausibly inferred; a species is "the smallest exclusive monophyletic group" (Baum, 1992).

It goes without saying that, under the PSC, species should be monophyletic. This is not a requirement of the BSC: cases are known where well-differentiated subspecies have gone on interbreeding (and so, under the BSC, remained conspecific), while a more recently differentiated form has apparently achieved genetic isolation; some of these cases are discussed by Groves (1989).

How the PSC works in practice has recently been exemplified by Cracraft (1992) in his revision of the birds-of-paradise. Some commonly recognized subspecies of these birds are "diagnosably different", so are ranked by Cracraft as full species; others represent mere subdivisions of clines, so are suppressed. The result is that the 40-43 species of earlier revisions become 90 ... and there are no subspecies! The informal category "species group" is used to delimit monophyletic clusters of species within a genus.

Not all PSC supporters necessarily abhor subspecies, as we will see below. All of them, however, would agree to recognize all discretely diagnosable entities as species. Does this sound familiar? It is a return to the museum taxonomist's working definition (e.g. Deraniyagala, 1955; Miller, 1934) above!

**Subspecies and the phenotypic plasticity question**

There is no doubt but that the phylogenetic taxonomists are right: the subspecies has been all things to all people in the past. As Cracraft (1992) remarks, "degrees of morphological difference among allopatric populations lead the investigator to speculate about the degree of reproductive isolation that might obtain if or when these populations might ever come into contact". In other words, we cannot base a formal taxonomic scheme on mere speculation - let us treat those that are diagnosably different (i.e. discrete) as species, and reject the rest.
Nixon & Wheeler (1990) are not so dismissive. While agreeing that the diagnosable entities are species, it is still worth recognizing groups that are "centric, not monothetic" with subspecific names.

The problem with subspecies has always been that there has been a tendency to reify them, as if they were simply "minor species", with only one or two diagnostic features rather than ten or twenty. They may indeed be population groups in the process of generating the kind of variation that will eventually lead to speciation (Groves, 1989), but if anything they represent the point at which such variation has reached a high enough frequency to attract attention, and do not by any means exhaust the spectrum of intraspecific geographic variation.

This last point is important in present-day conservation contexts, as was forcefully pointed out more than ten years ago by Greig (1979). A case cited by him has since achieved some notoriety: a population of Capra ibex successfully translocated to the Tatra Mountains was augmented by well-meaning persons with C. aegagrus from Turkey and C. nubiana from Sinai, causing the whole hybridized complex to rut earlier, so giving birth in winter, leading to unacceptable infant mortality and eventual extinction. The three species of Capra in this case history have at times been treated as subspecies, so the case may be relevant here; but in any case this well-known example has tended to overshadow other cases where some ill-conceived translocation at, or even below, subspecific level had similar unfortunate consequences. Greig (1979) cites the translocation of bighorn sheep, Ovis canadensis, from Jasper National Park to Oklahoma, where the species - possibly in a separate subspecies, possibly not - formerly existed; it failed. The addition of red deer, Cervus elaphus elaphus, from Germany to a Norwegian population caused the entire indigenous stock to die out. The lesson which he draws from this is that subspecific traits at a morphological level may be in effect the outwardly visible markers of physiological differences; we may go further, and claim that physiological differences may tend to characterize populations not even morphologically separable. This simply reminds us that, ultimately, what we aim to preserve (where we still have the option) is not just species or even subspecies, but gene-pools.

The question which this immediately raises, of course, is: are genes inevitably involved, even where visible differences appear to exist? Or can the appearance of two different taxa be generated by environmental differences alone?

In two groups of artiodactyls, it is well known that there certainly is a remarkable degree of phenotypic plasticity: these are deer and pigs. Hammond (1965) documents the remarkable degree to which domestic pigs may be stunted by undernutrition yet retain their general health and fertility. Huxley (1931) records the evidence for such plasticity in red deer: deer Cervus elaphus elaphus, of largely British origin, with a little German admixture, when translocated to optimal-quality habitat in New Zealand grew to sizes "hardly inferior to good Carpathian stags" Cervus elaphus maral; and in localities where environmental quality deteriorated, the size declined again. Specifically, the mean body weight of Scottish stags of the heaviest weight class (Huxley, 1931, Table III) is 128.7 kg, and of English (slightly mixed) stags is 169.0 kg, while that of the largest weight-class Carpathian stags is 230.7 kg; the New Zealand stags would be over 200 kg (one estimated weight of 250 kg is noted). The size of the antlers varies allometrically with body size (Huxley, 1931). Let it be noted, however, that other characters of antlers, and pelage colour, do not approach C. e. maral, and the differences in colour pattern, pelage disposition, antler type and gross body size between red deer and wapiti C. e.
canadensis, likewise introduced to New Zealand (and sometimes hybridizing with red deer), remain fixed. That is to say, environmental plasticity has its limits.

Van Bemmel (1949) described the rusa deer Cervus timorensis of Peucang Island, a small island 500 metres off the coast of the Ujung Kulon peninsula, West Java, as a subspecies (laronesiotes) different from that on the mainland (russa). The difference resided entirely in the smaller size: condylobasal length of two adult males 282-290 mm, compared to a range of 312-328 mm on the mainland. Hoogerwerf (1970) pointed out that wildlife and much (if not all) of the vegetation of Peucang were almost certainly eliminated by a tidal wave following the colossal eruption of the volcano Krakatao in 1883; thus the deer population must have originated since then, by swimming across from the opposite mainland, and have either become very rapidly genetically dwarfed or, more likely given the New Zealand data, be phenotypically stunted (despite being a healthy, self-perpetuating population). Only breeding experiments can resolve this question. I may note that in 1978 I picked up a wild pig Sus scrofa vittatus skull on Peucang, fully mature and perfectly normal but in size way below the range for those from the mainland of Java (Grovès, 1981a). Patton & Smith (1989) find much the same phenomenon in pocket gophers Thomomys bottae: environmental quality in this species affects size, but not shape parameters.

Developmental plasticity is likely, therefore, to be a very real phenomenon in some groups of ungulates and some other mammals, but its known effects are limited to size and correlated features (such as horn size). This reinforces the commonly-held notion that taxa described on the basis of size alone must always be regarded with some suspicion; on the other hand, since conservation of gene pools is in question, the null hypothesis should be that a described difference - even one of size - is genetically based until proven otherwise. There is clearly a need for breeding experiments along these lines: stocks of a given species from one region would be reared alongside stocks from a different region showing slight phenotypic differences. The identical conditions of rearing would allow determination of what genotypic differences actually do exist.

Material and methods

For taxonomic studies of gazelles going back to Groves (1969), I have studied specimens in museums all over the world, the most important collection being that held at the Natural History Museum, London - formerly the British Museum (Natural History). During my 1992 visit to the Arabian peninsula for the symposium on which this volume is based, I measured skulls of gazelles at the King Khalid Wildlife Research Center, Thumamah, Saudi Arabia, and at the Al-Areen Wildlife Park, Bahrain. I am most grateful to Dr Doug Williamson and Dr Jaime Samour, respectively, for these facilities.

Skin characters were noted (use of colour standards was abandoned as unexpectedly subjective), and skull measurements and observations were made as detailed in Groves (1969). The means, standard deviations and sample sizes of skull and horn measurements are given in Tables 2.2, 2.3 and 2.4.

A series of multivariate analyses, using SPSS Discriminant, was run on different subsets of these measurements. The graphs of first and second Discriminant Functions are shown in Figures 2.3 and 2.5, as follows; Figure 2.3 (a) G. gazella group, male cranial variables (variables 1 and 4-13) and (b) female cranial variables (same list), and (c) male horn variables (nos. 1-4); Figure 2.5, G. saudiya and bennetti, female (a) cranial and (b) horn variables (list numbers as above).
In order to test the PSC (Phylogenetic Species Concept) status of the taxa concerned, 27 skull and horn characters were coded and analyzed cladistically using Hennig86, version 1.5, then examined in detail with branch-swapping using MacClade. At the suggestion of Wilhelmus Rebholz (pers. comm.), G. d. pelzelni and other African subspecies of G. dorcas were included in the analysis. The characters used, their codes, and the data matrix are given in Table 2.5. The trees generated by this analysis are shown in Figure 2.6.

Results

- Pelage: Gazella bilkis is the darkest of the Arabian gazelles overall; G. g. gazella, erlangeri and muscatensis are probably equally dark on the dorsum, but are lighter on the face (so that the dark face stripes are conspicuous, which they are not in G. bilkis), and become suddenly lighter on the haunches. The white of the underside extends down the hindleg only to the hock in most specimens of G. gazella, but to the pasterns in G. bilkis. In G. bilkis there is a thin red stripe below the dark flank stripe; this does not occur in specimens of G. gazella as far as my experience goes.

G. g. cora is much lighter than other subspecies of this group; the haunch transition occurs, but is inconspicuous because of the much lighter overall body tone. It varies considerably in colour, from pale sandy to medium reddish fawn; the darker specimens have a well-marked but thin black flank-stripe, with a zone paler than the body colour just above it, the paler ones lack the light stripe and have the merest trace of a dark one. The forehead and midface are darker fawn to dark chestnut; a smudgy black nose-spot occurs in 11 out of 20 skins in the London collection, and 8 skins have a sprinkling of white hairs on the forehead.

Other members of the G. gazella group are darker coloured; dark fawn in G. g. gazella, and a very dark grey-brown, sometimes with a silvery sheen, in erlangeri and muscatensis, and by virtue of the dark hue the transition on the haunch to the fawn tone of the leg is more marked. The black flank-stripe is conspicuous, as is the lighter zone above it; there is a dark pygal band, of which barely a trace exists in cora. The face stripes are more clearly expressed than is usual in cora; the midface and forehead are dark brown in gazella, dark chestnut in the other two, and there is always a well-defined black nose-spot.

G. dorcas is coloured like G. g. cora, but the facial markings are clearer and sharper. The Saharan subspecies are often a very pale, sandy colour, but G. d. isabella, which is found along the Red Sea coast from Eritrea to the Negev, on the borders of Saudi Arabia, is darker and more reddish and commonly has a nose-spot; many skins of G. d. isabella could be mistaken for G. g. cora.

G. saudiya averages lighter, more sandy brown, than G. dorcas; there is scarcely any trace of a flank stripe, and the face stripes are not sharply differentiated. The white face stripes and the white of the underside are suffused with fawn tones.

The type (and only known) skin of G. arabica is medium to dark red-brown, comparable to darker specimens of G. g. cora; Neumann (1906) seems to have overdone the "strong red" part of his description, unless the specimen has lost this tone in the meantime. There is a dark grey flank band with a trace of a red-brown stripe beneath it, and the white goes down the inside of the hindleg to the pasterns; in these features it resembles G. bilkis but it is by no means as dark or as uniform; most importantly, it has a striking transition between dark dorsal and light limb tones on the haunch.
All subspecies of *G. subgutturosa* are characterized by yellowish body tones without strong markings, and by the invasion of the midfacial region by white with maturity. *G. s. marica* is very pale in colour; *G. subgutturosa* specimens from Iraq, which are as small as *G. s. marica*, are however the same darker, yellow-brown colour as Iranian *G. s. subgutturosa*. It remains to be determined whether the Iraqi populations form a stable race, or are simply intergrades between peninsular and Iranian subspecies.

- **Horns:** Horn shape in the male differs characteristically between taxa. Horns of *G. subgutturosa* and *G. dorcas* bow outward, then turn in (and forward) at the tips; *G. g. cora* and *muscatensis* show the same form to a lesser degree (in Table 2.2, note that the span in the male in *cora* is greater than in *gazella*, but the tip-to-tip distance is less). *G. g. gazella* and *erlangeri*, *G. saudiya*, *G. bilkis* and *G. arabica* males have horns that are straighter, little if at all bowed outward: indeed, those of the type of *G. arabica* are slightly turned out at the tips, and those of *G. bilkis*, shorter than in *G. g. gazella*, are nearly parallel. In the females of *G. g. gazella* and *cora*, the horns tend to be rather short and fragile, easily broken; they are longer in *G. g. erlangeri* and *muscatensis*, and even more so in *G. bilkis*.

### Table 2.2 Skull/horn measurements of taxa of the *G. gazella* group.

<table>
<thead>
<tr>
<th>Variable</th>
<th>gazella</th>
<th>cora</th>
<th>erlangeri</th>
<th>bilkis</th>
<th>Thumamah</th>
</tr>
</thead>
<tbody>
<tr>
<td>Horn length, straight</td>
<td>243.5</td>
<td>219.3</td>
<td>215.0</td>
<td>229.0</td>
<td>254.9</td>
</tr>
<tr>
<td>s.d.</td>
<td>16.23</td>
<td>18.57</td>
<td>18.98</td>
<td>-</td>
<td>18.01</td>
</tr>
<tr>
<td>Tip-to-tip (ditto)</td>
<td>91.0</td>
<td>87.7</td>
<td>102.0</td>
<td>69.0</td>
<td>97.7</td>
</tr>
<tr>
<td>s.d.</td>
<td>20.06</td>
<td>19.95</td>
<td>16.12</td>
<td>-</td>
<td>15.18</td>
</tr>
<tr>
<td>Greatest span across horns (ditto)</td>
<td>120.5</td>
<td>134.4</td>
<td>119.0</td>
<td>94.5</td>
<td>108.4</td>
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<tr>
<td>s.d.</td>
<td>12.81</td>
<td>12.80</td>
<td>16.11</td>
<td>-</td>
<td>14.40</td>
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<tr>
<td>Greatest width across bases of horn</td>
<td>67.2</td>
<td>65.0</td>
<td>60.5</td>
<td>66.5</td>
<td>65.0</td>
</tr>
<tr>
<td>s.d.</td>
<td>2.66</td>
<td>2.11</td>
<td>3.87</td>
<td>-</td>
<td>2.16</td>
</tr>
<tr>
<td>Width of nasal bones (anterior)</td>
<td>24.3</td>
<td>20.3</td>
<td>22.3</td>
<td>24.0</td>
<td>21.7</td>
</tr>
<tr>
<td>s.d.</td>
<td>1.40</td>
<td>1.80</td>
<td>1.26</td>
<td>-</td>
<td>1.11</td>
</tr>
<tr>
<td>Width of nasal bones (posterior)</td>
<td>27.7</td>
<td>22.5</td>
<td>24.0</td>
<td>26.0</td>
<td>23.7</td>
</tr>
<tr>
<td>s.d.</td>
<td>2.01</td>
<td>1.85</td>
<td>2.83</td>
<td>-</td>
<td>1.80</td>
</tr>
<tr>
<td>Greatest length of nasal bones</td>
<td>47.0</td>
<td>46.5</td>
<td>42.5</td>
<td>41.0</td>
<td>46.3</td>
</tr>
<tr>
<td>s.d.</td>
<td>4.65</td>
<td>5.15</td>
<td>8.88</td>
<td>-</td>
<td>3.99</td>
</tr>
<tr>
<td>Greatest skull length</td>
<td>191.1</td>
<td>184.5</td>
<td>178.5</td>
<td>191.0</td>
<td>190.3</td>
</tr>
<tr>
<td>s.d.</td>
<td>5.02</td>
<td>5.99</td>
<td>3.70</td>
<td>-</td>
<td>2.69</td>
</tr>
<tr>
<td>Greatest skull breadth (biorbital)</td>
<td>89.9</td>
<td>81.6</td>
<td>81.3</td>
<td>87.0</td>
<td>84.9</td>
</tr>
<tr>
<td>s.d.</td>
<td>2.53</td>
<td>2.28</td>
<td>4.92</td>
<td>-</td>
<td>3.13</td>
</tr>
<tr>
<td>Preorbital skull length</td>
<td>96.6</td>
<td>95.0</td>
<td>88.0</td>
<td>98.0</td>
<td>96.3</td>
</tr>
<tr>
<td>s.d.</td>
<td>2.45</td>
<td>3.97</td>
<td>4.08</td>
<td>-</td>
<td>2.29</td>
</tr>
<tr>
<td>Palate width (outside molars)</td>
<td>53.2</td>
<td>45.6</td>
<td>47.5</td>
<td>52.5</td>
<td>52.1</td>
</tr>
<tr>
<td>s.d.</td>
<td>2.21</td>
<td>2.14</td>
<td>2.65</td>
<td>-</td>
<td>1.86</td>
</tr>
<tr>
<td>Braincase width</td>
<td>61.2</td>
<td>60.1</td>
<td>56.8</td>
<td>63.5</td>
<td>56.9</td>
</tr>
<tr>
<td>s.d.</td>
<td>2.42</td>
<td>2.34</td>
<td>4.11</td>
<td>-</td>
<td>1.21</td>
</tr>
<tr>
<td>Braincase length (nasion to inion)</td>
<td>111.5</td>
<td>104.3</td>
<td>99.3</td>
<td>110.0</td>
<td>108.4</td>
</tr>
<tr>
<td>s.d.</td>
<td>4.21</td>
<td>4.55</td>
<td>4.57</td>
<td>-</td>
<td>3.41</td>
</tr>
</tbody>
</table>
In the skulls from the Thumamah breeding stock, the horns of the males are on average longer than in any other sample of the G. gazella group, and more nearly parallel than any but G. bilkis. The horns of females are shorter than in G. bilkis but longer than in G. gazella except for erlangeri.

The distance across the horn bases is broad in G. g. gazella, G. g. cora and G. bilkis (Table 2.2).

G. dorcas isabella has bowed horns remarkably similar to those of G. g. cora, but longer in the female. The near identity in horn shape recalls the great external similarity in general (Figure 2.1). In contrast, the horns of G. saudiya are very long and straight in both sexes, with very little inturning at the tips; they are not very divergent, resembling in this respect the horns of most subspecies of G. bennetti (Table 2.4), but are narrower across the bases.

The horns are closely ringed in the male, with more than 20 rings, in G. subgutturosa and G. saudiya; in the latter the rings are more prominent than in most Arabian gazelles. The rings are much fewer in number, 12-15, in G. g. muscatensis, G. bilkis and G. arabica, with about 15-20 in the other forms.

Horn shapes in Arabian gazelles are well illustrated in Morrison-Scott (1939, Plate VI); the specimens figured could hardly have been better selected to illustrate the manner in which the range of variation within a taxon, considerable though it may be, does not obliterate the differences between taxa. In this plate are figured three male and one female G. saudiya (Figures 1-3 and 10, respectively); one adult and one subadult male G. s. marica (Figures 14 and 15 respectively); seven male and one female G. g. cora (Figures 4-9 and 13, and 11 respectively, all captioned "G. arabica");
Figure 2.2 Naso-frontal suture shapes of a) *Gazella dorcas dorcas* (BM 1939.2560, from Air, Niger); b) *Gazella gazella cora* (BM 40.289, from Dhalm, Saudi Arabia).
two adult male and one adult female *G. g. muscatensis* (Figures 16-17 and 12 respectively); one *G. g. erlangeri* (Figure 18) and one *G. bilkis* (Figure 19). For comparison, two male and two female *G. d. isabellae* are figured by Ferguson (1981, Figure 1, though some are incorrectly identified as *G. d. dorcas* or inter-subspecific hybrids).

- **Horn Cores:** The horn cores in males are longitudinally grooved. In *G. dorcas* the 3-4 grooves on the anterior face are short (restricted to the proximal end) and shallow, their edges bevelled; on the posterior face there are one or two deeper, sharp-edged grooves which run for most of the length of the core. In *G. gazella* the anterior grooves are somewhat deeper and broader. In *G. subgutturosa* the anterior grooves are longer, and there is a deep, more sharp-edged groove on the antero-lateral corner; there are two exceedingly deep, sharp-edged grooves on the posterior surface. It was not possible to take off the sheaths of any other species to examine the grooves.

The cores in male *G. subgutturosa* are close together (Figure 2.6). They are also very stout basally, so that their medial edges are even closer together. Other species have more widely spaced horns: width across the bases is relatively greater in *G. gazella* and its relatives than in *G. dorcas* and *G. saudiya* (Figure 2.6).

- **Skull:** Table 2.2 records skull measurements (means and standard deviations) in the *G. gazella* group - *muscatensis* excepted, because despite a fair sample of this taxon most specimens are incomplete, only a single adult male and female skull being available.

*G. g. cora* differs from *G. g. gazella* in both sexes in that the nasals are much narrower, especially posteriorly, and the skull is shorter, primarily due to the shorter braincase, and narrower; the palate is much narrower.

*G. g. erlangeri* in the male differs from *gazella* in that the nasals are slightly narrower and much shorter, and the skull is shorter (both pre- and postorbitally) and narrower. Compared to *cora*, the nasals are slightly broader, much shorter; the skull is shorter but no narrower, the palate being actually broader in the male.

In *G. bilkis*, compared to *G. g. gazella*, the nasals are slightly less broadened posteriorly, and much shorter; the female, but not the male, is larger. Compared to *cora* the nasals are broader and much shorter, and the skull is much longer (especially postorbitally), and broader. Compared to *erlangeri* the nasals are slightly broader, and the skull is much longer and broader.

Male skulls of the Thumamah "idmi" stock are narrower than *G. g. gazella*, with much narrower nasals, and a slightly shorter, considerably narrower braincase (Table 2.2). The female skulls are slightly shorter than *G. g. gazella*, and have somewhat longer, narrower nasals. They have a broad palate and narrow braincase compared to *cora*, and the nasals are narrower in the female, especially anteriorly. The nasals are much longer and narrower than in *G. bilkis*, and the skull, especially the braincase, is rather narrower.
Figure 2.3a

Figure 2.3b
Figure 2.3c

Figure 2.3 Discriminant Function analysis of skull and horn measurements of the *G. gazella* group. In all comparisons, abscissa is Function 1, ordinate is Function 2. a) Skull and b) horn measurements of males; c) skull measurements of females. 1 = *gazella*, 2 = *cora*, 3 = *erlangeri*, 4 = *bilkis*, 5 = *idmi* from KKWRC, Thumamah.

Measurements of *G. dorcas isabella*, a species that may occur within the Kingdom (see below), are given in Table 2.3. The skull is strikingly similar metrically to that of *G. gazella cora*.

Table 2.3 Skull/horn measurements of *G. dorcas isabella*.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Male</th>
<th>Female</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mean</td>
<td>s.d.</td>
</tr>
<tr>
<td>Horn length, straight</td>
<td>218.1</td>
<td>16.61</td>
</tr>
<tr>
<td>Tip-to-tip (ditto)</td>
<td>84.2</td>
<td>25.43</td>
</tr>
<tr>
<td>Greatest span across horns (ditto)</td>
<td>138.2</td>
<td>19.11</td>
</tr>
<tr>
<td>Greatest width across bases of horn</td>
<td>61.5</td>
<td>2.30</td>
</tr>
<tr>
<td>Width of nasal bones (anterior)</td>
<td>20.1</td>
<td>1.69</td>
</tr>
<tr>
<td>Width of nasal bones (posterior)</td>
<td>20.4</td>
<td>2.34</td>
</tr>
<tr>
<td>Greatest length of nasal bones</td>
<td>45.2</td>
<td>3.46</td>
</tr>
<tr>
<td>Greatest skull length</td>
<td>179.7</td>
<td>4.41</td>
</tr>
<tr>
<td>Greatest skull breadth (biorbital)</td>
<td>80.5</td>
<td>2.53</td>
</tr>
<tr>
<td>Preorbital skull length</td>
<td>90.3</td>
<td>2.77</td>
</tr>
<tr>
<td>Palate width (outside molars)</td>
<td>45.9</td>
<td>1.18</td>
</tr>
<tr>
<td>Braincase width</td>
<td>58.5</td>
<td>2.05</td>
</tr>
<tr>
<td>Braincase length (nasion to inion)</td>
<td>100.7</td>
<td>3.53</td>
</tr>
</tbody>
</table>
G. saudiya is compared in Table 2.4 with two subspecies of G. bennetti, both newly described from Iran, including the very small sized G. b. karamii from the Bushehr district. The skull is narrower than in any G. bennetti, both biorbitally and across the palate but not across the braincase, and very narrow across the nasals which are always narrower posteriorly than anteriorly. Male and female skulls of G. saudiya are illustrated in Figure 2.4.

In non-metrical features, there are a few characteristic differences among members of the G. gazella / dorcas complex. Most consistent is the shape of the naso-frontal suture, which is arrow-shaped in G. dorcas but rounded-arch-shaped in G. gazella (Figure 2.2); this is one of the few features in which G. g. cora resembles other members of the G. gazella group rather than G. dorcas. In G. saudiya the shape is essentially as in G. dorcas; in G. bennetti it is similar but somewhat less markedly wedge- or arrow-shaped. Skull differences of G. bilkis from G. gazella (and G. dorcas) are described and figured by Groves & Lay (1985).

G. subgutturosa always has a large long-oval vacuity in the lacrimal bone, of unknown function. It is also consistently present in G. bennetti, G. saudiya and, unexpectedly, in G. bilkis (also in G. leptoceros and G. cuvieri). The occasional presence of a small vacuity in G. gazella is recorded.

Table 2.4 Skull/horn measurements of taxa of the G. bennetti group.

(1) MALES

<table>
<thead>
<tr>
<th>Variables</th>
<th>G. b. shikarii</th>
<th>G. b. karamii</th>
<th>G. saudiya</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>n=5</td>
<td>n=1</td>
<td>n=6/8</td>
</tr>
<tr>
<td>Horn length, straight s.d.</td>
<td>255.8</td>
<td>228</td>
<td>268.8</td>
</tr>
<tr>
<td>Tip-to-tip (ditto) s.d.</td>
<td>141.3</td>
<td>190</td>
<td>101.8</td>
</tr>
<tr>
<td>Greatest span across horns (ditto) s.d.</td>
<td>156.2</td>
<td>210</td>
<td>115.0</td>
</tr>
<tr>
<td>Greatest width across bases of horn s.d.</td>
<td>63.0</td>
<td>58</td>
<td>56.3</td>
</tr>
<tr>
<td>Width of nasal bones (anterior) s.d.</td>
<td>22.9</td>
<td>21</td>
<td>18.6</td>
</tr>
<tr>
<td>Width of nasal bones (posterior) s.d.</td>
<td>24.4</td>
<td>22</td>
<td>17.6</td>
</tr>
<tr>
<td>Greatest length of nasal bones s.d.</td>
<td>54.8</td>
<td>41</td>
<td>42.4</td>
</tr>
<tr>
<td>Greatest skull length s.d.</td>
<td>192.4</td>
<td>173</td>
<td>172.8</td>
</tr>
<tr>
<td>Greatest skull breadth (biorbital) s.d.</td>
<td>85.7</td>
<td>84</td>
<td>77.8</td>
</tr>
<tr>
<td>Preorbital skull length s.d.</td>
<td>97.0</td>
<td>-</td>
<td>86.5</td>
</tr>
<tr>
<td>Palate width (outside molars) s.d.</td>
<td>49.8</td>
<td>49</td>
<td>44.6</td>
</tr>
<tr>
<td>Braincase width s.d.</td>
<td>63.7</td>
<td>58</td>
<td>57.5</td>
</tr>
<tr>
<td>Braincase length (nasion to inion) s.d.</td>
<td>103.4</td>
<td>98</td>
<td>97.6</td>
</tr>
</tbody>
</table>

24
<table>
<thead>
<tr>
<th>Variable</th>
<th>G. bennetti (mixed) n=7(horns)/10(crania)</th>
<th>G. saudiya n=6</th>
<th>Bahrain n=1</th>
</tr>
</thead>
<tbody>
<tr>
<td>Horn length, straight s.d.</td>
<td>165.9</td>
<td>209.7</td>
<td>238</td>
</tr>
<tr>
<td>Tip-to-tip (ditto) s.d.</td>
<td>66.1</td>
<td>73.0</td>
<td>102</td>
</tr>
<tr>
<td>Greatest span across horns (ditto) s.d.</td>
<td>80.6</td>
<td>85.8</td>
<td>114</td>
</tr>
<tr>
<td>Greatest width across bases of horn s.d.</td>
<td>52.3</td>
<td>48.7</td>
<td>49</td>
</tr>
<tr>
<td>Width of nasal bones (anterior) s.d.</td>
<td>21.0</td>
<td>17.8</td>
<td>21</td>
</tr>
<tr>
<td>Width of nasal bones (posterior) s.d.</td>
<td>21.9</td>
<td>15.8</td>
<td>20.5</td>
</tr>
<tr>
<td>Greatest length of nasal bones s.d.</td>
<td>49.2</td>
<td>40.3</td>
<td>50</td>
</tr>
<tr>
<td>Greatest skull length s.d.</td>
<td>179.7</td>
<td>164.0</td>
<td>174</td>
</tr>
<tr>
<td>Greatest skull breadth (biorbital) s.d.</td>
<td>81.2</td>
<td>70.8</td>
<td>81</td>
</tr>
<tr>
<td>Preorbital skull length s.d.</td>
<td>92.6</td>
<td>85.2</td>
<td>88</td>
</tr>
<tr>
<td>Palate width (outside molars) s.d.</td>
<td>48.3</td>
<td>43.0</td>
<td>46</td>
</tr>
<tr>
<td>Braincase width s.d.</td>
<td>59.5</td>
<td>52.5</td>
<td>55</td>
</tr>
<tr>
<td>Braincase length (nasion to inion) s.d.</td>
<td>95.5</td>
<td>91.5</td>
<td>91</td>
</tr>
</tbody>
</table>

The premaxilla always ascends the margin of the nasal aperture to some degree, and may actually reach and suture with the nasal. It usually fails to meet the nasal in G. g. gazella, muscatensis and bilkis, and in the skull of arabica, but usually does meet the nasal in other taxa.

The anterior ends of the nasals are abruptly truncated in the genus Gazella (and in Antilope), and have lateral flanges. The median tips are recessed to or behind a line joining the tips of the lateral flanges in most Arabian taxa and some others, but not usually in G. g. gazella et erlangeri, and not in the type skull of G. arabica. This is perhaps connected with the puffy dorsal inflatability of the nasal cavity, which is so noteworthy in the north-east African G. spekei but can be detected in some other taxa as well.

The supraorbital foramina, generally sunk into triangular pits at the bases of the horns, are commonly multiple in G. subgutturosa, also in G. arabica and some non-Arabian species such as G. bennetti, but not, as far as the data go, in other Arabian taxa.

Canonical analyses of skull and horn measurements in Arabian gazelles were depicted in Groves (1989), and new analyses, designed to examine the affinities of the KKWRC "idmi" group and of the Al-Areen breeding group assigned to G. saudiya, are shown in Figures 2.3 and 2.5. Briefly, G. g. gazella and cora are well-distinguished, with erlangeri somewhat intermediate but (especially as far as the females are concerned) closer to cora; G. bilkis is close to G. g. gazella in the male, rather separate in the female; and the KKWRC specimens segregate independently, overlapping.
(in the males) with *erlangeri*. The reputed *saudiya* of Al-Areen does indeed assort with *G. saudiya*, not with *G. bennetti*.

The cladistic analysis generated a single most parsimonious tree, of length 124 and consistency index 41, but there proved to be trees of almost equal length when this was modified using MacClade (Figure 2.6). In the first of the cladograms generated by Hennig86 (Figure 2.6a), in some agreement with the descriptive observations above, a comb-like tree is produced, with *dorcas, osiris, isabella* and *pelzelni* branching successively off the main stem leading to the *G. gazella* group. In this tree, the similarities between *isabella* and *cora* are evidently to be interpreted as plesiomorphic. The Thumamah taxon branches off next; but this may be an artefact of its incomplete data set. The terminus of the branch is a bifurcation between *bilkis* and *arabica*. The initial split is between *bennetti* on the one hand, and the *subgutturosa / saudiya* and *gazella / dorcas* groups on the other.

![Figure 2.4 Skulls of Gazella saudiya (left) male, BM 40.303, from Wadi Markha and (right) female, BM 40.305, from Arq Abu Da’ir.](image)
In the two other equally parsimonious trees, the subspecies of *G. dorcas* except for *pelzelni* are on a single branch together, thus dissolving the peculiar *isabella / cora* affiliation; one (Figure 2.6b) retains the comb-like asymmetry of *pelzelni* plus the *gazella* group; the other (Figure 2.6c) places *gazella* and *muscatensis* in a branch of their own.

**Table 2.5** Data set for cladistic analysis of Arabian gazelles.

(a) **Character description**

<table>
<thead>
<tr>
<th>Character Description</th>
<th>States</th>
</tr>
</thead>
<tbody>
<tr>
<td>0 - nasofrontal suture:</td>
<td>0 - wedge, 1 - arch</td>
</tr>
<tr>
<td>1 - lacrimal fenestra:</td>
<td>0 - usually no, 1 - yes</td>
</tr>
<tr>
<td>2 - premaxilla:</td>
<td>0 - usually contacts nasal, 1 - usually not</td>
</tr>
<tr>
<td>3 - median nasal tip:</td>
<td>0 - longer than lateral flanges, 1 - shorter</td>
</tr>
<tr>
<td>4 - supraorbital foramen:</td>
<td>0 - single, 1 - multiple</td>
</tr>
<tr>
<td>5 - horn rings:</td>
<td>0 - less than 15, *1 - 16-20, 2 - more than 20</td>
</tr>
<tr>
<td>6 - female horn length:</td>
<td>0 - &gt;skull length, *1 - 85-100%, 2 - 70-85%, 3 - &lt;70%</td>
</tr>
<tr>
<td>7 - (male) horn span:</td>
<td>0 - &lt;50% of horn length, *1 - 50-60%, 2 - 60-70%, 3 - &gt;70%</td>
</tr>
<tr>
<td>8 - (male) horn tip-to-tip distance:</td>
<td>0 - &gt;85% of span, 1 - 65-85%, 2 - &lt;65%</td>
</tr>
<tr>
<td>9 - nasal length:</td>
<td>0 - &gt;27% of skull length, 1 - 22-27%, 2 - &lt;22%</td>
</tr>
<tr>
<td>10 - nasal width (posterior):</td>
<td>0 - &lt;45% of nasal length, *1 - 45-53%, 2 - 53-60%, 3 - &gt;60%</td>
</tr>
<tr>
<td>11 - anterior nasal width:</td>
<td>0 - &lt;90% of posterior width, 1 - 90-100%, 2 - &gt;posterior width</td>
</tr>
<tr>
<td>12 - preorbital length:</td>
<td>0 - &gt;98% as long as postorbital, 1 - 90-98%, 2 - &lt;90%</td>
</tr>
<tr>
<td>13 - braincase width:</td>
<td>0 - &gt;58% of braincase length, 1 - &lt;58%</td>
</tr>
<tr>
<td>14 - palate breadth:</td>
<td>0 - &lt;50% of preorbital length, 1 - 50-55%, 2 - &gt;55%</td>
</tr>
<tr>
<td>15 - horn ring prominence on anterior surface</td>
<td>0 - very prominent, 1 - prominent, well-spaced, 2 - closer together, 3 - poorly expressed, close together</td>
</tr>
<tr>
<td>16 - longitudinal ridges between horn rings</td>
<td>0 - none, 1 - barely visible, 2 - fairly well-marked</td>
</tr>
<tr>
<td>17 - anterior angulation of horn rings:</td>
<td>0 - absent (rings circular), 1 - slight</td>
</tr>
<tr>
<td>18 - posterior prominence of rings:</td>
<td>0 - just as prominent as on anterior surface, 1 - less so</td>
</tr>
<tr>
<td>19 - posterior angulation of rings:</td>
<td>0 - absent, 1 - slight, 2 - strongly expressed</td>
</tr>
<tr>
<td>20 - preorbital fossa:</td>
<td>0 - deep, 1 - less so, 2 - shallow</td>
</tr>
<tr>
<td>21 - lacrimal bone:</td>
<td>0 - not, or hardly, extending into preorbital fossa, 1 - extends into about one-quarter of fossa, 2 - about one-half</td>
</tr>
<tr>
<td>22 - ethmoid fissure:</td>
<td>0 - long, slit-like, 1 - broader, 2 - triangular or block-like</td>
</tr>
<tr>
<td>23 - ventral premaxillary ridges:</td>
<td>0 - strongly raised, crest-like, 1 - simple, ridge-like, 2 - very weak, not extending to level of premolars</td>
</tr>
<tr>
<td>24 - premaxillary tips:</td>
<td>0 - broad, shovel-like, 1 - rounded-pointed</td>
</tr>
<tr>
<td>25 - female skull length:</td>
<td>0 - &gt;97.5% of male, 1 - 95-97%, 2 - &lt;95%</td>
</tr>
<tr>
<td>26 - male horn length:</td>
<td>0 - &gt;140% of skull length, 1 - 130-140%, 2 - 125-130%, 3 - &lt;125%</td>
</tr>
</tbody>
</table>

* indicates primitive state; otherwise, 0 is primitive.
(b) Character state matrix

<table>
<thead>
<tr>
<th>Species</th>
<th>State Matrix</th>
</tr>
</thead>
<tbody>
<tr>
<td>*rufifrons</td>
<td>000001111001000001100000000</td>
</tr>
<tr>
<td>subgutturosa</td>
<td>01011203201210111010121013</td>
</tr>
<tr>
<td>bennetti</td>
<td>01001120002101100021120102</td>
</tr>
<tr>
<td>saudiya</td>
<td>01010200010320110002112713</td>
</tr>
<tr>
<td>isabella</td>
<td>000101122112201311111221110</td>
</tr>
<tr>
<td>gazella</td>
<td>1010003112021222112221021</td>
</tr>
<tr>
<td>cora</td>
<td>1001013221111101112221120</td>
</tr>
<tr>
<td>erlangeri</td>
<td>100001210121311002211111</td>
</tr>
<tr>
<td>muscatensis</td>
<td>10110132332021221002221120</td>
</tr>
<tr>
<td>bilkis</td>
<td>111100201231211201112111000</td>
</tr>
<tr>
<td>arabica</td>
<td>1010107002332112011121111072</td>
</tr>
<tr>
<td>Thumamah</td>
<td>10000130011211111111111111111111111111111</td>
</tr>
</tbody>
</table>

* outgroup

Figure 2.5a

Figure 2.5b

Figure 2.5 Discriminant Function analysis of Gazella saudiya and G. bennetti female a) skulls and b) horns. 1 = saudiya, 2 = bennetti, # = skull from Al-Areen, Bahrain
Figures 2.6a-d
Figure 2.6 Cladograms of Arabian gazelles, from data in Table 2.5. a, b, c) the three shortest trees found by Hennig86: length 124, consistency index 0.41; d, e, f) next shortest trees, found by MacClade: length 125, c.i. 0.41; g, h) next shortest trees, found by MacClade: length 126, c.i. 0.40.
By branch-swapping, using MacClade, three trees were found with a length of 125, one step longer than the first three, but with the same consistency index. The first of these (Figure 2.6d) retains the asymmetry of the shorter trees, but returns *isabella* to the stem leading to the *gazella* group, and makes *pelzelni* the sister taxon to the entire *dorcas*/*gazella* clade. The second (Figure 2.6e) places the *bilkis*/*arabica* branch as sister-group to all the *G. gazella* group except *erlangeri*, and unites *cora* with *muscatensis*, *gazella* with the Thumamah taxon. The third (Figure 2.6f) puts *erlangeri* on the *bilkis*/*arabica* stem.

To reunite *pelzelni* with other subspecies of *G. dorcas* requires an increased tree length of 126, and a slightly lower consistency index. When this is done, either *cora* is the sister species to the rest of the *gazella* group, and *G. g. gazella* is part of the *bilkis*/*arabica* cluster (Figure 2.6g), or it falls within the *G. dorcas* cluster, as sister group to *isabella* (Figure 2.6h). In either case, Thumamah can be added to the *gazella*/*bilkis*/*arabica* cluster at no extra cost.

Interestingly, *G. subgutturosa*, with a low chromosome number like *G. dorcas* and *G. gazella*, cannot be added to their branch with a tree length below 127. Placing *G. bennetti* and *G. saudiya* on a branch together requires a tree length of at least 128, though the consistency index is still 40.

- **Body Build:** *G. bilkis* appears more sturdily built than other Arabian gazelles, and *G. g. cora* more slenderly; but in the absence of extensive external measurements it is difficult to quantify this. Harrison and Bates (1991) and Mendelsohn and Yom-Tov (1987) give some measurement data (Table 2.6). For their size *G. saudiya*, and to a lesser extent *G. s. marica*, clearly have extremely large ears; they appear to be short-legged, but the above measurements suggest that the difference is in the hind limbs, which are elongated in *G. gazella* (as represented by *G. g. muscatensis*) but not in the other two species. *G. s. marica* also has a relatively longer tail.

Table 2.6 Body build measurements for Arabian gazelles (data for both sexes combined).

<table>
<thead>
<tr>
<th></th>
<th>Head+Body length</th>
<th>Tail length</th>
<th>Hindfoot length</th>
<th>Ear length</th>
<th>Shoulder height</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>gazella</em> (19-20)</td>
<td>1016.5</td>
<td>105</td>
<td>-</td>
<td>117.5</td>
<td>-</td>
</tr>
<tr>
<td><em>cora</em> (1)</td>
<td>1041</td>
<td>-</td>
<td>-</td>
<td>120</td>
<td>610</td>
</tr>
<tr>
<td><em>muscatensis</em> (2)</td>
<td>943.5</td>
<td>105.5</td>
<td>276.5</td>
<td>114.1</td>
<td>559</td>
</tr>
<tr>
<td><em>saudiya</em> (1)</td>
<td>928</td>
<td>90</td>
<td>255</td>
<td>123</td>
<td>600</td>
</tr>
<tr>
<td><em>marica</em> (1-2)</td>
<td>966.5</td>
<td>152</td>
<td>272</td>
<td>125</td>
<td>-</td>
</tr>
</tbody>
</table>

*Note: hindfoot lengths given by Mendelsohn and Yom-Tov are not comparable to those given by Harrison and Bates.*

Skeletal postcranial measurements are available only for *G. g. gazella*, *G. dorcas isabella*, *G. s. subgutturosa* and a single reputed *G. saudiya* (author's data). The last of these is in the collection of Al-Areen Wildlife Park, Bahrain. These data are given in Table 2.7 (sexes combined). As far as these measurements can be extended to the Arabian peninsula representatives of their respective groups, this appears to confirm that *G. gazella* have elongated hindlimbs compared to forelimbs, but shorter distal segments; *G. saudiya* is generally short-legged; *G. subgutturosa* has elongated metapodials but not an elongated tibia.
Table 2.7 Skeletal postcranial measurements for certain Arabian gazelles
(data from both sexes combined).

<table>
<thead>
<tr>
<th>Species</th>
<th>Humerus length</th>
<th>Foreleg: hindleg</th>
<th>Tibia: femur</th>
<th>Metatarsal: femur</th>
<th>Hindleg: skull</th>
</tr>
</thead>
<tbody>
<tr>
<td>gazella (20)</td>
<td>125</td>
<td>78</td>
<td>127</td>
<td>100</td>
<td>302</td>
</tr>
<tr>
<td>dorcas (11)</td>
<td>119</td>
<td>81</td>
<td>133</td>
<td>111</td>
<td>314</td>
</tr>
<tr>
<td>saudiya (1)</td>
<td>116</td>
<td>80</td>
<td>130</td>
<td>109</td>
<td>298</td>
</tr>
<tr>
<td>subgutturosa (10)</td>
<td>125</td>
<td>81</td>
<td>127</td>
<td>109</td>
<td>290</td>
</tr>
</tbody>
</table>

Discussion

It is probable that, according to a Phylogenetic Species Concept, all the following taxa would be regarded as separate species: saudiya, arabica, bilkis, erlangeri, gazella, muscatensis, and cora. The status of marica vis-à-vis G. subgutturosa was not tested, but both morphologically (Groves & Harrison, 1967) and genetically (Kingswood et al., this volume) there is ample reason to regard it as part of the same species. Similarly, there seems little doubt that isabella and other forms of G. dorcas are conspecific (Groves, 1981b). As little other than metrical data was collected on the Thumarnah crania, the position of this quasi-taxon on the cladogram remains somewhat hypothetical. The status of the other taxa will be discussed in turn.

- Status of Gazella saudiya: That Gazella saudiya is totally distinct from G. dorcas is confirmed; as Rebholz et al. (this volume) have concluded, it is much closer to G. bennetti. It would be difficult to propose uniting them specifically, however. Metrically, G. saudiya falls outside the range of variation of G. bennetti, and the skull is a different shape from the similarly small-sized G. b. karamii (Table 2.4). In addition it shares some derived states with G. subgutturosa which are not seen in G. bennetti (Figure 2.6): nasal tip shortening, ethmoid fissure shape, greater sexual size difference, horn length in both sexes, more horn rings. Unless the polarities of these characters are incorrect, or there is an unsuspected degree of homoplasy, this does imply that G. bennetti and G. saudiya may not be sister species.

A question that must be asked is whether the Al-Areen (Bahrain) breeding group, phenetically resembling G. saudiya, is pure-bred or has been mixed with G. bennetti (see Rebholz et al., this volume, for discussion). The only detailed evidence is the morphology (mainly craniometry) of a female specimen made available courtesy of Dr Jaime Samour, formerly of the Al-Areen Wildlife Park. This specimen (Table 2.4) is considerably larger than wild-collected G. saudiya in the Natural History Museum, London (the only existing study sample), but is in proportion; compared to G. bennetti, it has a narrow skull, especially the braincase and across the horn bases, and the nasals are narrower posteriorly than anteriorly. The horns are extremely long, like G. saudiya, and spread more widely than either (on average), though they would be easily within the 2-standard-deviation limits of G. saudiya; but it must be borne in mind that the female of G. bennetti karamii, whose horns are exceptionally widely flared for that species, is unknown. In Figure 2.5 this skull, entered as an unknown in a Discriminant Analysis comparing G. bennetti and G. saudiya, falls within the range of the latter, confirming its identity in shape.

There is consequently only one character in which the Al-Areen specimen falls outside the expected range of G. saudiya: absolute size. It is possible that this is an effect of captivity (see the discussion above on subspecies and phenotypic plasticity); it is also possible that it derives from a population outside the known area of distribution of G. saudiya (Appendix 2.1).
On my first visit to Al-Areen, in 1987, the breeding group now called *G. saudiya* were listed as "Qatari subgutturosa". This implies that they had originated from Qatar, but no-one at Al-Areen had any record of their date of arrival or their origin. Dr Faris Al-Timimi (Doha, Qatar) informed the group visiting him (Drs Rebholz and Sayeed, Mr Kitchenside and myself) in November, 1992 that there are gazelles, of unknown species and origin, in a free-ranging government-owned facility in the north of Qatar, and that gazelles reputed "Qatari" in other countries are likely to be from there. If this is the case for the Al-Areen group, it re-opens the possibility that some of them may be of mixed stock. There is an urgent need to study this stock intensively; all skeletal remains should be saved, and breeding records should be kept so as to see whether matings between animals of different karyotypes (see Rebholz *et al.*, this volume) are associated with reduced fertility.

- *Gazella arabica* and *Gazella bilkis*: These two species are very close (Groves, 1987: Figures 1, 2; this paper, Figure 2.6), though not identical; they are not dissimilar in pelage characters either. The cladistic analysis always links them. A case could be made for uniting them conspecifically.

- Is *Gazella "gazella" cora* related to *Gazella dorcas*? The "spoilers" in many of the cladograms, rendering *Gazella gazella* polyphyletic, are *G. dorcas isabella* and *pelzelni*, one or other of which often emerge as the sister-group to *G. gazella*, especially *G. g. cora*. The similarity of *isabella* and *cora* in pelage characters and horn shape was noted above; they are, in fact, exceedingly easy to confuse when alive. Most of their skull codes are identical, in view of which their potential cladistic closeness is perhaps little surprise. In fact, the shape of the naso-frontal suture (Figure 2.2) is the only strikingly different aspect of skull morphology. The possibility that this relationship is real, an alternative to the general association of *cora* and *gazella* in the same species, was raised previously (Groves, 1989).

It is difficult to see *cora* as close to *G. g. gazella*. In discriminant analysis of cranial variables both sexes separate completely (Figures 2.3 a,b; Groves, 1989: Figures 1,2); on horn characters, they separate almost completely (Figure 2.3c). The only form of *G. gazella* with which it is sometimes linked in the shortest trees (Figure 2.6) is *muscatensis*.

In the light of the conclusions of Rebholz *et al.* (this volume) and Vassart *et al.* (this volume), these findings must be regarded as unexpected. One possible explanation could be that there has been simple misidentification of some reddish-toned *cora* as *dorcas*, and that specimens identified as *cora* for genetic study were actually something else. Alternatively, gross morphological characters are so replete with homoplasy as to cause a spurious linkage on some of the cladistic analyses and in the discriminant analysis; it is less plausible that the DNA segments sequenced by Rebholz *et al.* (this volume) or the blood protein loci analyzed by Vassart *et al.* (this volume) might be subject to extreme homoplasy. The problem is difficult but not intractable. For the moment it does seem better to adopt the conservative course and retain *cora* in *G. gazella*, but this option must be tested and re-tested in the future.

- The status of *Gazella "gazella" erlangeri*: Though formerly confused with *G. g. cora* (for example, Groves & Lay, 1985), and only recently identified as a separate taxon (Groves *et al.*, in press), this form turns out to be thoroughly distinct both metrically (Figures 2.3 a,b,c: but note small
sample sizes) and cladistically (Figure 2.6). It is also readily distinguished in the flesh. The map (Figure 2.7; see also localities listed in Appendix 2.1) shows a striking anomaly: undoubted erlangeri are known from coastal localities north of Jeddah, as well as from Yemen; yet cora is known from the coastal plain as well, in intervening localities. There is no evidence of gene exchange. Under such circumstances it would seem perverse to retain the two taxa in the same species.

Figure 2.7 Distribution map of taxa assigned to, or related to, *Gazella gazella* in the Arabian peninsula.

Externally, it is very close to muscatensis, as noted above; but skull characters and horn shape distinguish them (see above, and Figure 2.6). The cladistic analysis never associates them; indeed, as noted above, it refuses to associate erlangeri with any other member of the *G. gazella* group except, in one tree (Figure 2.6f) *G. bilkis* and arabica.

**What are the Thumamah idmi?** The large, very dark, straight-horned idmi, identified as *Gazella gazella* cf. *gazella*, in the breeding pens at the King Khalid Wildlife Research Center, Thumamah, Saudi Arabia, together with the rheem (*G. subgutturosa marica*) held at the same Center, were the subjects of a thorough behavioural study by Habibi (1991). They closely resemble *G. g. gazella* externally, but differ craniometrically (see above), especially in their straighter horns, narrower nasals and overall narrower skulls. The horns of the females are longer. The ascending
branch of the premaxilla generally touches the nasals, unlike *G. g. gazella* and many *G. g. cora*. Discriminant analysis of both male and female crania separates them completely from both *gazella* and *cora*; that of horns nearly separates them. The cladograms (Figure 2.6) tend to separate the Thumamah gazelle as the sister-group to most other members of the *G. gazella* group; but this is likely to be a spurious effect of the incomplete data set.

Conclusions

- **Relationships of Arabian Gazelles:** The interrelationships of Arabian gazelles are complex. The *G. gazella* group has produced compactly built, dark representatives with stout, straight horns in more mesic highland regions (*G. g. gazella* in the Levant, *G. bilkis* in Yemen) and small, dark forms in coastal zones (*G. g. erlangeri* along the Red Sea coast, *G. g. muscatensis* along the Batinah coast). The pale desert form, *G. g. cora*, is strikingly like *G. dorcas*. If the desert morphology is primitive, then the highland and coastal forms have converged; if the remarkable resemblance between *G. g. gazella* and *G. bilkis* is due to retention of primitive features, then the convergence of *G. g. cora* on *G. dorcas* is extraordinary. Either way, it seems that these gazelles exhibit an ability to adapt genetically to a wide range of environments.

The affinities of *G. saudiya* are puzzling. Cranially the species in many respects recalls *G. dorcas*, with which indeed it has generally been considered conspecific. Chromosomally, however, it resembles *G. bennetti* much more; and its suppressed colour contrasts increase this resemblance. The most westerly subspecies of *G. bennetti* lives in the region of Bushehr, on the Gulf shores of Iran; this is also the smallest subspecies. Skull measurements of the single available skull, compared to males of *G. saudiya* (n=6), are given in Table 2.4. Skull size, as measured by the greatest length, is exactly equal to that of *G. saudiya*. However, it has the typical broad nasal bones of *G. bennetti*, wider posteriorly than anteriorly; the skull is broader, the teeth are larger, the horns are shorter but very widely bowed outwards. In other words, the two may be sister species, but *G. saudiya* is not simply a westward extension of *G. bennetti*.

I have considered whether the type skull of *G. arabica* might actually be a misplaced specimen of *G. bilkis* (in which case, of course, the prior available name would be *arabica*). While Hemprich and Ehrenberg obtained the specimen on Farasan (Groves, 1983), it is possible that they did not themselves shoot it but that it was brought there, alive or dead, from the mainland. The skin is redder and less dark than of *G. bilkis*; the skull is narrower, and has a longer braincase and very short nasal bones. Cladistic analysis (Figure 2.6) always associates them. It seems likely that they are subspecies of the same species. Though generally associated with *G. gazella* in the cladograms, this is not obligatory (Figure 2.6f), and they are not clearly part of that species.

While the evidence is not complete, it seems likely that *cora* is a subspecies of *G. gazella*, as are *muscatensis* and the Thumamah taxon. Efforts to identify the origin of this apparently subspecifically distinct form need to be intensified. But *erlangeri* is surely not part of the same species. Cladistically it always appears as the sister-group to the rest of the species *G. gazella* (unless it is the sister-group to *G. arabica* / *bilkis*). Moreover its distribution would seem to overlap or interdigitate with that of *G. g. cora* (see above), without any indication of gene flow between them.

The position of *G. subgutturosa* is unclear. It is the most readily differentiated of the Arabian species, but this may be simply a matter of adaptation to a different environmental setting. There is also the matter of the number of subspecies to be considered: those of Iraq and, perhaps,
Syria, are small like *G. s. marica* but like *G. s. subgutturosa* in colour and in the females being normally hornless - are they simply intergrades, or a stable subspecies? Are the representatives on Bahrain Island different from those on the mainland?

I propose the following classification of Arabian gazelles:

- *G. subgutturosa marica*
- *G. saudiya*
- *G. dorcas isabella* (in Israel and Sinai, and perhaps extending into Saudi Arabia, on the evidence of Bedouin suppliers of specimens to Al Wabra)
- *G. erlangeri*
- *G. arabica arabica*
- *G. gazella gazella*
- *G. gazella* (Thumamah subspecies)
- *G. gazella cora*
- *G. gazella muscatensis*

**Acknowledgements**

I am very grateful to Drs Arnaud Greth and Doug Williamson for the invitation to participate in the symposium which gave rise to this volume; to Prof. Abdulaziz Abuzinada and his associates for the facilities and hospitality during the symposium; and to Charlie Kitchenside and Drs Wilhelmus Rebholz, Marc Vassart, Arnaud Greth, Khushal Habibi, Doug Williamson, Sayeed Mubarak, Faris al-Timimi, Mubarak al-Dosri and Jaime Samour for information, discussions and assistance in various ways.

**References**


Thomas, O. 1897. On a new gazelle from Central Arabia. *Annals and Magazine of Natural History (6):* 162-163.


**Appendix 2.1** Gazelle specimens and localities from the Arabian peninsula. Unless otherwise stated, all specimens are in the Natural History Museum (London).

*Gazella gazella cora*

Ain al Rizat (3 skins, 1 skull).

Arq Abu Da'ir, 4,000 feet: 16°40'N, 45°15'E (1 skin, 1 skull).

15 miles north of Ashiera: 22°00'N, 41°00'E (1 skull).

Buaiman, coastal plain: 21°38'N, 39°13'E (1 skin).

Buaimi: 24°15'N, 55°45'E (2 skulls).

Dhalm: 22°50'N, 41°40'E (1 skull).

'Garshawr (Qilwah) area (light red-brown gazelles, photos 4a and b of NCWCD Protected Area Report no. 18).

Hadhramaut: ±15°50'N, 48°50'E (1 skin).

Wadi Hammam: 14°50'N, 46°36'E (1 skin, 1 skull).


Haraj plain: 14°50'N, 46°40'E (1 skin, 1 skull).

Hudhaiyab al Aranib, 3,300 feet: 20°30'N, 42°40'E (1 skin, 1 skull).

Jurfaih: 17°00'N, 54°10'E (1 skin, 1 skull).

Manwakh: 16°57'N, 48°06'E (Figures 2.1a, b, this article).

Wadi Markha: 14°57'N, 46°35'E (1 skin, 1 skull).

Mughshin: 19°28'N, 54°57'E (2 skulls).

Qinfida: 19°00'N, 41°00'E (1 skin, 1 skull).

Rabigh Qasr: 22°50'N, 39°02'E (1 headskin, 1 skull).

Raqba plain: 22°30'N, 41°40'E (2 skins, 9 skulls).

South Arabian coast at 49°50'E (4 skulls).

Sudaihat, 3,000 feet: 16°00'N, 45°50'E (1 skin, 1 skull).

Tarf Al Ain, 2,500 feet: 15°50'N, 47°40'E (1 skin, 1 skull).

Uqla-Jifr plain, 3,000 feet: 15°25'N, 46°50'E (1 skin, 2 skulls).

Plain between Uqla and Wadi Mudhaib al Jifr (1 skin).

*Gazella gazella erlangeri*
Aden: 12°50'N, 45°03'E (4 skins, 2 frontlets; also one skull in Paris Museum).
Ma'bar, 7,400 feet: 14°46'N, 44°21'E (2 skins and skull, one a fawn, Field Museum, Chicago).
Najran Emirate: 17°30'N, 44°20'E (NWRC, Taif).
Taif district: 21°10'N, 40°45'E (1 skin of a fawn).
Thuwal, Hejaz Tihama: ± 22°30'N, 30°00'E (3 skulls, 3 skins and 2 head-skins).

Gazella gazella muscatensis
Abieat, north of Muscat (Harrison Museum, Sevenoaks, Kent, U.K.
Baikit et Maze, Oman (1 skin and skull).
Khode: 23°37'N, 58°08'E (2 skins, 2 skulls).
Muscat: 23°37'N, 58°38'E (1 skull, 2 skins; also one skull in Booth Museum, Brighton, U.K., and one skull in Harrison Museum).
Saham: 24°10'N, 56°53'E (2 skulls, Harrison Museum).
Sohar area: 24°23'N, 56°45'E (11 skulls, Harrison Museum).

Gazella bilkis
Mocha: 13°15'N, 43°15'E (1 skull).
El Hauban, Wadi Maleh, 5 miles east of Ta'izz: 13°36'N, 44°07'E (1 skin, 1 skull, Field Museum, Chicago).
Ta'izz, 4,100 feet: 13°35'N, 44°02'E (1 skin, 1 skull, same).
Usafira, 4,000 feet: 13°36'N, 44°00'E (1 skin, 1 skull, same).
Jebel Zarba, 7,000 feet, east of Ta'izz: 13°30'N, 44°03'E (1 skin, 1 skull, same).

Gazella sousiya
"Arabia" (2 skulls).
Alam Abyadh: 16°00'N, 45°42'E (1 skin and skull).
Arq Abu Da'ir: 16°40'N, 45°15'E (1 skin and skull).
Dhalm: 22°50'N, 41°40'E (7 skins and skulls).
Kuwait: ± 29°N, 48°E (1 skin and skull).
Wadi Markha: 14°57'N, 46°35'E (1 skin and skull).
Wadi Naq'a: 15°30'N, 47°15'E (1 skin and skull).
Ruwaik tract: 15°55'N, 46°10'E (1 skin and skull).
Sirr al Yamani: 16°20'N, 46°50'E (1 skin and skull).
Taraf al Ain: 15°50'N, 47°40'E (1 skin and skull).

Gazella subgutturosa marica
Arabia, 29°15'N, 47°E (1 skin and skull).
Arabia, 29°45'N, 40°28'E (1 skin and skull).
Arabia, 29°46'N, 40°56'E (1 skin and skull).
"Arabia" (2 skins and skulls).
Afalil: 46°30'N, 15°45'E (1 skin and skull).
Baisita plain.
Jebel Dhalm, between Alif and Khuna: 22°50'N, 41°40'E (1 skin and skull).
Dibdibbah, 60 miles south-west of Kuwait: 29°10'N, 46°50'E (1 skin and skull).
Harrath al Arrat, Saudi/Jordan border: ± 30°N, 38°E (NWRC, Taif).
Kuwait.
Ibri, Nejd: 23°15'N, 56°35'E (2 skins and skulls).
Es Taisiya Nejd, 27°30'N, 44°20'E (2 skins and skulls).
Safala plain, 27°N, 39°E (1 skin and skull).
3. Gazelle Distribution and Status in the Arabian Peninsula

Doug Williamson and Hany Tatwany

Abstract: This paper provides a concise outline of what is currently known about the distribution and status of gazelles in the Arabian Peninsula for the benefit of people who either are not familiar with the region or are unaware of the results of recent studies of gazelle distribution and status. Both free ranging and captive populations are considered. The presentation concludes with an examination of the conservation value of captive populations in the region.

Keywords: gazelle, afri, idmi, rheem, status, conservation, Saudi Arabia.

Introduction
Since the distribution and conservation status of gazelles in Saudi Arabia have recently and comprehensively been reviewed by Thouless et al. (1991) and gazelle distribution in Arabia has also recently been reviewed by Harrison and Bates (1991), an exhaustive review of these subjects would be redundant. This presentation therefore has the strictly limited purpose of providing a concise outline of what is currently known about the status and distribution of gazelles in the Arabian Peninsula for the benefit of people who are either unfamiliar with the region or are unaware of the results of recent findings on gazelle distribution and status. Both free-ranging and captive populations are considered, but only the species level is discussed. Subspecific issues are addressed in other articles in this volume. Much of the paper simply summarizes Thouless et al. (1991), but there is a discussion of captive populations which raises issues not previously addressed in an explicit manner.

The historical distribution and abundance of the gazelles of the Arabian region were poorly documented and there are reasons for believing that the original distribution of gazelles has been radically disrupted by human activities. Motorized hunting has been widespread since World War II and domestic livestock populations have greatly increased their range because of access to artificial water supplies and supplementary feeding, and have also greatly increased in numbers. Given the paucity of historical information and the scale and intensity of recent disturbances, it is difficult to see how a clear picture of undisturbed gazelle distribution and abundance can ever be constructed.

Despite this lack of information, it is clear that all Arabian gazelle species have been drastically affected by hunting and habitat degradation. One species, the Saudi gazelle (English) or afri (Arabic) *Gazella saudiya* is almost certainly extinct in the wild and the other two species, the sand gazelle (English) or rheem (Arabic) *Gazella subgutturosa* and the mountain gazelle (English) or idmi (Arabic) *Gazella gazella* have been reduced to a few relict populations. Each species will be individually reviewed. Since their status is considered further in other presentations, the reviews will be brief.
Afri

This species is currently the subject of dire confusion, to the point where it is no longer clear whether the word "afri" refers to one or two species. Historically the species was recorded only on the western side of the Arabian Peninsula, except for one anomalous specimen from Kuwait. Afri were found on gravel and sandy plains between 15-30 degrees north. Apart from the Kuwaiti specimen, all records of afri are west of 47 degrees east.

It seems likely that the afri is extinct in the wild. Occasional reports of it are received from rangers in the northern reserves of Harrat al-Harrah and Al-Khunfah (Figure 3.1), but these are vague and unconfirmed. It is also said to occur on an island in the Gulf, but most of the islands in the Gulf which support gazelles have been artificially stocked, so there must be serious doubts about the origins of any such animals.

The confusion about the afri arises from the results of cytogenetic research on animals in three collections in the Gulf - the Al Areen Wildlife Park in Bahrain, the Al Ain Zoo & Aquarium in the U.A.E. and the Al Wabra estate in Qatar. The animals in all three collections are said to be afri, but those from Al Wabra are karyotypically very different to those from the other two collections. The Al Wabra animals have the same karyotype as the African dorcas gazelle *Gazella dorcas*, while those from the other two collections have a surprisingly variable karyotype, which most closely resembles that of the chinkara *Gazella bennetti*. It is claimed that the founders of the Al Wabra group were obtained in Saudi Arabia, but the origins of the groups in the other two collections are unknown.

Clarification of the status of this species will require further taxonomic research, field surveys to investigate reports of their occurrence in the wild and investigation of reports of afri being held in private collections in Saudi Arabia. It is likely that it will take years to solve the problems relating to the afri, if, indeed, they can ever be completely resolved.

Rheem

There are historical records of the occurrence of rheem in areas as far apart as the gravel plains and basalt deserts to the north and west of the Nafud desert and the north-eastern and south-eastern fringes of the Rub Al Khali (Figure 3.1). They were also recorded on the plains to the east of Medina and Makkah and on the northern fringes of Saudi Arabia, including the plains along the Gulf coast. Populations may well have been migratory or nomadic and recorded herd sizes range from 50-100 to thousands.

The only two areas of Saudi Arabia where rheem can with certainty be said to survive are in the reserves of Harrat al-Harrah and Al-Khunfah (Figure 3.1) to the north and west of the Nafud. The total number surviving in these areas is probably less than 1,000. Protection is being given to these populations and they are likely to increase as a result of this. There are unconfirmed reports of rheem in the vicinity of Sharourah, on the south-western edge of the Rub Al Khali. Checking out the veracity of these reports would clearly be a worthwhile undertaking.

An NCWCD expedition to the Rub Al Khali early in 1990 collected the remains of rheem freshly hunted on the north-eastern edge of this desert, probably in Oman. A few animals may survive in this vicinity and rheem are also found in the Wahiba Sands of Oman. Since the numbers of rheem remaining in the wild are rather small, they must be considered vulnerable, but ongoing protection efforts give cause for hope that their status in the wild will improve.
The NCWCD has over 1,000 rheem in captivity (around 400 at Thumamah and more than 600 at Qassim) and there are reports of large numbers in captivity in Bahrain, Qatar and on islands in the Gulf. It is likely that the total number of rheem in captivity runs into several thousands. However, as is so often the case, the value of the captive rheem populations is clouded by uncertainty about the origins and pedigrees of the animals.

Rheem from the NCWCD's two captive populations are currently being reintroduced to the Mahazat as-Sayd protected area, 150 km north-east of Taif. Early indications are that the animals are adapting well to a free-ranging situation. A recent estimate (Smith, pers. comm.) puts the population of the protected area at 200.

![Figure 3.1 Arabian Peninsula, showing major geographical features. Stippled area shows major sand deserts. (Redrawn from Thouless et al., 1991).](image)

**Idmi**

In Saudi Arabia, relict populations of idmi occur in the northern reserves of Harrat al-Harrah and Al-Khunfah and in various places in the Tihama coastal plain and the Hejaz and the Sarawat mountains. In addition a population of more than 500 occupies the Farasan archipelago (Figure 3.1).

All historical and recent records of idmi in Saudi Arabia are from the western side of the Kingdom. The absence of records from the remainder of the region illustrates the inadequacy of the historical record, because local informants are adamant that idmi also occurred in the eastern part of the Arabian Peninsula.
One area where local people are insistent about the previous occurrence of idmi is the Ibex Reserve, which spans the Tuwayq Escarpment about 150 km south of Riyadh. Since the inception of an idmi reintroduction project in this reserve, reports have been received of a few gazelles surviving in a wadi about 50 km north of it. A survey of the area found signs of gazelle, in the form of tracks and dung pellets, but no animals were seen. Reports of idmi signs have also been received from well south of the reserve and local inhabitants from as far south as 'Uruq Bani Ma'arid, more than 500 km south of Riyadh, are also insistent that idmi previously occurred there. It thus seems plausible that they occurred along the entire length of the Tuwayq Escarpment, which runs roughly north/south for well over 1,000 km.

The situation of idmi in captivity is different to that of rheem, with relatively few collections being known to have large numbers of idmi. The NCWCD's herd of around 200 animals at Thumamah is almost certainly the largest captive group of idmi in the world. Animals from this herd are currently being reintroduced to the Ibex Reserve, with early indications being that the released animals are thriving. To date a total of 54 animals have been released over a period of two years. The number of births has exceeded the number of deaths by nearly three times and the population was approaching 80 by the end of 1992.

Discussion

One of the most interesting issues in gazelle conservation in Arabia is the future role of captive animals. Because all gazelle species have been radically depleted in the wild while at the same time there are substantial numbers of gazelles in captivity, the role of captive animals in restoring free-ranging populations could vary from being important, in the case of rheem, to being absolutely essential in the case of the afri. The role that captive animals will actually have in restoring free-ranging populations will depend on how idealistic or pragmatic attitudes are and on how successfully the problems associated with captive animals can be overcome.

Choices between idealism and pragmatism occur, for example, when decisions have to be made in restoration projects as to whether it is better to make use of animals already in captivity, even if there are questions about their origins and taxonomic status, or whether it is better to capture wild animals and start new captive populations for eventual replenishment of wild populations. In my view there is no single correct answer to this type of question because restoration projects may be undertaken in a variety of circumstances and for a range of different but equally valid objectives. The prerequisites for finding optimal answers to such questions are familiarity with relevant information, clear thinking and keeping an open mind.

Common problems which have to be overcome when working with captive animals are ignorance about their origins and pedigree and lack of genetic variability due to an inadequate number of founders or to inbreeding. If a number of captive populations of a given species exists, then increasing genetic variability by exchange of breeding animals between the different populations is relatively easy.

On the other hand, determining the taxonomic status of animals of unknown origin can be a very difficult problem. This is one context in which modern cyogenetic and molecular genetic techniques are likely to prove of great value. Application of such techniques is warranted because captive populations may be a repository of genetic material which has been lost in the wild.
Good management of captive stocks requires a sophisticated understanding and application of the principles of taxonomy and genetic management, which cannot realistically be expected from the many private animal collections in the Gulf region. Because many of these collections could contain valuable genetic resources for gazelle conservation, there is an urgent need to devise ways of screening them and encouraging and assisting their owners to maintain the conservation value of the animals in their custody.

Although the role of captive breeding in gazelle conservation is an important and interesting subject, it is vital to remember that there are compelling reasons for giving priority to in situ conservation of surviving free-ranging populations. The extent to which biodiversity can be replenished by reintroduction and restoration is subject to clear financial, practical and theoretical limits which preclude the possibility of ever recreating the past. Protecting intact habitats and their resident fauna is therefore not only the most efficient way of conserving diversity, but also the only defence against its continuous erosion.

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References
4. The Relationship Between Taxonomy and Conservation

Douglas Williamson

Abstract: Two conclusions that can validly be drawn from the history and current status of taxonomy are that:

1) There is no single, unifying purpose to current taxonomic activities;
2) Because of differing objectives and criteria for classification it is essential to consider whether existing taxa have been delimited in a way which is relevant to conservation.

It is also essential to understand that there is often a lack of congruence between the methods of taxonomists and the needs of conservationists.

Although modern DNA technology offers objective and relevant criteria for classification, it is far from being a panacea for all taxonomic problems and it is likely that conservationists will have to live with taxonomic uncertainty for a long time yet.

Prerequisites for dealing with taxonomic uncertainty include a clear understanding and articulation of the purposes of conservation in general and of individual projects in particular and a commitment to focusing activities on achievable goals.

Keywords: taxonomy, conservation, reintroduction

Introduction

Attempts by conservationists to base practical programmes on existing taxonomic divisions have raised doubts about the latter's importance and utility (e.g. USFWS, 1991). This paper explores the sources of these doubts and proposes an approach for dealing with them. The argument developed in this paper rests on the following propositions:

1) The traditional approach to taxonomy - based on the typological or essentialist concept of a species - is flawed from the point of view of conservation because the criteria used for the delimitation of species are subjectively chosen and no distinction is made between genetic and environmental effects;
2) The results of classification depend on the purpose with which it is undertaken;
3) From the plethora of existing species concepts it is clear that no single purpose for systematics exists;
4) Since purpose influences the results of classification it is essential for conservationists to be clear about their own purposes before they attempt to make decisions about the utility of existing classifications and about the levels of variability that can feasibly be protected.

On the basis of these propositions an approach to dealing with taxonomic issues is discussed. The discussion does nothing more than illustrate the approach. Treatment of the issues raised is neither comprehensive nor definitive because a comprehensive treatment would require a book and a definitive understanding of the issues remains a distant goal.
The traditional approach to taxonomy
All attempts to understand the order of living Nature and to express it in an equivalent logical structure are based on shared identical features, similarities and differences between organisms. For the purpose of grouping organisms together, similarities in structure and function are used. Although this seems like a logical procedure "nobody could deny that judgements and procedures of this sort are mere unobjectifiable expressions of opinion until there is some causal understanding of the resemblances between various organisms" (Ax, 1987).

The lack of objective delimiting criteria was a feature of all efforts to classify the natural world from the zoology of Aristotle (384-322 BC) to the Systema Naturae of Linnaeus (1707-1778). Throughout this more than two thousand year period the essentialist or typological approach to classification was dominant. In terms of this approach, organisms were placed together in units on the basis of the shared possession of particular features, which were chosen subjectively and set up as essential characteristics.

As well as lacking in objectivity this approach is inherently problematic because it uses static categories to classify dynamic entities which are being modified by the ongoing process of evolution - in other words, it is an attempt to impose pattern on process. It has the further weakness that it ignores the question of whether the shared features selected as essential characters are genetically or environmentally determined.

From the point of view of conservation this approach is particularly unsatisfactory because it allows virtually anybody to decide that virtually any level of variability is worthy of either specific or subspecific status. This means that there is uncertainty both about the nature and the consistency of what is being protected. In other words it raises the questions:

- What kinds of entities are we protecting?
- Are we always protecting the same kinds of entities?

The typological or essentialist approach was challenged when the emergence of evolutionary theory provided a causal explanation for the diversity of the natural world. Darwin himself (1859) pointed out that classifications should ideally be genealogies, thus suggesting a new basis for systematics.

The purpose of classification
The importance of the purpose of classification is pointed out by De Bono (1990): "Just as we can analyze things in different ways so we can classify them in different ways. We need to choose the basis of classification and then stick to it... The choice of classification basis depends very much on the purpose of your thinking. What do you want to do with the classification?"

Given the range and the complexity of natural diversity, there is so much scope for differences in purpose that it is questionable whether unified methods and criteria for taxonomy are practical or even possible (Rojas, 1992). It is therefore not surprising to find that in modern taxonomy differences in aims and methods seem to be the rule rather than the exception.
The current status of taxonomy

Adopting a new basis for systematics to take account of evolutionary theory has proved to be difficult and more than a century after Darwin's death there was still "a stormy argument as to the aims of systematics" and "an embittered debate for and against a consistently phylogenetic system" (Ax, 1987).

There has also been an enduring lack of consensus about basic taxonomic concepts. In a recent review Rojas (1992) identifies more than ten different species concepts and shows that the existence of different species concepts has practical implications. Thus the genus *Drimys* may be divided into one or thirty species, depending on which species concept is used, and estimates of the number of existing plant and animal species range from 5 to 30 million.

The actual concepts and criteria used for classification "will depend on the purposes of the researcher, on what is to be investigated and explained" (Rojas, 1992). In a theoretical or academic context there is no reason why people should not have any purpose they choose, but conservationists need to be aware that taxonomic divisions may be motivated by different purposes. If a classification has been made for purely theoretical or academic purposes, there may well be limitations on its practical utility.

It is important to appreciate that existing difficulties are unlikely to be easily resolved by the advent of new molecular technologies, which enable genetic differences to be detected between different individuals, as well as different taxa. One problem with the use of such powerful techniques of discrimination is that groupings of individuals are usually made on an arbitrary basis. This means that we are still left with the problem of finding a rigorous basis for making decisions about which level of variability is significant.

A further difficulty with these techniques is that the great majority of identified molecular changes are almost entirely phenotypically neutral and therefore have no functional significance (Kimura, 1983). Although on the one hand this means that, for example, DNA techniques can be used to establish times since divergence between taxa (because rates of molecular change are uncoupled from selective pressures), on the other hand it makes it impossible to make inferences about the relationship between molecular differences and adaptation to the environment. If it is found that there are molecular differences between two taxa, this currently tells us nothing about their adaptation to particular environments, which is an issue of critical importance to conservation.

Because of these difficulties, and the "noisiness" of the data (which are full of unrecognizable homoplasies) the new molecular technologies will probably not be a panacea for resolving all the current problems of systematics. These techniques, and those of cytogenetics, are certainly powerful and valuable means for testing the validity of existing classifications, able as they are to produce trees of the phylogenetic history of a taxonomic group and identify "cryptic" species - but they do not remove all the problems associated with establishing valid and workable alternative classifications where existing ones are found to be wrong.

The purpose of conservation

Since there is evidently a relationship between the purpose of classification and its results, it is logical to propose that conservationists should use their own purposes as a basis for assessing the importance and practical implications of prevailing taxonomic divisions. In the context of antelope
conservation, taxonomic problems have usually related to divisions at the specific and subspecific levels, so the ensuing discussion will ignore supraspecific questions.

Just as taxonomists have different purposes so do conservationists, but most people involved in conservation would probably agree that one of its overall objectives is the maintenance of existing levels of biodiversity. The logical basis for maintaining biodiversity is that this will provide a capability for maintaining biological production in the face of environmental change. If species diversity is high, then there are likely to be species that will thrive in whatever conditions arise in the future.

From this point of view it is those attributes of individual species and groups of species that make them either adapted or adaptable to a specific environment or to a range of environments which are important to conservation. The importance of taxonomic divisions to conservation should therefore depend on the degree to which these divisions can be shown to reflect environmental adaptation.

Using taxonomy in conservation

The confidence with which conservationists can use existing taxonomic divisions as a basis for maintaining biodiversity is undermined by the fact that in the past taxonomists have often used delimiting criteria that have no relationship to environmental adaptation or have an unknown relationship to it. This lack of congruence between the needs of conservation and the methods of taxonomy probably arises because conservationists are concerned with the management of whole, living organisms and dynamic systems and processes, whereas taxonomists have in the past frequently worked in museums and have often been obliged to base their methods on a very limited amount of preserved material from dead specimens.

A similar lack of congruence could arise with laboratory based cytogenetic, allozyme and DNA studies, because the adaptational significance of differences revealed by these methods is seldom known. However, since these methods involve direct determination of genetic characteristics, they provide much more important evidence of relationships between individuals or groups of individuals than can be obtained, for example, from arbitrarily selected morphological characters which could be either genetically or environmentally determined.

For the purposes of conservation, taxonomic divisions should ideally be based on a comprehensive overview of biology, ecology, demography and biogeography, following the approach of Greth et al. (Article 5, this volume) to the question of gazelle subspecies in Saudi Arabia and their conservation. In reality, circumstances are seldom ideal and it is often difficult or impossible to collect adequate information on all aspects relevant to the establishment of taxonomic divisions.

Even where a compelling case can be made for the validity of taxonomic divisions, they may be of limited significance to practical conservation. The rapidity with which biodiversity is being lost and the limits on the resources available for dealing with this crisis require that conservationists should define "achievable goals" and "move from didacticism to pragmatism" (Western, 1991). These imperatives mean that conservationists may, for instance, be obliged to work at levels of variability which are lower than those recognized by taxonomists. The level of variability which is recognized as significant in a specific project will depend on its objectives and the circumstances in which it is being implemented.
There is much scope for conflict between didactic idealism and pragmatism in relation to restoration ecology in general and reintroduction in particular. In my view idealistic efforts to recreate the past are both naive and futile because even a limited analysis demonstrates clearly that by the time restoration or reintroduction have become necessary it is impossible to recreate the past.

A putative antelope reintroduction will be used to illustrate this point. It is assumed that the original population has been exterminated and that the habitat has been disturbed to an unknown degree. In this situation recreating the past has at least two impossible requirements:

1) Knowledge of all the interacting variables that govern the ecological and evolutionary processes which affect the life histories of individual animals;
2) The management capability to restore the ecosystem to the condition that it was in when the population was exterminated and to return the development of the system to the path it was on before disturbance.

In even the best known ecosystems relevant information is unavailable because there is no way of identifying all the events, processes and interactions that have shaped the system over the course of its development. In many situations virtually all the information is missing and will never be available because of changes that have taken place. For example, evolution is influenced by demographic features such as population structure and the number of equivalent phenotypes and if a population is exterminated before it is studied, then this information is irretrievably lost.

Our ability to manage reintroduced populations is limited by our ignorance of which variables govern the system and the evolution of the population and the critical values of these variables, both in the past and in the present, and by our lack of understanding of how evolution works in the wild (Endler, 1986). As Endler points out, the latter is illustrated by the lack of agreement over the relative importance of natural selection and mutation in determining the rate of evolution.

To formulate achievable goals for reintroduction we need to be continuously aware of our own ignorance and to be aware that problems can be approached in more than one way. For example one way of taking account of intraspecific variability is to appreciate that every discrete population is on its own unique evolutionary track. Once this track is terminated by extinction there is no way of putting a different group of animals onto the same track, whether or not they belong to the same race, subspecies or whatever. Because discrete populations are effectively evolutionary units, it would be perfectly logical to regard them as units for conservation and thus to bypass the whole controversy over subspecific classifications.

It is important also to appreciate that even where populations are not extinct the course of evolution has almost certainly been changed by human intervention. According to Soulé (1989): "the direction of evolution of virtually all surviving species will change".

In Saudi Arabia it is easy to see how selective pressures on, for example, antelope populations could have been affected by human activity. Motorized and other forms of hunting have occurred on a massive scale, there has been widespread and serious disturbance of plant cover, top carnivores have been exterminated, domestic animals have invaded new areas and have vastly increased in numbers, bringing with them new pathogens and parasites. All these changes are very likely to have created new selective pressures, resulting in the emergence of new phenotypes.

In these circumstances it is naive to believe either that it is possible to restore the past or that the future will be like the past. Recreating the past is quite simply not an achievable objective. The
most that can be done is to simulate what was previously present and to restore the ecological and evolutionary processes which generate diversity. The latter is what the priority for the future should, in my view, be.

A pragmatic approach to reintroduction should draw on all the knowledge available in behavioural ecology, genetics, small population biology, taxonomy and so forth, but it should not be sidetracked by idealistic and impossible objectives and it should not be inhibited by undue caution. Our factual and conceptual ignorance of all the factors that impinge on reintroduction is so great that risk and trial and error are unavoidable. Thus it may well transpire that carefully conducted experimental reintroductions with achievable objectives will do more to increase our capacity for restoring biodiversity than idealistically motivated, elaborate and painstaking efforts to recreate a largely unknown and unknowable past.

The whole enterprise of reintroduction, indeed of conservation, is so new that there is not only scope for a diversity of approaches and objectives but also a positive need for flexibility and openness.

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References
Abstract: Classifications at the subspecies level have frequently been criticized because of the irrelevant criteria used in reaching them and, by some authors, because of their lack of biological significance. There are however ethical, ecological and phylogenetic considerations which validate the subspecies concept.

A systematic approach to assess the validity of a subspecies is proposed which is based on consideration of the range, natural history and ecology of the taxon and its investigation by morphometric, cytotaxonomic, allozyme and DNA analysis. The cases of the sand gazelle (Gazella subgutturosa) and mountain gazelle (Gazella gazella) in Saudi Arabia are presented as examples of the subspecific classification of wild and captive populations.

Keywords: taxonomy, subspecies, conservation, Gazella subgutturosa, Gazella gazella, Saudi Arabia.

Introduction

The conservation of our planet's vanishing biodiversity has gained increasing attention over the last decade among scientists and even politicians. Considering the increasing rate of extinction and economic constraints, it is necessary to define what biodiversity is and which taxa deserve our specific help and attention to restore and maintain it. To answer these questions we first have to know what taxa there were and are and by what unique characteristics they are classified. With certain taxa this is difficult, especially when trying to delineate subspecies. One genus that exemplifies these problems and that is an integral part of the biodiversity of Saudi Arabia is Gazella.

Gazelles belong to the family Bovidae, the subfamily Antilopinae and the genus Gazella de Blainville, 1816. At this level, disagreements mainly concern taxonomists and have few implications for conservation, because the species level is internationally recognized as the unit for conservation.

Within the genus Gazella there is, however, still some dispute as to how many genuine species to recognize. Gazella consists of 12 to 16 species (12 species: Honacki et al., 1982; 15 species: Groves, 1988; Corbet and Hill, 1991; 16 species: Nowak, 1991). This picture gets even more puzzling when the numerous subspecies within each species are examined. One subspecies may have a wide distribution with several scattered populations, each of which experiences different evolutionary pressures. At which level should conservationists invest their efforts to conserve biodiversity?

Errors in systematics can lead to the recognition of taxonomic groups that share little evolutionary differentiation or, at the other extreme, to a lack of taxonomic recognition of phylogenetically distinct forms. In both cases, conservation efforts for endangered taxa may be
misdirected with respect to the goal of protecting biological diversity (Avise, 1989). Financial and socio-political implications must also be taken into consideration in the current conservation struggle.

Should the subspecies level be considered in conservation projects? The answer is relatively simple for *in situ* conservation because projects concern areas where native populations exist. The question becomes more sensitive with *ex situ* conservation programmes involving the translocation of animals. Should *ex situ* conservation focus on populations, subspecies, or species? What is the best policy to adopt in restocking or reintroduction programmes when the only animals available are of different geographic origin from the native current or past taxon?

**The subspecies concept: definition and controversy**

In order to understand the subspecies concept, let us first recall the definition of the species. The species concept was originally based on morphological criteria identified using museum specimens. More recently, the Biological Species Concept has emphasized reproductive isolation as the basic criterion (Mayr, 1963). Since then, various criteria, based on phylogeny, ecology, and genetic cohesion, among others, have been used to delineate species (see Rojas, 1992 for a review). As yet, however, no common agreement has been reached on what true species are. Modern molecular techniques have recently allowed access to genotypes, which contain the heritable information of an animal (Hillis, 1987). These techniques provide more reliable tools for studying genetic similarity or phylogenetic relationships between taxa, increasing the understanding of certain taxa (Avise, 1989).

The concept of subspecies is even more vague and controversial (Mayr, 1963). Avise and Ball (1990) proposed that subspecies should be defined as "groups of actually or potentially interbreeding populations phylogenetically distinguishable from, but reproductively compatible with, other such groups. Importantly, the evidence for phylogenetic distinction must normally come from the concordant distributions of multiple, independent, genetically based traits". Consideration of geographical, morphological, behavioural and genetic factors may suggest that isolation and independent evolution of a geographical race has occurred, implying the likelihood that populations of this race (or subspecies) may possess genes rare or absent in other conspecific taxa (Ryder *et al.*, 1988). Members of a subspecies should share a unique geographic range or habitat, a group of phylogenetically concordant phenotypic characters, and a unique natural history relative to other subdivisions of the species (O’Brien and Mayr, 1991). This concept emphasizes the importance of local adaptation. To enhance the success of reintroduction projects, it seems logical to release animals that have the best chances of fitting within the ecosystem. Although the subspecies concept represents a biological reality, its application requires a good understanding of the distribution of the different local races within a species and their comparative degree of differentiation. As such information is often lacking, it is difficult to find clear features to define the subspecific level.

The traditional classification of subspecies, based mainly on small numbers of morphological characters, is being subjected to more and more justified criticisms and is increasingly controversial. Should we consider this taxonomic level in wildlife management? The following sections present arguments for and against the consideration of subspecies in conservation.

**Arguments against subspecies consideration**

The arguments against the recognition of subspecies in conservation biology can be divided into four categories: taxonomic, technical, biological and practical.
- **Taxonomic argument:** The divisions of species into subspecies were mainly created by taxonomists in view of the need for nomenclature. In the past, subspecies have often been described on the basis of minor, arbitrary, equivocal, inconclusive or outdated criteria. For example, minor cranial and external morphological differences (e.g. size, colouration, pelage pattern) have been widely used. Further shortcomings appear in the methodology used in the past, such as descriptions which were often based on very few specimens, synonyms which have not yet been properly sorted out and overlap of characteristics between neighbouring subspecies. Because of these methodological failures, many described subspecies cannot be validated as they do not correspond to biological realities but to artificial subdivisions.

- **Technical argument:** Molecular genetic techniques, particularly DNA sequencing, are now so precise that it is possible to distinguish individuals. This raises the question of how to establish the arbitrary threshold that fixes the level below which distinctions between the specimens studied should be ignored (Avise and Ball, 1990; Avise, 1989). With allozyme data, the overlapping ranges of values of genetic distances associated with different taxonomic levels (population, subspecies, species, subgenera) makes it difficult to use these criteria for deciding whether two (or more) compared taxa should be placed in one or another category (Duplantier *et al.*, 1990).

- **Biological argument:** Some of the proposed reintroduction sites (where the concerned species no longer occurs) have been altered to such a degree that animals of the subspecies formerly occupying the area might be less, or only equally, suitable compared to any other subspecies. Moreover, reintroduced animals of uncertain status (such as subspecific hybrids) may have a higher fitness due to their genetic mixture and consequently increased adaptability. The reintroduction of the peregrine falcon *Falco perigrinus* into the eastern U.S.A. was achieved by releasing young birds derived from genetic stocks of various geographical origins (Spain, Scotland, Chile, Alaska, the Aleutian Islands, the Queen Charlotte Islands and California). The reintroduction was successful despite the fact that the birds were genetically very different from the aboriginal population (Barclay and Cade, 1983).

- **Practical argument:** Due to the accelerating rate of extinctions, species conservation is increasingly becoming a race against the clock. Considering subspecific taxonomic levels will cost money and time and therefore cause the delay of conservation action in particular reintroduction projects.

**Arguments for subspecies consideration**
The arguments in favour of subspecies can be divided into three categories: ethical, phylogenetic and ecological arguments.

- **Ethical argument:** The main role of conservation is to maintain biodiversity. Reintroduction projects should therefore aim to restore former biodiversity. Reintroduction of an alien subspecies into the range of a native subspecies would decrease biodiversity, except if the historical subspecies is extinct. It has been emphasized by IUCN (1987) and different authors (Brambell, 1977; Stanley-Price, 1989) that the animals involved in reintroduction should be the
"closest available race to the original stock and preferably be the same race as that previously occurring in the area" (IUCN, 1987). For restocking, the recommendations are even stronger, emphasizing that "only individuals from a similar climatic or ecological zone (should be) used since interbreeding with individuals from an area with a milder climate may interfere with resistant and hardy genotypes on the population’s edge" (IUCN, 1987). The guidelines of the Re-introduction Specialist Group of IUCN (Re-introduction Specialist Group, 1992) are more specific, recommending that the animals should be of the same taxonomic unit as those which were extirpated and that taxonomic investigation, using molecular genetic studies if necessary, should be undertaken in case of doubt. Depending on the success of the operation, reintroductions can become restocking if the reintroduced animals expand their range and interbreed with remnant local populations. This kind of process, depending on the species' survival, could be irreversible. It implies a responsibility towards future generations, and therefore all possible precautions should be taken. An assessment of the taxonomic status of individuals to be reintroduced and of the local existing or historical subspecies should be a prerequisite to any such programme.

- **Ecological argument**: Many species are distributed over a geographical range that encompasses a range of environmental conditions that influence the animals' ability to survive or reproduce. Under these conditions, local populations of the species will often adapt to the local environment (Templeton et al., 1986). This is of particular importance in species where dispersal is limited. Hybridization between different local populations could result in outbreeding depression, a decrease in fertility and viability of the progeny, and the production of animals with genetic make-ups inappropriate for a given environment (Templeton, 1986). To enhance the success of reintroduction programmes, animals must be well adapted to their environment. The subspecies that previously occurred locally is in all probability the most adapted taxa, except in the case of a drastic and recent change in the environment. A famous example that illustrates the risk of mixing subspecies is the reintroduction of ibex into Czechoslovakia. *Capra ibex ibex* from Austria were successfully reintroduced after the extinction of the locally adapted Tatra mountain ibex *C. i. ibex*, due to overhunting. But, some years later, bezoars *C. i. aegagrus* from Turkey, and Nubian ibex *C. i. nubiana* from the Sinai peninsula were added to reinforce the local herd. The resulting fertile hybrids dropped their kids in February, three months earlier than the pure *C. i. ibex* population, and the coldest month of the year, resulting in total kid loss. As a consequence, the entire population became extinct (Greig, 1979).

- **Phylogenetic argument**: The process of species formation and dynamics includes geographic isolation and genetic differentiation of populations below the species level. The subspecific designation accounts for this process and recognizes the potential of isolated subspecies to acquire ecological adaptations through natural selection, and, in some cases, to become new species.

It is clear that there is a real problem in assessing the validity of subspecies. However the subspecies concept has a phylogenetic and ecological significance that cannot be ignored. The recent evolution of modern taxonomy and the availability of molecular techniques should provide a more reasonable basis for a proper recognition of evolutionarily significant units (Ryder, 1986). Molecular assays provide access to a specified and usually significant sample of genetic material, whereas
conventional taxonomic characters typically have an unknown or a limited genetic basis and may be primarily environmentally determined (Avise, 1989).

This taxonomic revolution will need a tremendous investment of time, effort and financial resources to redefine the levels of all taxa. Effort should first concentrate on endangered taxa where disputes about taxonomy are hampering appropriate conservation measures.

**An overall approach for evaluating the validity of a subspecies**

One general approach to evaluate the validity of a particular subspecies is to consider objectively all available information resulting from the application of different analytical tools to the concerned taxon (Ryder, 1986). If the information is convergent and reveals a taxonomic distance from other subspecies, or not, the validity of the subspecies should then be accepted, or rejected. If the data are inconclusive because of the lack of data or the complexity of the case, other methods should be applied.

- **Range and distribution, natural history, ecology:** These simple data can be useful for investigating speciation and geographic adaptation and thus assessing the validity of some subspecies within a species. Because populations constituting distinct subspecies are reproductively compatible, subspecies are normally allopatric, except in secondary hybrid zones (Avise and Ball, 1990). The characteristics of the range will determine the different habitats to which the species become adapted. An extended range, particularly on a north-south axis, will probably present a wide variety of climatic conditions. The distribution of the species, continuous or in patches, and of the different subspecies are also important factors for genetic isolation. An insular distribution will favour the speciation process. The natural history of the populations should also be considered carefully. The longer the geographic isolation, the greater the opportunity for genetic divergence. The problem is to determine what constitutes a significant period of reproductive isolation (Avise and Ball, 1990). This isolation time should of course be interpreted in terms of generation time. The founder size of the population and the initial growth rate, when known, are also key factors in understanding the differentiation process. It must be kept in mind that the distribution of many taxa has been recently modified due to human factors. All the ecological differences, such as type of habitat, behaviour, reproductive performances and physiological adaptations, between two taxa should be taken into account. Their dispersal habits (e.g. migratory, erratic, sedentary) will also influence gene pool isolation.

- **Morphometric analysis:** Morphometrics, the quantification of the phenotypic similarities of populations, is a powerful tool if applied on a scientific basis in which large numbers of variables such as measurements of skulls, skeletons, horns, etc. are subjected to multivariate statistical analysis. Before any premature judgement is reached, the whole geographic variation of the species should be considered and genetically independent characters should be studied before grouping the different races into valid subspecies (Wilson and Brown, 1953).

For example, Fabricius et al. (1989) developed a simple field method to distinguish the two subspecies of *Damaliscus dorcas*, the bontebok *D. d. dorcas*, and the blesbok *D. d. phillipsi*, and their hybrids. They proposed a discriminant function obtained by measurements of the white patches on the hind quarters (based on photographs).
- **Cytogenetic analysis:** Chromosomal studies can help to identify subspecies by the comparative study of their karyotypes. Karyotypes obtained with conventional colouration as well as with different banding techniques should be compared for each pair of chromosomes. Chromosomal differences could explain any observed reduced fertility of hybrids between two subspecies.

Thus, karyotypes of the two subspecies of orang-utan, *Pongo pygmaeus pygmaeus* and *P. p. abelii*, differ by a pericentric inversion involving chromosome pair 2 (Seuanez et al., 1979). These two taxa can also be identified by morphological and behavioural differences.

- **Protein electrophoresis:** All ozyme study can be a powerful tool in identifying subspecies, but only if there is a sufficiently large degree of protein heterozygosity within the species, with polymorphic loci and variation in allele frequency (Ryder et al., 1988). The required level of heterozygosity is not present in all mammalian families. Protein polymorphism may be low, as, for example, in the Mustelidae (O'Brien et al., 1989). Some alleles may be discriminant between the two samples. Genetic distances between subspecies may also be calculated and compared with data in related species, and used as a criterion for distinguishing subspecies.

For example, a study of six different Alpine chamois *Rupicapra rupicapra* populations revealed Nei genetic distances that allowed the validation of one population as a subspecies, *R. r. cariusiana* (Pemberton et al., 1989). No loci displaying fixed differences were detected but the genetic distances calculated on allele frequencies were of the same order of magnitude as the distances between named red deer *Cervus elaphus* subspecies (Gyllensten et al., 1983).

- **Mitochondrial DNA analysis:** The mitochondrial genome consists of a closed circular DNA molecule. This DNA has a rapid rate of evolution in comparison with the rates of change in nuclear genes (Brown et al., 1979). The rate is also relatively constant and provides an "evolutionary molecular clock". It has been suggested that the evolution rate ranges from 0.5% to 2% per million years (Brown et al., 1979; Harrison, 1989). Mitochondrial DNA is haploid, maternally inherited without recombination, has a simple sequence organization, and thus, represents an unambiguous marker of maternal phylogeny (Harrison, 1989). It can therefore be used to investigate systematic relationships between related taxa with recent times of divergence (Avise et al., 1979; Brown and Simpson, 1981; George and Ryder, 1986). Nevertheless, it is apparent that there is considerable variability among taxa in relative and absolute rates of change, which necessitates caution about the hypothesis of the molecular clock (Hillis, 1987). This clock should first be demonstrated as valid within a taxonomic group. The relative rate test, using phylogenetic data (Sarich and Wilson, 1973) and the study of fossils can provide comparative data for this purpose. Molecular data should always be analyzed in parallel with unrelated suites of characters and historical biogeographic data. Taxonomic subdivisions should be recognized when all this information is concordant and clear phylogenetic discontinuities resulting from long-term population separation appear (Avise, 1989).

Analysis of the mitochondrial DNA of the bontebok and the blesbok shows 0.47% sequence divergence which would translate into a time of divergence of about 250,000 years ago (Essop et al., 1991). This confirms the subspecific level for these two taxa.

Another study estimated the genetic distances between the two most numerous subspecies of the black rhinoceros, *Diceros bicornis michaeli* and *D. b. minor*, to determine whether they could be mixed for conservation management purposes (Ashley et al., 1990). The estimated percent sequence
divergence between the mitochondrial DNA of the different populations ranged from 0% to 0.39%. This result suggests that all these populations have a very recent common ancestry, and that they would not suffer from outbreeding depression if subspecies merging occurred.

Cronin's (1992) study considering intraspecific variation in mitochondrial DNA of North American Cervidae is an interesting example of the concordance, or lack of it, between existing subspecies and molecular data. No variation was detected between the four moose Ales alces subspecies and little in elk Cervus elaphus subspecies. Caribou Rangifer tarandus and white-tailed deer Odocoileus virginianus possessed considerable variation, but the characteristic mitochondrial DNA genotypes identified were not concordant with the geographic distribution of existing subspecies. Only the mule deer Odocoileus hemionus was characterized by high divergence between, and limited divergence within, subspecies. However these data should be interpreted with caution, by analyzing a variety of information, not only mitochondrial DNA, because of the history in some of these cervid populations of recent colonizations, including human transplantations, and gene flows following Pleistocene climate changes (Cronin, 1992).

The cost of similar studies would represent only a small fraction of the overall financial investment needed for any captive-breeding or reintroduction programmes of threatened taxa. It would also perhaps help to prevent errors that could be difficult to correct once the programme has been implemented.

**Two case studies: Gazella subgutturosa ssp. and Gazella gazella ssp.**

Classification of the genus Gazella has raised questions among taxonomists, and has been subject to many revisions, not only at the subspecies level, but even at the species level (Groves and Harrison, 1967; Groves, 1969). Taxonomic difficulties are probably due to the recent origin of many taxa (Gentry, 1966; Furley et al., 1988). Considering the confusing taxonomic relationships and the vast distribution of the genus, Blandford (1873) supposed that this group had recently gone through a period of rapid expansion. The range of colouration and cranial morphological variation within the species is so large that there is an overlap between intra- and interspecific variation. The number of museum specimens of precise geographic origin is also too small for a quantitative analysis. Moreover, zoo specimens are often of unknown origin, due to the uncontrolled trade of live animals, and are subject to hybridization. Two of the most taxonomically studied gazelle species, both native to Saudi Arabia, illustrate some of the problems relating to subspecific status.

**The goitred gazelle or sand gazelle (Gazella subgutturosa Güldenstäedt, 1780)**

- **The problem:** The goitred or sand gazelle, typical inhabitant of desert steppes, sandy and stony deserts, is said to belong to a separate subgenus, Trachelocele (Ellerman and Morrison-Scott, 1951), shared with the slender-horned gazelle G. leptoceros. Four subspecies of the sand gazelle are usually distinguished (Groves, 1985):
  - G. s. subgutturosa, the Persian gazelle. Ranges from eastern Turkey through Iran, Pakistan and Soviet Central Asia;
  - G. s. marica, the Arabian sand gazelle or rheem. Formerly found throughout the Arabian Peninsula except for mountainous areas, ranging north through eastern Jordan and Iraq;
  - G. s. yarkandensis, the Xinjiang goitred gazelle. Found in the deserts of the Tarim Basin, Xinjiang, China;
G. s. hillieriana, the Mongolian goitred gazelle. Occurs in the Gobi and Caidam areas in Mongolia.

Firstly, there is some taxonomic uncertainty at the species level. G. s. marica was initially placed with G. leptoceros in an earlier classification (Ellerman and Morrison-Scott, 1951). Later, it was proposed that G. leptoceros itself should be included in G. subgutturosa (Lange, 1972). This example reflects the dilemma within the genus Gazella that exists even at the species level. Finally Groves and Harrison (1967) identified marica as a subspecies of G. subgutturosa on the basis of obvious skull similarities. For the taxon leptoceros, no final answer has yet been given (Furley et al., 1988).

The sand gazelle was once abundant in the open country of central Saudi Arabia and was particularly numerous in the north (Thouless et al., 1991). It probably migrated in large numbers along a north-south axis to Syria. Only two small known populations have persisted today in two protected areas in the northern part of the country, Harrat al-Harrah and Al-Khunfah. Two captive populations, managed for future reintroductions, exist. The King Khalid Wildlife Research Center (KKWRC) near Riyadh, holds a herd of about 400 individuals. The other captive population is at Qassim and numbers about 600 individuals. No reliable data are available on the origin of these two captive populations, which both originate from private collections of the Royal family. Princes used to hunt in neighbouring countries and collect live specimens from various origins for their private collections. Due to the proximity of the geographic range of G. s. subgutturosa, it is possible that this subspecies was mixed with G. s. marica in both collections.

The lack of historical data for both captive herds, as well as the existing biological and taxonomic data concerning the species, raises many questions:

1) How can it be established whether the animals bred in the NCWCD collections (at KKWRC and Qassim) are pure G. s. marica?
2) What is the genetic distance between G. s. subgutturosa and G. s. marica? Should they be considered as valid subspecies?
3) If hybridization with G. s. subgutturosa is suspected, should these animals be used for reintroduction within the historical range of G. s. marica in Saudi Arabia?

Data synthesis

- **Natural history information:** The majority of historical records derived from the north of the country. According to Philby (1923), sand gazelles occurred in "thousands". It is possible that these populations were migratory or nomadic, depending on food availability (Thouless et al., 1991). These migrations could have generated regular genetic exchanges between populations of the two subspecies.

- **Range and distribution data:** The range of the two subspecies is clearly defined, with G. s. subgutturosa in Azerbaijan, Afghanistan and Iran, and G. s. marica in all the Arabian peninsula, ranging north through eastern Jordan. Judging by morphometric and cytogenetic data (see below), there might have been a possible range overlap in Iraq with possible hybridization (Harrison and Bates, 1991; Kingswood and Kumamoto, 1988).
- **Morphometries:** Some morphological criteria allow distinction between the two subspecies. Adult females of *G. s. subgutturosa* tend to be hornless, but female *G. s. marica* have well developed horns (Groves and Harrison, 1967; Harrison and Bates, 1991). *G. s. marica* is also smaller, is more rotund, lighter, and has a whiter face than *G. s. subgutturosa*. However, some specimens cannot be assigned with certainty to one of the two subspecies by relying on external criteria because of the intergradation zone. Some individuals from southern Iraq showed mixed characteristics of each subspecies (Harrison and Bates, 1991). Groves and Harrison (1967) also found an intergradation zone between *subgutturosa* and *marica*, situated in the Tigris-Euphrates valley. Specimens from this zone had intermediate characters in skull measurements, horn length and occurrence of horns in female.

Al Bassri and Thouless (1988) have conducted a preliminary morphometric study on the KKWRC population using horn and skull measurements. They compared eight specimens from KKWRC with museum specimens of the subspecies *marica, subgutturosa* and *hillieriana*. Despite the small sample size and the methodological biases, it was shown that the KKWRC specimens' measurements were closest to the *marica* subspecies.

- **Cytogenetic analysis:** The two subspecies normally have different numbers of chromosomes: 30, 31 for female and male *subgutturosa* respectively (Wurster, 1972) and 32 and 33 chromosomes for *marica* (Kingswood and Kumamoto, 1988).

Cytogenetic studies performed on the North American zoo population of sand gazelles, originating from Jordan, found a chromosomal polymorphism involving two acrocentric pairs of chromosomes (Kingswood and Kumamoto, 1988). The same polymorphism was discovered, with different frequencies, in the captive populations at Qassim and at KKWRC by further studies (Granjon et al., 1991; Vassart et al., 1993b). This results in a variation in the possible number of chromosomes, with females having a diploid chromosome number of either 30, 31 or 32, and males having either 31, 32 or 33.

There are two different hypotheses about the origin of this chromosomal polymorphism, inducing two controversial views about reintroduction policy. First, the polymorphism could be the consequence of the introduction of individuals of the *subgutturosa* subspecies into the *marica* population (Granjon et al., 1991). In this case, the hybrid individuals should not be used for reintroduction, since they are not pure *marica*. The second hypothesis is that the polymorphism could occur naturally as the result of a Robertsonian translocation. A similar polymorphism has already been found in some wild populations of impala *Aepyceros melampus* (Wallace and Fairall, 1967) and waterbuck *Kobus ellipsiprymnus* (Ryder et al., 1990). In the Arabian sand gazelle, such a polymorphism could be further complicated by a natural chromosomal cline between *G. s. subgutturosa* and *G. s. marica*, with a zone of intergradation and populations with different chromosome numbers in the north and south of Arabian peninsula. According to this hypothesis, the diploid number 32/33 would then become more common along a gradient towards the southern end of the Arabian peninsula, and the diploid number 30/31 less common. The Arabian sand gazelles in Oman would presumably all be 32/33. A similar cline has already been found in the Iranian wild sheep (Valdez et al., 1978), which has two cytologically distinct populations and a hybrid zone including individuals with heterogeneous and intermediate karyotypes. If this hypothesis is valid,
then animals with different karyotypes can be reintroduced, since they constitute part of the natural variability.

The only way to solve the problem was to karyotype rheem from wild populations. Such a study was initiated by KKWRC and, to date, eight wild rheem caught in Al-Khunfah have been karyotyped. The Robertsonian translocation was found in four wild-caught females (2n=31) and in two males (2n=31; 2n=32), indicating that this polymorphism is a natural phenomenon. It is planned to capture a larger number of animals from Al-Khunfah to provide a more comprehensive picture.

The polymorphism does not appear to confer a reproductive disadvantage. A study of spermatogenesis did not indicate any problem with male reproductive fitness associated with the different chromosome numbers (Kingswood, pers. comm.).

- **Protein electrophoresis:** A study on 20 blood allozyme loci was performed by Granjon et al. (1991) on 30 animals originating from KKWRC. The results will need to be compared with an allozyme study of *G. s. subgutturosa*.

- **Restriction mapping of mitochondrial DNA:** Although not yet undertaken this study would be of tremendous help in defining more clearly the taxonomic relationships between the different subspecies. It should be performed with specimens of known origin. If no live animals can be sampled, DNA could be extracted from museum material.

The data presented above gave convergent information concerning the taxonomic status of the two subspecies with identical implications for the reintroduction of rheem from KKWRC and Qassim captive populations. The historical distribution suggests some overlap between *G. s. subgutturosa* and *G. s. marica*. The morphological study of KKWRC specimens confirms that they belong to *marica*. The natural chromosomal polymorphism also found in the Al-Khunfah rheem population raises serious doubts about the hypothesis of hybridism in captivity. All this information suggests the existence of a north-south cline between the two subspecies.

Thus, KKWRC and Qassim captive rheem populations can be objectively considered suitable for reintroduction into Saudi Arabia. Animals with different karyotypes could also be reintroduced, as part of the natural polymorphism occurring in the wild (Robinson and Elder, 1993).

- **Recommendations:** Additional studies would be helpful to obtain a better picture of the distribution and genetic distance between the two subspecies and to clarify the hypothesis of a cline.

1) The study initiated by Al Bassri and Thouless (1988) should be continued, by comparing the data of Groves (1969) with a larger sample of captive specimens from Qassim and KKWRC, museum specimens and specimens collected in the wild in Harrat al-Harrah and Al-Khunfah.

2) Genetic distances between *G. s. subgutturosa* and *G. s. marica* should be estimated by the use of electrophoresis and mitochondrial DNA techniques. For *G. s. marica*, individuals from Al-Khunfah or Harrat al-Harrah should be sampled.

3) A study of the genetic status (morphometrics, karyotype, molecular techniques) of rheem in the south of the Arabian peninsula would help to clarify the distribution of both subspecies. It would also help to answer the question of the taxonomic cline. A co-
operative programme could be set up with Omani authorities to obtain samples. Museum specimens from the south of Saudi Arabia, Oman or Yemen could also be used.

The mountain gazelle (Gazella gazella Pallas, 1766)

- The problem: The mountain gazelle includes a large number of subspecies and covers a wide range. In an earlier classification, G. cuvieri of North Africa and G. bennetti of India were both classified as subspecies of G. gazella (Schwarz, 1937; Ellerman and Morrison-Scott, 1951). Both taxa were later assigned true species status because of morphological and cytogenetic characteristics (Groves, 1969; Kumamoto and Bogart, 1984 for G. cuvieri; Furley et al., 1988 for G. bennetti). Seven subspecies are currently recognized:

G. g. gazella: This large, dark gazelle occurs in the mountains of northern Israel, southern Lebanon and the border areas of Syria (Groves, 1985).

G. g. cora: This is the common form, known as the Arabian gazelle, once occurring throughout all the Arabian peninsula. The dividing line between G. g. gazella and G. g. cora in the north of the peninsula is not clear since no museum specimens have been collected in the northern half of Saudi Arabia (Thouless et al., 1991). It has been suggested that this taxon could be the Arabian representative of G. dorcas (Groves, 1989). This hypothesis was refuted by cytogenetic studies (Vassart et al., 1993a). Wild populations of mountain gazelles, G. g. cora, are very scattered in Saudi Arabia. They occur in the foothills of the Asir mountains, in the Tihama coastal plain and in the Hejaz, in most places at low density. They are also present in small numbers in both protected areas in the north, Harrat al-Harrah and Al-Khunfah. It is not sure whether these latter populations belong to cora or gazella subspecies. Thousands of G. g. cora are reported from Oman (Thouless et al., 1991).

G. g. farasani: Described by Thouless and Al Bassri (1991), and restricted to the Farasan Islands, approximately 80 km off the coast of southern Saudi Arabia in the Red Sea. The population of the Farasan Islands, divided among three islands and numbering at least 500 individuals (Flamand et al., 1988), is now well protected and may soon be limited by density-dependent effects.

G. g. erlangeri: This small dark-coloured gazelle is in the process of being described by Groves et al. (in press) as a subspecies of G. gazella. However, its taxonomic relationships with other taxa, especially the Bilkis gazelle, G. bilkis, need to be clarified (Greth et al., 1993). Although no reliable data concerning the distribution of this taxon are available, it probably occurs in Yemen and possibly also in the south-west of Saudi Arabia.

G. g. acaciae: Restricted to southern Israel and considered endangered, only one small population is known.

G. g. muscatensis: Restricted to the coastal strip of northern Oman.

G. g. ssp.: In the process of being described as a subspecies from Farrur island in Iran by Karami and Groves (1992).

A captive population of about 200 mountain gazelles is maintained at the KKWRC. The origin of the founder individuals is unknown. A reintroduction project has been initiated in the Ibex Reserve at Hawtat Bani Tamim, where about 50 mountain gazelles bred at the KKWRC have been released.
Again some questions, related to the validity of the different subspecies of *G. gazella* on the Arabian peninsula, and subsequent management options, arise.

1) Should *G. g. cora* and *G. g. gazella* be considered as two valid subspecies?

2) How can we assess the subspecific status of the KKWRC collection? In which geographic areas are these animals suitable for reintroduction, given the historical distribution of the different subspecies in Saudi Arabia?

3) What is the genetic distance between *G. g. farasani* and *G. g. cora*? Could we use the surplus animals of the Farasan Islands for reintroduction on the mainland?

4) What is the real taxonomic position of *G. g. erlangeri*? Depending on this, is its protection a high priority?

**Data synthesis**

- **Natural history information**: The mountain gazelle is more or less a sedentary species. Males are typically solitary and territorial and females live in small groups (Mendelsson, 1974). They seem to have occupied a wide range of habitats of the Arabian peninsula, occurring at lower density in sandy areas (Thouless. et al., 1991). Very little information is available on the biology and ecology of the different subspecies in Saudi Arabia.

  Different hypotheses have been proposed to explain the existence of the Farasan gazelle. The gazelles may have been isolated from the mainland during the last Ice Age about 15,000 years ago (Thouless and Al Bassri, 1991). This period represents quite a short time on the biological scale of evolutionary change (about 10,000 generations). Another hypothesis suggests that the population originated from a few founders brought in by fishermen to establish a primitive game ranching operation. In this case, the validity of the subspecies would be doubtful, because of the short period of time over which the speciation process has occurred. Genetic drift due to the founder effect could alone explain the morphological differences found between *G. g. farasani* and *G. g. cora*. It is very likely that some introductions of gazelles have recently occurred from the mainland.

- **Range and distribution data**: Two subspecies of *G. gazella* are distributed on a north-south axis, with *G. g. gazella* in Israel, Lebanon and Syria and *G. g. cora* in the Arabian peninsula. Considering ecological variations in this gradient and climatic changes, the concept of subspecies can be easily understood with adaptation to local conditions. However, data about the former distribution of *G. gazella* subspecies are very imprecise.

  Most of the museum specimens of the Arabian gazelle, *G. g. cora*, come from the western part of the country but reports exist from many other parts of the country as well (Thouless et al., 1991).

- **Morphometrics**: *G. g. gazella* is larger than *G. g. cora*. The coat is said to be lighter than in *G. g. cora*. The horns of *G. g. cora* are also more lyrate and narrower across the base than in *G. g. gazella* (Groves, 1969).

  Al Bassri and Thouless (1988) conducted a study on the KKWRC mountain gazelle population. Measurements from eight skulls were compared with *G. g. gazella* and *G. g. cora*
museum specimens (data extracted from Groves, 1969). Their results seem to indicate that the G. gazella population of KKWRC belongs to the Palestinian subspecies gazella.

The description of G. g. farasani is mainly based on skull measurements from a sample of 13 specimens (or even less depending on the characters considered and the state of the skulls) that were compared with G. g. cora specimens from the British Museum of Natural History (Thouless and Al Bassri, 1991).

With its small size and dark coat, G. g. erlangeri seems different from the other subspecies of G. gazella in its phenotypic appearance.

- **Cytogenetic analysis:** So far, all the individuals from the subspecies studied (eight gazella, eight cora, 22 erlangeri, three farasani) have had the same diploid number by conventional staining: 34 chromosomes for the females and 35 for the males (Vassar et al., 1993a). Chromosomal polymorphisms have not been found in these taxa. This supports their assignment to the same species. Banding techniques also confirm that they all are closely related taxa (Vassar et al., 1993a).

- **Protein electrophoresis:** An allozyme study based on 18 loci showed that G. g. gazella, G. g. cora, G. g. erlangeri and G. g. farasani appear to be genetically similar. The levels of observed differences in allelic frequencies are similar to those observed between separate geographic populations in other ungulates considered as separate subspecies (Vassar et al., 1994). These results support their classification as different subspecies of G. gazella.

- **Restriction mapping of mitochondrial DNA:** No data are currently available for the different subspecies of G. gazella.

- **Recommendations:** Our knowledge about the different subspecies of G. gazella is much weaker, and the subspecific level more complex, compared with rheem. There are a large number of subspecies of G. gazella, inhabiting a wide range of ecological conditions, and several relict populations occur. A reassessment of the validity of the different subspecies should be the first step in any reintroduction or restocking project.

1) The genetic distance between G. g. gazella and G. g. cora and their status as distinct subspecies should be reassessed. Samples of G. g. gazella should be obtained from the Palestinian populations. Samples of G. g. cora should be obtained from populations in the south-west of the Arabian peninsula and Oman. These samples should be compared with some taken from specimens from Al-Khunfah and Harrat al-Harrah, to determine the subspecific status of the mountain gazelle populations found in these areas. Hairs, cell cultures, blood samples or organ samples could be used to extract and amplify the mitochondrial DNA.

2) The genetic relationship between the KKWRC mountain gazelle herd and G. g. gazella should be studied using mitochondrial DNA techniques. According to the results of this study, the historical distribution limit between G. g. cora and G. g. gazella and their subspecific status, a geographic range for the reintroduction of KKWRC animals should be defined - assuming reliable data can be gathered.
3) Considering the threatened status of relict populations of *G. g. cora* due to overhunting, particularly in the south-west of Saudi Arabia, and the fact that no captive population exists, immediate conservation measures including detailed surveys and the establishment of protected areas should be a high priority for NCWCD. A captive population could be established at KKWRC by capturing the remaining individuals of non-viable populations, if the subspecific status of *cora* is validated. The subspecific status of the populations occurring in Oman should be verified to ensure that the subspecies is safeguarded on an international level.

4) The confirmation of the subspecies *farasani* should be reviewed with caution considering the different hypotheses concerning the origin of this population and the small sample size of the skulls examined. Molecular techniques based on mitochondrial DNA should be applied to estimate the genetic distance and the approximate time of speciation separating *G. g. farasani* and *G. g. cora*. The results would allow conservationists to take a sensible position concerning the translocation of founders from the Farasan population for restocking or reintroduction purposes on the mainland.

5) In view of the morphological characteristics of *G. g. erlangeri*, a taxon believed to be endemic to Saudi Arabia and Yemen, taxonomic studies should be encouraged to evaluate genetic distances between *G. g. erlangeri*, *G. g. cora* and the enigmatic *G. bilki*. Depending on the results, immediate conservation actions should be implemented *in situ*.

**Conclusion**

This article has illustrated and summarized taxonomic uncertainties that may exist with subspecies classifications. Before adopting conservation measures to protect and rebuild the Kingdom’s biodiversity, we should know what we are protecting. While the subspecies dilemma should not become a philosophical debate, with its bitter enemies and its devoted supporters, it can not simply be ignored or rejected. The best approach is a case by case study for each particular threatened taxon. When all available information is gathered, and if necessary, further studies performed, a critical and objective evaluation of the subspecies validity can be made. The resources allocated to this part of the conservation process will be minimal compared to the financial investment needed for *in situ* and particularly *ex situ* programmes. Ultimately, it will help to avoid misdirected conservation measures.

The classification status of many gazelle species is currently the subject of so much controversy and research that we have to consider the subspecies level, and at the same time be aware of the risk of neglecting major taxa. Many problems have been identified concerning the Arabian peninsula taxa. In the past few years, taxonomic studies have been initiated and the first results are now available. The use of new techniques, such as mitochondrial DNA analysis, should be encouraged. This will add valuable information to permit informed management decisions.

When feasible, priority should be given to *in situ* conservation of local populations, like those of *G. g. cora* in the western part of the Kingdom. It is the safest way to protect subspecies, by respecting their natural geographic distribution.

Prior to any reintroduction programme, the genetic suitability of stock of unknown origin should be assessed as completely as possible, even if it should delay the project. Comparison with remaining wild populations is necessary to ensure genetic compatibility. A multinational strategy should be developed to ensure implementation of a coherent regional and global action plan.
Acknowledgements

This work was carried out under the auspices of H.R.H. Prince Saud Al Faisal, Prof. Abdulaziz Abuzinada, Secretary General of the National Commission for Wildlife Conservation and Development and Abdul-Rahman Khoja, Director of the National Wildlife Research Center. Jean Francois Asmodé, Phillipe Gaucher, Colin Groves, Eric Harley, Chris Hillman, Steven Kingswood, Chris Magin, Steven O'Brien, Ulysses Seal and Chris Thouless, all gave useful comments on the early draft. The authors also acknowledge Nick Lindsay and Frank Rietkerk for their constant support during this exercise.

References


6. Modern Techniques in Taxonomy and their Reliability

Eric H. Harley and Marc Vassart

Abstract: Cytogenetics is still a useful tool for taxonomy especially when modern techniques are used (single or double thymidine synchronization for example) to obtain high resolution banded karyotypes. In the present communication, examples of the recognition of species and subspecies by cytogenetic means and protein electrophoresis are given, and techniques which were in use at the National Wildlife Research Center (NWRC) in Taif, Saudi Arabia, are described. In recent years biochemical methods of DNA analysis have developed a degree of versatility and sophistication that enables their use in a whole range of new applications. One of the most rapidly developing of these is in addressing problems of relationships between organisms, and the versatility of these techniques is demonstrated by their use at levels ranging from differentiation between subspecies to interrelationships between phyla. Characteristics of the types of DNA used, an outline of methods, and their reliability, will be discussed.

Keywords: cytogenetics, protein electrophoresis, DNA analysis, taxonomy.

Introduction
Problems of relationships between species are not only of great concern for taxonomy but also from the point of view of conservation. Conventional cytogenetic techniques still offer a great deal of information to scientists, since the chromosomal constitutions of natural populations of wild mammals are poorly known. However, modern techniques based, for example, on single or double thymidine synchronization appear to be a more powerful tool than conventional ones and are greatly informative for taxonomy and conservation. Other methods involving deoxyribonucleic acid (DNA) analysis also find a whole range of applications in addressing problems of taxonomy. Different methods and their possible applications are presented in this article.

Is cytogenetics still a useful tool for taxonomy?
Cytogenetic techniques describe the number and structure of chromosomes. This was the aim of classic animal cytogenetics, but today, cytogeneticians also use the modern tools of molecular biology to locate precisely the position of genes on chromosomes. Fluorescence in situ hybridization is now the most used tool for this task. Cytogenetic laboratories around the world mainly receive funds to work on domestic animals and are studying the gene maps of cattle and pigs. Cytogenetic techniques such as resolution banding methods are also available, and can be used to describe more precisely the structures of chromosomes. It is now possible to obtain very long chromosomes by the use of thymidine synchronization on fibroblast cell culture or the use of actinomycin. For example, a conventionally banded karyotype of the Corsican deer *Cervus elaphus corsicanus* distinguished a maximum of 400 bands compared to 600-900 bands with high resolution techniques (Rubini et al., 1991). Precise descriptions of chromosomes promises the recognition of a higher degree of chromosomal differentiation between closely-related species or even subspecies. Such results have
been obtained with *Gazella gazella* species. Among Bovids, centric fusions have been the predominate chromosomal rearrangements detected by conventional techniques. By examination of high-resolution banded chromosomes, complex re-shapings of the chromosomes, such as pericentric or paracentric inversions have been found in goat, cattle and sheep (Hayes *et al.*, 1991).

**Cytogenetics and the recognition of species**

- **Bovids**: It was formerly believed that one karyotype was a characteristic of a particular species. However, with increases in sample sizes, chromosomal polymorphisms have been frequently found, e.g. in *Madoqua guentheri* and *M. kirki* (two dik-dik species) (Ryder *et al.*, 1989); Arabian oryx, *Oryx leucoryx*, (Cribiu *et al.*, 1990; Cribiu *et al.*, 1991; Vassart *et al.*, 1991); waterbuck, *Kobus ellipsiprymnus* (Ryder *et al.*, 1990); goral, *Naemorhedus goral*, Sika deer, *Cervus nippon*, Bactrian wapiti, *Cervus elaphus bactrianus*, and tufted deer, *Elaphodus cephalophus* (Shi, 1987); impala, *Aepyceros melampus*; and blackbuck, *Antilope cervicapra* (Effron *et al.*, 1976). Benirschke *et al.* (1984) found 12 different karyotypes in Soemmerring's gazelle *Gazella soemmerringi* because of different centric fusions and Arryo Nombela *et al.* (1990) have described a centric fusion in *Gazella dama*. Centric fusion leading to chromosomal polymorphism has also been found in *G. subgutturosa* (Kingswood and Kumamoto, 1988; Granjon *et al.*, 1991; Vassart *et al.*, 1993).

To be a valid criterion for the recognition of a new species the chromosomal difference between two forms has to be large enough to lead to their reproductive isolation.

- **Rodents**: Conventional techniques are still very useful for recognizing different species inside one genus, as for example, in the case of *Mastomys* from Senegal (Duplantier *et al.*, 1990). Specific assignations can be attributed partly on the basis of chromosomal characteristics: *Mastomys erythroleucus* (diploid chromosome number 2n = 38; chromosomal arm number or fundamental number FN = 52), *M. huberti* (2n = 32, FN = 44) and *M. natalensis* (2n = 32, FN = 54). Each of these karyomorphs has its own ecological characteristics; the first is a generalist species, the second is restricted to humid biotopes and the last is commensal.

Similarly Tranier *et al.* (1973) found that *Taterillus conicus* (Gerbillidae) was specifically different from *T. lacustris*, the first having 54 chromosomes and the second 28 chromosomes. Cytogenetics has also been used to recognize sibling species in the genus *Hylomyscus* (Iskandar *et al.*, 1988).

**Cytogenetics and the recognition of subspecies**

One example of the use of cytogenetics to distinguish subspecies comes from a study of the black spider monkey, *Ateles paniscus*. Two subspecies, *A. p. paniscus* and *A. p. chamek*, can be distinguished by their chromosome number: 2n = 32 in the former and 2n = 34 in the latter (De Boer and de Bruijn, 1990). The difference is most probably the result of a tandem fusion between chromosomes 4 and 13 of the original *Ateles* karyotype (2n = 34) to form a unique metacentric chromosome in *A. p. paniscus*. Even intra-subspecific karyological variation in *A. p. chamek* was detected. Cytogenetics has also been used to differentiate nine different subspecies from one single species of night monkey *Aotus* sp., previously described from its phenotype as a single species (Hershkovitz, 1983).
Is protein electrophoresis still a valid technique for systematics?

Allozyme electrophoresis can be a powerful tool in recognizing cryptic species: a single fixed genetically-determined electrophoretic difference is sufficient to recognize two cryptic species as it demonstrates that interbreeding is not occurring. A fixed difference occurs when two species fail to share any alleles at a locus. For example, if a sample of 10 individuals is considered from a population of a supposed single species consisting of five individuals homozygous for one allele at a locus and five individuals homozygous for an alternative allele at that locus (Richardson et al., 1986), the null hypothesis under test is that the 10 individuals come from a single population of a single species which is in Hardy-Weinberg Equilibrium. Estimated allele frequencies are 0.5 in both cases. The expected proportion of heterozygotes is therefore 2pq = 0.5. The probability of not obtaining any heterozygotes in a sample of 10 individuals is then 0.5^{10} = 0.00098 = 0.1%. The null hypothesis is therefore rejected. In order to be sure that the fixed difference is under simple genetic control and that the gels have not been misinterpreted, it is important that a minimum of two diagnostic fixed differences are used. As shown, sample sizes needed are surprisingly small. For three fixed differences the probability becomes 0.001^3 = 0.1%^3 = 0.0000001%. The number of loci sampled should be as large as possible. It is far more important to screen a few individuals for many loci than it is to screen many individuals for a few loci.

Among vertebrates, populations of the same species seldom differ at more than 14% of loci. Therefore allopatric populations with fixed differences at more than 20% of loci can be considered separate species. Screening of between three and five individuals per population should be enough for taxonomic purposes because electrophoretic studies of a large number of vertebrates have shown that most populations are monomorphic at an average of 85% of isozyme loci. Therefore a single individual is representative of the whole population for, on average, 85% of electrophoretic characters. Even for the 15% of loci that are polymorphic a single individual will be partly representative of the whole population. For a locus with two alleles with frequencies of 0.8 and 0.2 there is a 96% chance that a single individual will carry at least one copy of the more common allele.

Phylogenetic reconstruction

Closely related species of birds usually share electromorphs at almost all loci, so electrophoresis is not likely to aid in elucidating phylogenetic relationship between species of birds of the same genus. For most other groups of animals however, closely related species differ at an average of about 10% of loci, and electrophoresis is therefore a useful tool for elucidating species relationships. There is an upper limit of usefulness at about 60-70% divergence. The taxonomic level at which this occurs varies between groups: below the genus level for frogs; around the subfamily level among mammals. Many factors other than time since divergence might affect genetic distance estimates: the kind of proteins used, the detectability of protein differences (due to different laboratory techniques), and sampling errors (a large number of loci should be used to obtain a reliable estimate of genetic distance). Furthermore when the time since divergence between two species is great, the relationship between D and t is no longer linear. As stated by Nei (1987) "if D is too large (say D > 1) its variance becomes very large even if a substantial number of loci are studied, so that the reliability of dating declines".
It appears that protein electrophoresis is still a powerful technique for taxonomy. For example Nei (1987) showed that the resolving power of mitochondrial DNA, judged on the number of nucleotides assayed by both techniques, is not necessarily higher: 33% of nucleotide substitutions result in amino acid changes, and of these, 25% are detectable by electrophoresis, a total of 8.3% overall. There are 400 amino acids in an average protein (1,200 nucleotides in the gene), therefore electrophoresis will survey about 1,200 x 0.083 = 100 nucleotides per locus. If 30 loci are examined, protein electrophoresis is equivalent to studying 3,000 nucleotides, which is larger than the number of nucleotides sequenced in many mitochondrial DNA studies.

**DNA methods**

Animal cells contain two types of deoxyribonucleic acid (DNA), and both may be used for taxonomic purposes: 99.9% of the cell's DNA is found in the nucleus and the rest is found in the mitochondria (mtDNA). The latter evolves (i.e. accumulates mutations) at a faster rate than nuclear DNA: about five to ten times faster in mammals. This, coupled with its maternal, haploid mode of inheritance, small size (it is typically 16,000 - 17,000 base pairs in length, compared to some three billion base pairs in nuclear DNA), and ease of preparation make mtDNA very useful for addressing problems in systematics and population genetics, especially in closely related animal groups such as the gazelles.

Mutations accumulate in a stochastic (random) manner. This is an essential concept for understanding evolutionary processes and an illustration is instructive: assume that stochastic events occurring at a rate of five per minute are observed and watched for three one minute periods (it could be radioactive decay in a sample, or cars passing a point on the road). Although on average about five events per minute are observed, a measure over only one minute can give a very inaccurate estimate, for example 4, 2, or 8 events per minute (Figure 6.1). However, if the same process is observed over three ten minute periods, figures such as 41, 58, and 52, i.e. estimated rates of 4.1, 5.8, and 5.2 events per minute respectively may be obtained, which is a marked improvement in accuracy. As can be seen, the stochastic error is inversely proportional to the number of events measured.

```
1  ||  \\
2  ||  \\
3  ||  |  |
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**Figure 6.1** Graphic representation of three sequences of stochastic events occurring at a rate of five per minute.

There are many places in the DNA where mutations do not alter the way in which it is expressed. The mutations measured by DNA techniques are therefore all essentially phenotypically neutral (Kimura, 1983) since the phenotypically deleterious are eliminated by selection, and the advantageous are rare. This gives them the useful property (unlike morphological characters) of being uncoupled from selective pressures. Thus measurements of divergence between the DNA of any two taxa gives a useful estimate of the time since they diverged from their common ancestor, provided enough mutational events are recorded to reduce the stochastic error to an acceptably low value. This will be on a relative time scale unless appropriate calibration of the mutation rate (the
"molecular clock") has been established, e.g. from a good fossil record, for the group under study. A number of practical approaches to obtaining measurements of DNA divergence are outlined below:

- **The Restriction Fragment Length Polymorphism (RFLP) approach:** This is a quick and easy technique, of low penetrance (i.e. it will not "see" far into the past) but good for obtaining a quick indication as to whether two populations justify specific or sub-specific status. The RFLP patterns produced (by one enzyme only - normally 10-20 would be used to give a range of patterns) for three taxa are illustrated in Figure 6.2. Taxa 1 and 2 share nearly all the bands, suggesting a close relationship. Taxon 3 shares only one band with the others, suggesting a more distant relationship. A distance estimate comparing these taxa measures the proportion of shared bands (restriction fragments) in a pairwise manner, summing over all the restriction enzymes used. This method is not good for cladistic analyses since it violates the assumption of independence of characters required by the cladistic approach (i.e. a fragment in one taxon may be equivalent to two in another taxon if the latter has a new restriction site in the former fragment). Fingerprinting is an equivalent approach used on nuclear DNA and has great potential for population genetic studies. However, it is still fraught with methodological and interpretive problems (Lynch, 1988) which will limit its use until methods improve.

```
  1      2      3
       -      -      -
       -      -      -
       -      -      -
       -      -      -
       -      -      -
```

*Figure 6.2  Schematic Restriction Fragment Length Polymorphism patterns produced by one enzyme for three different taxa.*

- **Restriction site mapping:** This is a development of the RFLP method in which the sites where the restriction enzymes cut are mapped to a linear or circular representation of, for example, the mitochondrial genome. This method has better penetrance, but is much more time consuming. However, it does provide good characters for cladistic analyses. RESOLVE (Harley, 1992), a computer programme designed to produce, store, manipulate, and perform phylogenetic analysis on restriction data, is an invaluable asset and time-saver.
- **Sequencing:** With the advent of the Polymerase Chain Reaction (PCR) (Saiki, 1988) this most versatile of the DNA-based techniques is becoming more practicable for the general biochemical or biological laboratory. The PCR technique has two key features:
  a) Specificity: The ability to select precisely the segment of DNA studied from the three billion or so bases of the typical mammalian genome.
  b) Amplification: The ability to amplify the segment of DNA selected by over a million-fold in a matter of an hour or so, to give sufficient quantities of DNA for sequencing.

Sequencing is not a difficult method to apply, although it needs some skills, understanding of basic biochemistry, and experience. It is surprisingly effective even on poor quality or old starting material. Figure 6.3 illustrates DNA sequence data from three related taxa which have been aligned - not always a trivial task - to provide data for either distance measures (counts of the pairwise proportion of shared bases) or cladistic characters (although the latter will always require at least four taxa in the analysis). Taxa 1 and 2 have two base differences giving a proportion of shared bases of $30/32 = 0.94$, or a sequence divergence of $(1-0.94) \times 100 = 6\%$. Taxa 1 and 3 show a 22\% sequence divergence, as do taxa 2 and 3. Given time, sequencing can provide unlimited amounts of data for use at all levels of investigation, but is of most use in detailed systematic studies.

1. GGACTGAGTCTCTCTAAAAGCTAGCATGGATC
2. GAACCTGAGTCTCTCTCAAGAGCTAGCATGGATC
3. GAATCGAGTTCTCCTGAAAAGGCTAGCAAGGATC

**Figure 6.3** Schematic illustration of DNA sequence data from three related taxa which have been aligned to provide data for either distance measures or cladistic characters.

**Conclusion**

Although DNA-based methods provide large quantities of objective data for cladistic or distance based studies, they are not infallible. With more distantly-related taxa, the data sets can present many homoplasies. This impairs the ability of cladistic (e.g. maximum parsimony) methods to reveal the correct topology. For closely related-taxa, accumulating sufficient data to overcome stochastic error is difficult, and this impairs the ability of distance-based methods to reveal the correct topology even when the rate of change in the DNA is the same (see Figure 6.1). DNA methods are best seen as an excellent complement to morphological, cytogenetic and allozyme approaches. Taken in this context, provided the appropriate quantity and quality of data are selected and analyzed correctly, DNA approaches are becoming increasingly valuable in providing answers of practical value in conservation management.

**Acknowledgements**

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References


7. Chromosomal Evolution in Gazelles and its Relevance to Conservation

Steven C. Kingswood and Arlene T. Kumamoto

Abstract: Chromosomes of gazelles (genus Gazella) vary in diploid number (2n) from 30 to 58. The fundamental number (FN) has been reported to range from 58 to 72. Chromosomal evolution in the genus is believed to have been predominated by Robertsonian translocations of the centric fusion type. Autosome-to-sex chromosome translocations have been documented in all species in which banding analyses have been conducted. Comparative cytogenetic studies support affinities, as established by morphological data, between certain taxa of gazelles. Chromosomal studies are unique in their ability to quickly document the complete genetic constitution of an organism, albeit at a gross level of resolution. Intraspecific chromosomal variation demonstrated in G. dama, G. soemmerringi, and G. subgutturosa illustrates the importance of cytogenetics in identifying biological diversity not detectable through other measures. Chromosomes have a major role in the concept of biological species because of the potential for chromosomal rearrangements to effect reproductive isolation. Thus, conservation efforts aimed at preserving biological diversity are served by studies that document chromosomal variation in gazelles.

Keywords: Gazella, chromosomes, evolution, cytogenetics, conservation, wildlife management.

Introduction

Nine taxa of gazelles (genus Gazella) are currently recognized by the World Conservation Union as threatened (IUCN, 1990). Conservation efforts for gazelles are complicated, however, by the uncertain taxonomy of the genus. Reviews by Gentry (1971), Corbet (1978), and Groves (1988) place 12 to 16 species in the genus Gazella, and taxonomic revisions based on morphological data continue to be made on a regular basis. Cytogenetic studies have demonstrated considerable chromosomal variation among gazelles, both interspecifically and intraspecifically, but the relationships between chromosomal and morphological variation are complex and not well-understood. However, chromosomal variation is well-established as a potential reproductive isolating mechanism, and the identification of chromosomal variation serves in the identification of biological species. Cytogenetic studies are relevant to conservation through the identification of biological diversity that may not be apparent morphologically and in documenting potential reproductive isolation among chromosomally divergent populations. The purposes of this paper are to discuss chromosomal evolution in gazelles, comparing the evolutionary implications of these data with taxonomic relationships inferred from morphological data, to discuss the role of chromosomes in the biological species concept, and to establish the relevance of chromosomal studies to the conservation of gazelles.
Chromosomal evolution in gazelles

Chromosomes of Gazella vary in diploid number (2n) from 30 in female G. dorcas, G. granti, and G. subgutturosa, to 58 in G. rufifrons and G. thomsoni (Table 7.1). Variation in diploid number among gazelles is primarily the result of fusions or fissions between chromosomal arms. This is evidenced by the fact that the chromosomal arm number (commonly referred to as the fundamental number or FN) for gazelles has little variation. The FN is usually 58 to 62 but may be higher in G. thomsoni and G. saudiya (Table 7.1). Compound sex chromosomes, formed by the fusion of an autosome (i.e. a chromosome other than a sex chromosome) to the X and/or Y chromosome, are common among gazelles. The findings of all known chromosomal studies of gazelles are summarized in Table 7.1.

Todd (1975) proposed that chromosomal evolution in artiodactyls, including gazelles, has been predominated by karyotypic fissioning, whereby metacentric (bi-armed) chromosomes of putative ancestors split at their centromeres. This resulted in an increase of the number of chromosomes as fission of a metacentric produced two acrocentric (single-armed) chromosomes. However, the most widely accepted theory emphasizes centric fusion events. Centric fusion between two acrocentrics would produce a single metacentric chromosome and result in lowering the diploid number. Chromosomal rearrangements of autosomes that involve centric fusions are often termed Robertsonian translocations.

In studies of mammalian karyotypic evolution, Robertsonian translocations are the most frequently encountered chromosomal rearrangements. Gallagher and Womack (1992) presented evidence supporting centric fusions as driving chromosomal evolution in the family Bovidae. Chromosomal evolution in the form of Robertsonian translocations has resulted in both interspecific and intraspecific variation in the diploid number of gazelles. Variation in the diploid number between gazelles of the subgenus Nanger (G. granti, G. soemmerringi, and G. dama) can be attributed to four Robertsonian rearrangements and an autosome-to-Y chromosome translocation. Intraspecific variation in the diploid number of G. dama, G. soemmerringi, and G. subgutturosa is due to Robertsonian translocations (Effron et al., 1976; Benirschke et al., 1984; Benirschke and Kumamoto, 1987). G. dama and G. subgutturosa are polymorphic for single centric fusions; G. soemmerringi is polymorphic for three centric fusions. It is important to note that Robertsonian translocations involve a change in the structure of the chromosomes, but do not involve loss or gain of genetic material, except for theoretical loss of minute centromeres.

Autosome-to-X chromosome translocation is another common chromosomal rearrangement found in gazelles. Twelve species studied to date have a compound X chromosome (Table 7.1). Previous studies did not identify G. thomsoni as having the autosome-to-X chromosome translocation, but banding analysis resulting in higher resolution of chromosomal structure indicates that G. thomsoni possesses this translocation (Kumamoto, unpublished data). This rearrangement involves the fusion of an acrocentric autosome to the X chromosome. Since males have only one X chromosome, one member of the autosomal pair remains unfused, and this usually results in males having an additional chromosome. However, in G. soemmerringi, G. dama, G. rufifrons, and G. thomsoni, an autosome-to-Y chromosome translocation also exists, giving these species compound X and compound Y chromosomes (Table 7.1). Analyses of G-banded karyotypes indicate that the autosome translocated to the X chromosome is the same in G. soemmerringi (Benirschke et al., 1984), G. subgutturosa (Kingswood and Kumamoto, 1988), G. dama (Arroyo Nombela et al., 1990),
and *G. gazella* (Vassart *et al*., Article 9). This suggests that the autosome-to-X chromosomal translocation may have occurred once during the evolution of gazelles.

**Table 7.1** Chromosomal data for gazelles. Species are listed and grouped following Groves (1985).  
2n = diploid number; F/M = females/males; FN = fundamental number, which includes sex elements;  
A = number of acrocentric chromosomes; M = number of metacentric chromosomes;  
X and Y = structure of sex chromosomes A (acrocentric), M (metacentric),  
cA (compound acrocentric), cM (compound metacentric).

<table>
<thead>
<tr>
<th>Gazella</th>
<th>2n (F/M)</th>
<th>FN</th>
<th>A</th>
<th>M</th>
<th>X</th>
<th>Y</th>
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<tr>
<td><em>granti</em></td>
<td>30/31</td>
<td>60</td>
<td>0/1</td>
<td>28</td>
<td>cM</td>
<td>A</td>
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<tr>
<td></td>
<td>30/31</td>
<td>60</td>
<td>0/1</td>
<td>28</td>
<td>cM</td>
<td>A</td>
<td>Benirschke, 1985</td>
</tr>
<tr>
<td></td>
<td>30/31</td>
<td>60</td>
<td>0/1</td>
<td>28</td>
<td>cM</td>
<td>A</td>
<td>Gallagher and Womack, 1992</td>
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<tr>
<td></td>
<td>30/31</td>
<td>60</td>
<td>0/1</td>
<td>28</td>
<td>cM</td>
<td>A</td>
<td>Benirschke <em>et al</em>., 1984</td>
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<tr>
<td><em>soemmerringi</em></td>
<td>34 to 39</td>
<td>60</td>
<td>8 to 20</td>
<td>18 to 24</td>
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<td>cM</td>
<td>Wurster and Benirschke, 1968</td>
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<td><em>dama</em></td>
<td>38</td>
<td>60</td>
<td>16 to 22</td>
<td>18 to 20</td>
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<td>A</td>
<td>Effron <em>et al</em>., 1976</td>
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<td>60</td>
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<td>28</td>
<td>M</td>
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<td></td>
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<td>62/61</td>
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<td>Hsu and Benirschke, 1974</td>
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|                | 32/33    | 60  | 4/5  | 26  | cM | A | Effron *et al*., 1976   | 79
If the karyotype is adaptive as other biological characteristics are to an organism, the chromosomal constitution of a taxonomic group of organisms can be expected to demonstrate evolutionary trends. This pattern of chromosomal evolution is referred to as karyotypic orthoselection (White, 1973). The numerous Robertsonian translocations found in the Bovidae are a good example of karyotypic orthoselection at the family level. Autosomal-to-sex chromosome translocations are common rearrangement patterns found in two bovid genera, *Tragelaphus* and *Gazella* (Wurster, 1972; Effron et al., 1976; Wallace, 1978). Wurster (1972) has documented similar relationships between characteristics of the sex chromosomes and taxonomic groups in other subdivisions of mammals.

Chromosomal variation among gazelles is considerable, both interspecifically and intraspecifically, but observed relationships between chromosomal and morphological variation can only be explained on theoretical grounds. For example, chromosomal evolution among marine mammals (cetaceans and pinnipeds) demonstrates phylogenetic relationships; however, the karyotype has not evolved in the same way as anatomical and physiological characteristics. Arnason (1972) attributed this to two factors; their reproductive biology (late sexual maturity) and ecology (mobility in a relatively uniform environment). Because of these factors, the chances are unlikely that two individuals with the same chromosomal rearrangement will meet and become founders of a population with a new karyotype.

In contrast to marine mammals, the reproductive biology and ecology of gazelles would seem to favour karyotypic change. Sexual maturity in gazelles is reached at an earlier age than in marine mammals. Perhaps most influential in the development of karyotypic diversity among gazelles were the series of Pleistocene climatic changes in Africa and Asia that diversified the environment by fragmenting habitats (Bishop and Clark, 1967). Savannas inhabited by gazelles receded due to the advance of forests during alternating periods of dry and moist climates. These geologically recent events might explain the interspecific karyotypic diversity among gazelles as the geographic isolation of populations facilitated the fixation of chromosomal rearrangements. Intraspecific chromosomal variation observed in *G. dama*, *G. soemmerringi* and *G. subgutturosa* indicate that the fixation of existing chromosomal rearrangements in some gazelle populations is not complete.

Cytogenetics can reinforce, or even clarify, evolutionary relationships postulated on the basis of morphological studies. For example, Thomson's gazelle *G. thomsoni* has historically been considered a separate species from the red-fronted gazelle *G. rufifrons*. Groves (1985) contended, however, that Thomson's gazelle was a subspecies of the red-fronted gazelle with "a chain of gradually changing subspecies which simply cannot be broken up into species". Chromosomal re-evaluation of Thomson's gazelle (Kumamoto, unpublished data) along with recent preliminary data from the red-fronted gazelle (Kumamoto et al., unpublished data) seems to support the contention of Groves (1985) that they are conspecific. Cytogenetic data also support relationships of *G. cuvieri* to *G. leptoceros* and *G. subgutturosa* based on skull measurements (Groves, 1985). G-banded karyotypes of *G. cuvieri* and *G. leptoceros* are nearly identical (Kumamoto and Bogart, 1984).

The systematic value of G-band studies has been reviewed by Baker et al. (1987). In phylogenetic analyses, variation in G-band patterns among taxa can be used as character states. Evolution of chromosomal rearrangements can be determined through the identification of primitive character states. Cladistic methods utilizing data from G-bands can be used to test phylogenetic relationships inferred from other data sets, such as morphology, protein electrophoresis, or DNA
analysis. Systematic relationships based on chromosomal evolution can independently challenge
traditional taxonomic groupings based on morphological specializations.

In a growing number of mammalian species complexes, chromosomal variation between
populations exceeds apparent morphological variation. If chromosomal variation reproductively
isolates morphologically similar, or even identical, populations, they are referred to as cryptic, or
sibling, species (Mayr, 1942). Reproductive isolation between two karyotypically distinct, but
morphologically indistinguishable, forms of the antelope *Madoqua kirki* has been demonstrated by
Ryder *et al.* (1989) in captive animals; suggesting the existence of cryptic species within this taxon.
The extensive chromosomal divergence among captive *G. soemmerringi* is believed to be responsible
for their poor reproduction in captivity (Benirschke and Kumamoto, 1991). Unfortunately, the origin
of these gazelles is unknown, making it impossible to correlate the observed chromosomal divergence
with geographical populations. The important point to recognize, however, is that biological
diversity in the form of chromosomal divergence can only be identified through cytogenetic studies.

**Biological Species Concept**

Chromosomal variation has the potential to effect reproductive isolation between populations. The
Biological Species Concept stresses that populations be reproductively isolated and possess a genetic
programme effecting such isolation (Mayr, 1970). Although the degree to which chromosomal
rearrangements operate in reproductive isolation varies among groups of organisms (White, 1978) the
rate of speciation is clearly associated with the rate of chromosomal evolution in vertebrates (Fredga,
1977). In mammals, rates of speciation and chromosomal evolution are strongly correlated (Bush *et al*.,
1977). Only rearrangements which can potentially result in chromosomal underdominance
(inferiority of heterozygotes, in comparison to homozygotes, with respect to characters such as
fertility) can play a role in speciation processes (King, 1987). Chromosomal underdominance of
translocation heterozygotes has been demonstrated in humans (Speed, 1989) mice (*Mus musculus*; De
Boer and De Jong, 1989) and domestic cattle (*Bos taurus*; Dyrendahl and Gustavsson, 1979). The
1/29 Robertsonian translocation that reduces fertility in cattle is of particular interest in considering
the fertility of gazelles with Robertsonian translocations. Poor reproduction of captive *G.
soemmerringi* is believed to be due to the "incompatibility" of 14 chromosomal cytotypes involving
three Robertsonian translocations (Benirschke *et al*., 1984; Benirschke and Kumamoto, 1991).

There is a deficiency of empirical data, particularly from wild populations, to test theoretical
aspects of mammalian chromosomal evolution (Baker *et al*., 1987). Many studies have reported
various translocations in domestic animals, and effects of these different translocations on
reproductive fitness varied intraspecifically and interspecifically (Long, 1988). It has been suggested
that the slow but positive increase of translocations in most domestic mammal species might be due
to a slight heterozygous advantage (heterosis). Another possibility is that the rearrangement in
heterozygotes is favoured through non-random assortment of chromosomes during meiotic
segregation. This has been documented in *G. subgutturosa* heterozygous for centric fusions
rearrangements may affect reproductive fitness in one organism but not in another, and the study of
meiosis is one key to determining the influence of chromosomal variation upon the reproductive
process.
Formation of normal gametes is dependent upon proper progression of chromosomal events at meiosis (Moses, 1980). Chromosomal homology is necessary for meiotic pairing and recombination; prerequisites to segregation, production of chromosomally balanced gametes, and reproductively fit individuals. The level of chromosomal homology required for recombination seems to be influenced by the particular species involved and the degree to which homology has been changed, or reduced, by chromosomal rearrangement. *G. dorcas* and *G. gazella* differ chromosomally by two Robertsonian translocations. They have hybridized in captivity when a *G. gazella* dam was involved; F₁ females had reduced fertility and males were sterile (Wahrman et al., 1973). However, based on extensive breeding records, reproductive fitness of sheep (*Ovis aries*) was not affected by three different Robertsonian translocations that produced heterozygotes with two to five translocation chromosomes (Bruere and Ellis, 1979).

Autosome-to-X chromosome translocations often have a considerable detrimental effect on fertility. Germ-cell death during meiosis is typical for male autosome-to-X translocation heterozygotes in humans (Speed, 1989) and mice (De Boer and De Jong, 1989). In cattle, there have been few reports of autosome-to-X translocations (Long, 1988), but reduced fertility was observed in female cattle heterozygous for an autosome-to-X translocation (P. K. Basrur, pers. comm.). However, autosome-to-sex chromosome translocations in two species of marsupials (Sharman, 1961) and several species of the rodent family Gerbillidae (Viegas-Péquignot et al., 1982) apparently do not reduce fertility. Occurrence of autosome-to-X translocations in 12 gazelle species studied to date (Table 7.1) suggest that pairing of the sex chromosomes is not disrupted. Meiotic studies in *G. subgutturosa* males, having both a Robertsonian and an autosome-to-X translocation, give no indication of reduced fertility in heterozygotes (Kingswood, 1992). Thus, chromosomal rearrangements can define potential reproductive isolation between karyotypically divergent populations, but are limited in defining reproductive isolation by the variability of meiotic systems.

Baker and Bickham (1986) have proposed a model of chromosomal speciation by monobrachial centric fusions in which fixation of single Robertsonian translocations is facilitated in populations by normal segregation and minimal meiotic problems. The model is based on the fixation of single fusions, involving different acrocentric chromosomes, by geographically-isolated populations. If secondary contact between the populations leads to hybridization, metacentric chromosomes having monobrachial homology (i.e. homology limited to only one of the two chromosomal arms) may experience meiotic problems. The finding that single Robertsonian translocations do not appear to cause meiotic problems in male *G. subgutturosa* (Kingswood, 1992) is consistent with this model. Extensive monobrachial homology among gazelles and other bovid taxa (Effron et al., 1976; Gallagher and Womack, 1992) suggests the involvement of monobrachial centric fusions in their speciation.

Relevance to conservation

From a conservation standpoint, it is important to recognize and preserve chromosomal variation simply because it exists. There is a need to consider quantitative measures of taxonomic distinctness in conservation (May, 1990), and chromosomal variation can and should be used with other measures to quantify biodiversity. The role of chromosomes in effecting reproductive isolation and biological speciation makes cytogenetics an important tool in identifying species diversity. As a practical application, cytogenetics can identify cryptic chromosomal variation that might jeopardize
management efforts, whether management involves captive breeding or the translocation of animals between geographically-distant populations (Robinson and Elder, 1992).

The application of chromosomal studies to conservation efforts for gazelles involving captive breeding has been discussed by Ryder (1987) and Benirschke and Kumamoto (1991). For example, the poor reproduction of captive G. *soemmerringi* is believed to be due to the "incompatibility" of different chromosomal cytotypes. As a result of the difficulty in identifying gazelle taxa, conservation programmes involving captive breeding have occasionally produced hybrids by unwittingly grouping individuals representing different species or subspecies. The captive population of *G. subgutturosa marica* in the United States was originally believed to represent *G. gazella*, and clarification of the taxonomic status of these gazelles was aided by chromosomal study (Kingswood and Kumamoto, 1988).

Most of our knowledge regarding chromosomal evolution in gazelles has been obtained from the study of a few specimens in captivity. The small sample sizes of these studies have probably not demonstrated the full range of chromosomal variation present in wild populations. Given the human threats to gazelle populations and the importance of cytogenetics in the identification and conservation of biological diversity, we believe it is important to document the karyology of all natural populations of gazelles.

Acknowledgements

Suellen Charter and Marlys Houck have given much toward the chromosomal studies of gazelles at the Center for Reproduction of Endangered Species, and the Zoological Society of San Diego has facilitated these efforts through its ongoing support of gazelle conservation and research. For the opportunity to participate in the workshop "Establishing priorities for gazelle conservation in the Arabian Peninsula", we thank the National Commission for Wildlife Conservation and Development of Saudi Arabia, particularly Prof. Abdulaziz Abuzinada, Arnaud Greth, Douglas Williamson, and Youssef Al-Wetaid. Marc Vassart, Arnaud Greth, and Wilhelmnus Rebholz gave helpful suggestions to improve the manuscript.

References


8. Use of DNA-based Methods in Mammalian Taxonomy and Population Genetics

Eric H. Harley, M. Faadiel Essop, Colleen O'Ryan, Nomusa Mda and Derek Ohland

Abstract: Examples of the use of three different methods of DNA analysis are given to illustrate their relative value in providing answers to questions of phylogenetic relationships as well as questions at the population genetic level, and to show how some of these can be of direct relevance to practical problems of conservation management. Restriction Fragment Length Polymorphism (RFLP), restriction mapping, and direct deoxyribonucleic acid (DNA) sequencing approaches are compared, with examples from studies on rhinoceros, antelopes, elephant, dolphins, and birds.

Keywords: DNA analysis, taxonomy, population genetics, conservation.

Introduction

Deoxyribonucleic acid (DNA)-based methods can be used to address many interesting aspects of systematics or population genetics in animals, plants, and micro-organisms, some with direct conservation relevance. There are a number of different approaches which can be used to implement such studies, and an outline of these approaches, and their reliability, has been discussed previously in these Proceedings (Harley and Vassart, Article 6). In this article some examples of the uses of these methods will be presented to illustrate the sort of problems which can be addressed by each of the different approaches.

Before DNA studies can be undertaken, it is necessary to obtain the appropriate tissue sample from which to extract the DNA, and to decide whether the problem is best solved using nuclear or mitochondrial DNA. In mammals, mitochondrial DNA evolves about five to ten times as fast as nuclear DNA, and has a number of properties (Harley and Vassart, Article 6) useful for studies which have conservation relevance, and the examples to be described will therefore concentrate on the use of mitochondrial DNA. This presents the investigator with a practical problem, since studies using the Restriction Fragment Length Polymorphism (RFLP) or restriction mapping approach are most easily performed using purified mitochondrial DNA. Unfortunately, such studies require significant quantities (between five and 100 g) of fresh tissue, usually heart muscle, skeletal muscle, or liver, which except in the case of the largest animals can only be obtained postmortem. However, the RFLP and to a lesser extent the mapping approach can be used on smaller samples requiring less invasive sampling procedures (blood, or cell cultures made from skin biopsies) but the more laborious Southern blotting laboratory approach is then required for analysis of the DNA. Fortunately the most powerful and versatile approach, DNA sequencing, poses the least problematic sampling problem, since almost any tissue sample is adequate. Unfortunately, the culture of cells remains an expensive technique.
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With very small dry samples or samples placed in alcohol, the Polymerase Chain Reaction (PCR) technique can be used for amplification before sequencing. In our laboratory we have found that cell cultures are an excellent medium for the long term storage of tissues from which DNA can be extracted. Being living tissue they are capable of very long term storage in liquid nitrogen, and have many other biochemical or cytogenetic uses. To date we have samples from over 150 individuals in culture representing 50 natural mammalian taxa - many of which are threatened with extinction - and three hybrids (Table 8.1). These cultures provide an invaluable and renewable biological resource. In the following sections practical examples of the application of various DNA analysis techniques are given.

The RFLP approach

Cell cultures were extracted from over forty individuals representative of four different subspecies of black rhinoceros: Diceros bicornis minor, D. b. bicornis, D. b. michaeli, and D. b. chobiensis. DNA extracted from these was restricted with fourteen different restriction endonucleases. Since total DNA was extracted, mitochondrial DNA restriction patterns required the Southern blotting technique to display them, using a radio-labelled rhinoceros mitochondrial DNA probe prepared previously from heart tissue obtained from an opportunistic death in the field. Three of the enzymes showed distinctive mitochondrial DNA morphs, illustrated diagrammatically in Figure 8.1, which were characteristic of, and monomorphic for, either the minor, the michaeli, or the bicornis subspecies, with chobiensis always giving patterns identical to minor. These RFLPs therefore provide useful markers for three of the subspecies and demonstrate a close genetic affinity of chobiensis to minor. The results also show low intra-subspecific genetic distances which suggest that outbreeding depression from mixing subspecies would be unlikely, should this ever be required to maintain
genetic diversity in a subspecies where numbers had dwindled to such low levels that inbreeding depression resulted.

Two populations of African elephant *Loxodonta africana* from the Kruger Park in the Eastern Transvaal and from the Addo National Park in the Eastern Cape Province were examined using the RFLP approach. Six individuals from Addo were darted and biopsied, with about 5g of muscle being sampled per individual. This provided enough purified mitochondrial DNA for direct analysis using twelve restriction enzymes. Whereas all patterns were monomorphic in this population, results from twelve Kruger elephants showed polymorphic patterns for three enzymes. However, the Addo patterns were always identical to one of the polymorphisms of the Kruger population, so it could be concluded that the Addo population was very closely related to the Kruger population, but that it was more inbred. Such results have direct relevance to conservation management decisions relating to translocating individuals from and between these populations.

![Figure 8.1](image)

**Figure 8.1** Diagrammatic representation of gel electrophoretic separations of restriction enzyme digests of mitochondrial DNA from 1) *D. b. chobiensis*, 2) *D. b. minor*, 3) *D. b. michaeli*, and 4) *D. b. bicornis*, using the restriction enzymes Stu I, Dra I, and Bcl I.

In contrast a similar study on two populations of *Damaliscus dorcas*, representing the well defined and morphologically distinct bontebok *D. d. dorcas* and blesbok *D. d. phillipsi*, showed genetic distances appropriate for their current subspecific status (Essop and Harley, 1991).

In summary, the RFLP approach is well suited to population genetic studies below the species level. It is also useful for the identification of cryptic species, and can be used for highlighting unexpected relationships between closely related species, as we have recently done in demonstrating affinities amongst species in the genus *Francolinus* (Crowe *et al.*, 1992).

**The Restriction Mapping approach**

This method is a development of the RFLP technique in which the sites where the restriction enzymes cut are mapped to a linear or circular representation of the mitochondrial genome. The technique is much more time consuming than the RFLP approach and is more suited to studies of systematics than population genetics. Restriction sites provide data appropriate for both cladistic analyses, sites being unweighted, unordered characters, and distance methods, since the molecular clock enables the
Figure 8.2 Illustration of the use of restriction mapping in systematics: a) Neighbour-joining distance dendrogram; b) Maximum Parsimony cladogram derived from restriction site maps of mitochondrial DNA from representatives of four bovid tribes. Numbers in a) reflect relative genetic distances, and in b) the number of synapomorphies supporting the node.
amount of change between individual species, represented by the proportion of shared sites, to be used not only to construct dendrograms, but to provide an indication as to when particular radiations took place.

For example, restriction mapping of mitochondrial DNA from both black and white rhinoceros has helped provide an estimate of their time of divergence from a common ancestor to compare with fossil evidence (O'Ryan and Harley, 1993). An illustration of the use of restriction mapping in systematics is shown in Figure 8.2. Dendrograms were constructed from mitochondrial DNA restriction maps for a number of individual bovid species taken from four tribes, Tragelaphini, Antilopini, Connochaetini and Alcelaphini, analyzed by a distance method and by maximum parsimony. In the absence of a suitable outgroup the maximum parsimony tree was rooted using information from the distance analysis. The only difference between the topologies produced by these two very different tree-building methods is in the positions of the Tragelaphine antelopes relative to each other, and the exchange of Red Hartebeest Alcelaphus caama and Tsessebe Damaliscus lunatus. It is noteworthy that in general the topologies are consistent with current classifications.

Cladograms are generally more concerned with the branching order than with branch lengths, although the number of shared derived characters supporting each node are frequently indicated, as here, and can provide an indication of relative branch length. Other statistical approaches, such as the consistency index, which here = 0.55, and the bootstrap (Felsenstein, 1985), can be used to assess the robustness or otherwise of the overall topology or of particular monophyletic groupings. The distance tree is particularly concerned with relative branch lengths, from which its estimate of the topology is derived, and if a calibration is available, can give an estimate of when lineages divided. A detailed critique of the relative merits of the two methods is beyond the scope of this article, but is the subject of much controversy (sometimes acrimonious). The major weakness of the cladistic approach for molecular data is the amount of unrecognized homoplasy in the data, and the major weakness of the distance approach is the degree of stochastic error when measuring small numbers of random events.

A similar study using the restriction mapping method was performed on mitochondrial DNA prepared from twelve members of the Odontoceti (toothed whales). Distance analyses showed surprisingly little variation between members of the Delphinidae (dolphins). This indicated an unexpectedly recent radiation in the Delphinidae, and therefore directs further study to a re-evaluation of the fossil record, or to the need for studies on the calibration of the molecular clock in marine mammals.

DNA Sequencing
This method is able to provide information at any level of phylogenetic analysis, and is the method of choice for definitive systematic studies. The ability to obtain sequence data from long dead tissues provides totally novel uses for museum material and the opportunity to demonstrate the phylogenetic affinities of extinct species. For example, DNA extracted and amplified from 14,000 year-old bones of the sabre-toothed cat Smilodon fatalis have affirmed the placement of Smilodon within the modern radiation of Felidae. The advent of the polymerase chain reaction (PCR) technique as a means of amplifying specific regions of DNA suitable for sequencing has greatly enhanced and simplified the use of DNA sequencing, making it the method of choice for many applications. Aligned DNA
sequences from related taxa provide the most direct approach to the production of character sets since the base position can represent the character, and the type of base (adenine, guanine, cytosine, or thymidine) can represent the character state. Distance matrices are readily derived from the pairwise proportion of shared bases.

Figure 8.3 illustrates the (at least initial) simplicity of evaluating DNA sequence data in a comparison of 100 bases of mitochondrial DNA from some Southern African Felidae, and gives an indication of the amount of change typically found at the generic and species level in this family. There are a number of features of note: there are changes at 18 positions; 10 of these are phylogenetically informative (marked with an *), meaning that they can be used by cladistic (e.g. parsimony) methods to construct a phylogenetic tree and require that each character state occurs at least twice, and not more than a number given by the total number of taxa less two (i.e. four in this example). The initial assumption of the cladistic approach is that at any one of these phylogenetically informative sites one of the shared bases represents a derived character state, or synapomorphy (the other representing the primitive state, or synapomorphy). The other positions represent autapomorphies and are not used by cladistic methods, (but are by distance methods).

![Figure 8.3 Comparison of 100 bases of mitochondrial DNA from some southern African Felidae.](image-url)

The major problem with the cladistic approach is the noise given by unrecognized homoplasies (parallel or reverse mutations) which are very common in sequence data. For example, the bases shared by the lion *Panthera leo* and caracal *Felis caracal*, but not by the leopard *Panthera*
*pardus,* at positions 38, 61, 64, and 79 tend to cluster these two taxa together. The lion and the leopard only share a unique character state at positions 28 and 34, although the monophyly of these two is more intuitive. Only a much larger data base, preferably over 500 base pairs of shared sequence, would show which of these are homoplasies and represent a sampling error. It can also be seen that 15 of the base changes are transitions, i.e. purine to purine or pyrimidine to pyrimidine, and only four are transversions, i.e. purine to pyrimidine or vice versa. This is typical especially of mitochondrial DNA, which shows a greater than 90% transition bias, and contributes to the frequency of parallel mutations.

There is another feature of interest in the caracal sequence and that is the three base deletion at positions 9 to 11. Although it is autopomorphic in this data set such DNA rearrangements represent very strong characters for phylogeny reconstruction, since they are less likely to be homoplastic than the individual site changes discussed above. Computational assistance in storing, editing, aligning, translating, and analyzing DNA sequence data is essential with the increasing rate with which sequence data can be generated, and with the mass of data now available in international data banks. DAPSA (Harley, 1993) is a user-friendly and versatile package for the IBM-compatible PC which has proved invaluable for this task.

**Conclusion**

As has been discussed by Harley and Vassart (Article 6) these DNA-based methods have a large number of applications, many of direct value to the conservation biologist. However, they need to be well understood and used only in ways appropriate for the problem in hand, and are not a panacea. They are best used as a complement to morphological, behavioural, developmental, and other data, where they can be genuinely useful in contributing to a complete picture.

**References**


Abstract: The relationships between four subspecies of Gazella gazella (gazella, cora, erlangeri and farasani) and Gazella subgutturosa were studied by protein electrophoresis and cytogenetics. Genetic distances, mean number of alleles per locus and proportion of polymorphic loci computed from allelic frequencies at 24 loci were given with G- and R-band karyotypes. C-band techniques revealed that the p arm of the X chromosome and the Y chromosome were heterochromatic. The karyotype of G. gazella consisted of 35 chromosomes for the male and 34 for the female due to an autosome-to-X chromosome translocation. No chromosomal polymorphism was found. All the results were compatible with the current subspecific status of gazella, cora, erlangeri and farasani.

Keywords: Gazella gazella, chromosomes, allozymes, subspecies, R-BG-band, GTG-band.

Introduction
Although the exact definition of a subspecies varies among authorities, there is general agreement that it should be considered an evolutionary significant unit. In order to avoid an unjustified multiplication of their number, subspecies should be defined on the basis of a number of convergent characters (Ryder, 1986; Patton and Smith, 1990). Moreover, they are generally considered as locally adapted gene pools, and this is of particular importance to conservation problems. Reintroduction programmes should take into account the specificity of populations (Ryder, 1986; O'Brien and Mayr, 1991). In this respect, gazelles (genus Gazella) are well-suited for the application of systematics to conservation problems. Several gazelle species are considered threatened (IUCN, 1990), and populations of G. gazella have recently declined in Saudi Arabia (Thouless et al., 1991; Magin, Article 14). Thus, genetic characterization of the different subspecies of G. gazella is increasingly important for conservation management. G. gazella consists of five subspecies: G. g. muscatensis, G. g. gazella, G. g. cora, G. g. farasani and G. g. erlangeri (Groves, 1989; Thouless and Al Bassri, 1991). The purpose of this study is to describe the subspecies of G. gazella, based on C-, G-, and R-banded karyotypes and protein electrophoresis.

Materials and Methods
- Origin of the sample animals: Gazella gazella erlangeri: This is a small dark gazelle commonly found in private collections in the south-western part of Saudi Arabia. There are no captive breeding programmes or protected areas in its natural habitat. Groves identified these gazelles from photographs and skulls as Gazella gazella erlangeri, different from Gazella bilkis described by himself in 1985 (Groves and Lay, 1985). At the end of 1991, the National Wildlife Research Center (NWRC) began to collect some individuals from private collections to establish the first captive breeding programme for this particular taxon. Gazelles were sent to the King Khalid
Wildlife Research Center (KKWRC), near Riyadh, (25^003'N, 46^045'E). This Center is today in charge of their captive propagation. From this group, 22 animals were karyotyped. Of these gazelles, 13 came from a private shop in Jeddah, five animals from NWRC, and four animals from private collections in Taif. The precise origin of the gazelles from Jeddah is not known, but they were collected from Aden (Yemen). The three founders of the NWRC nucleus were a gift from the Emir of Najran (in south-west Saudi Arabia). Organs of two gazelles from NWRC were available for protein electrophoresis.

Gazella gazella gazella: Tissue samples for electrophoresis were collected from 14 individuals from northern Israel. Eight animals were also sampled for cytogenetic studies. Organs were sampled during controlled hunting organized by the Israeli Nature Reserve Authority to limit overpopulation of gazelles.

Gazella gazella cora: Organs of two individuals originating from south-west Saudi Arabia and kept at NWRC were taken for electrophoresis. Eight animals from the same region were also karyotyped.

Gazella gazella farasani: Three animals from the Farasan Islands, a protected area located in the Red Sea, were karyotyped.

Gazella subgutturosa marica: Organs from five individuals born at KKWRC were used for protein electrophoresis. The KKWRC herd originated from wild animals caught in different regions of Saudi Arabia between 1976 and 1982. Fifty-eight gazelles from this population were karyotyped (Granjon et al., 1991; Vassart et al., 1993). The G-banded karyotype of G. s. marica is presented here to allow comparison of banding patterns with G. gazella.

- Electrophoresis: Horizontal starch gel electrophoresis was performed on kidney, liver and heart samples of G. g. gazella, G. g. erlangeri, G. g. cora and G. subgutturosa marica. Protein extraction, electrophoresis, protein staining, and scoring of the results were conducted according to Pasteur et al. (1988). Twenty-four presumptive genetic loci were scored in all individuals. Buffers used were tris citrate pH 6.4, 6.7 or 8.0 (TC), lithium hydroxide pH 8.3 (LiOH), tris maleate EDTA pH 6.9 (TME), tris borate EDTA pH 8.6 (TBE) and tris HCl pH 8.5 (TH). The electrophoretic loci were identified with the following format: enzyme, abbreviation, (Enzyme Commission Number, and buffer used). These included: adenylate kinase, AK, (E.C. 2.7.4.3, TC 6.4) from heart; alpha glycerophosphate dehydrogenase, GPD, (E.C. 1.1.1.8, TC 8.0) from kidney; aspartate aminotransferase, AAT, (E.C. 2.6.1.1, TME) from liver (2 loci); diaphorase, five esterases, ES, (E.C. 3.1.1, TME and TH) from liver; glycoxlase, GLO, (E.C. 4.4.1.5, LiOH) from kidney; glucose phosphate isomerase, GPI, (E.C. 5.3.1.9, TME) from liver; isocitrate dehydrogenase, IDH, (E.C. 1.1.1.42, TC 6.7) from kidney (2 loci); lactate dehydrogenase, LDH, (E.C. 1.1.1.27, TC 6.7) from kidney (2 loci); malate dehydrogenase, MDH, (E.C. 1.1.1.37, TC 6.7) from kidney (2 loci); mannose phosphate isomerase, MPI, (E.C. 5.3.1.8, LiOH) from kidney; nucleoside phosphorylase, NP, (E.C. 2.4.2.1, TME) from liver; phosphoglucomutase, PGM, (E.C. 2.7.5.1, TME) from liver; sorbitol dehydrogenase, SDH, (E.C. 1.1.1.14, TC 8.0) from kidney; superoxide dismutase, SOD, (E.C. 1.15.1.1, LiOH) from kidney; 6-phosphogluconate dehydrogenase, 6PGD, (E.C. 1.1.1.43, TC 6.7) from kidney; and total proteins (TC 6.4) from heart. Percentage of polymorphic loci, mean number of alleles per locus, and mean heterozygosities were calculated from allele frequencies. Nei and Roger's genetic distances were computed using the Phylip package of J. Felsenstein.
**Cytogenetic methods**: Chromosomes were obtained from lymphocyte and fibroblast cell cultures. For lymphocyte cell cultures, about 10 ml of peripheral blood were aseptically collected by jugular puncture in sterile heparinized tubes. Ten drops of blood (approximately 0.5 ml) were distributed into flasks containing 9.5 ml of HAM’S F12 nutrient medium supplemented with 20% foetal calf serum, antibiotics (100 UI streptomycin) and concanavalin A (10 mg/ml). The culture was incubated at 37°C for 72 h, and colcemid (final concentration 0.03 mg/l) was added 1 h before harvesting. Cell cultures were then treated with a hypotonic solution of sodium citrate (0.85%) for 20 min at 37°C, fixed with Carnoy’s fluid (3/1: methanol/glacial acetic acid), spread on pre-cooled slides, and stained in 4% Giemsa. Metaphases were photographed for preparation of karyotypes.

Table 9.1 Allelic frequencies for variable loci in 4 samples of *Gazella*; n = sample size; H = mean heterozygosity; A = mean number of alleles per locus; P99% = proportion of polymorphic loci. H, A and P calculated for the 24 loci studied.

<table>
<thead>
<tr>
<th>Locus</th>
<th>Allele</th>
<th><em>G. g. gazella</em> n = 14</th>
<th><em>G. g. erlangeri</em> n = 2</th>
<th><em>G. g. cora</em> n = 2</th>
<th><em>G. s. marica</em> n = 56</th>
</tr>
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<tr>
<td>PGD</td>
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<td>0.96</td>
<td>1</td>
<td>1</td>
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</tr>
<tr>
<td></td>
<td>110</td>
<td>0.04</td>
<td></td>
<td></td>
<td>0.1</td>
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<tr>
<td>IDH1</td>
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<td>0.18</td>
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<td></td>
<td></td>
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<td></td>
<td>100</td>
<td>0.82</td>
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<td>1</td>
</tr>
<tr>
<td>SDH</td>
<td>100</td>
<td>1</td>
<td>1</td>
<td>0.75</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>120</td>
<td></td>
<td>0.25</td>
<td></td>
<td></td>
</tr>
<tr>
<td>GPDH</td>
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<td>1</td>
<td>1</td>
<td>0.75</td>
<td>1</td>
</tr>
<tr>
<td></td>
<td>120</td>
<td></td>
<td>0.25</td>
<td></td>
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<td></td>
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</tr>
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<td>0.75</td>
<td>1</td>
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<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>ES1</td>
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<tr>
<td></td>
<td>100</td>
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<td>1</td>
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<tr>
<td></td>
<td>120</td>
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<td>0.5</td>
<td></td>
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<tr>
<td>ES2</td>
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<td>0.54</td>
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<td>0.5</td>
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<td></td>
<td>120</td>
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<td>0.8</td>
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<td>MPI</td>
<td>100</td>
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<td>1</td>
<td>1</td>
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<td>1</td>
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<td></td>
<td>120</td>
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<td></td>
<td>1</td>
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<tr>
<td>A</td>
<td>1.25</td>
<td></td>
<td>1</td>
<td>1.21</td>
<td>1.17</td>
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<tr>
<td>P99%</td>
<td>16.7</td>
<td></td>
<td>0</td>
<td>20.8</td>
<td>16.7</td>
</tr>
<tr>
<td>H</td>
<td>0.05</td>
<td></td>
<td>0</td>
<td>0.088</td>
<td>0.036</td>
</tr>
</tbody>
</table>

For fibroblast cell cultures, a biopsy of subcutaneous connective tissue or muscle was collected. After disruption and digestion of the biopsy in trypsin (2.5 g/l), the cells were grown at 37°C in a CO2 incubator as monolayer cultures in Falcon flasks (75 cm²) containing a medium similar to the one previously described for lymphocyte cultures. Once the cultures were initiated, cells were
grown in MEM medium supplemented with 10% foetal calf serum, antibiotics and glutamine. Cultures were synchronized with a single thymidine block during S phase (Viegas-Pequignot and Dutrillaux, 1978; Hayes et al., 1991) in order to increase the yield of metaphase and early metaphase cells. To induce R-banding, 5-bromo-2-deoxyuridine (BrdU Sigma 5002) was added to the medium at a final concentration of 10 or 20 g/ml. The cultures were incubated at 37°C until the number of mitotic cells reached a maximum, about 8 to 9 h after BrdU addition. To obtain RBG-bands, cells were treated according to the procedure described by Hayes et al. (1991) and Fluorochrome-Photolysis-Giemsa (FPG) staining was performed as described by Viegas-Pequignot et al. (1989).

G-banded karyotypes were prepared using a modified method of Seabright (1971). Chromosomes were ordered according to their size, shape and banding pattern. For G-banded karyotyping, numbering of chromosome pairs follows that of Kingswood and Kumamoto (1988). C-bands were obtained by the barium hydroxyde/saline/giemsa (BSG) technique (Sumner, 1972).

Table 9.2 Nei's genetic distances (upper right) and Roger's genetic distances (lower left).

<table>
<thead>
<tr>
<th></th>
<th>G. g. gazella</th>
<th>G. g. erlangeri</th>
<th>G. g. cora</th>
<th>G. s. marica</th>
</tr>
</thead>
<tbody>
<tr>
<td>G. g. gazella</td>
<td>0.054</td>
<td>0.017</td>
<td>0.152</td>
<td></td>
</tr>
<tr>
<td>G. g. erlangeri</td>
<td>0.074</td>
<td>0.017</td>
<td>0.075</td>
<td>0.169</td>
</tr>
<tr>
<td>G. g. cora</td>
<td>0.061</td>
<td>0.0115</td>
<td>0.135</td>
<td></td>
</tr>
<tr>
<td>G. s. marica</td>
<td>0.162</td>
<td>0.167</td>
<td>0.171</td>
<td></td>
</tr>
</tbody>
</table>

Results

Fourteen loci were found to be monomorphic in all samples. Allelic frequencies at the 10 polymorphic loci are listed in Table 9.1. The mean number of alleles per locus (A) ranged from 1 in G. g. erlangeri to 1.25 in G. g. gazella. The proportion of polymorphic loci (P%) ranged from 0 in G. g. erlangeri to 20.8 in G. g. cora, and mean heterozygosity ranged from 0 in G. g. erlangeri to 0.088 in G. g. cora. Nei and Roger's genetic distances appeared to be 2 to 15 times higher between G. subgutturos marica and the different subspecies of G. gazella than between subspecies of G. gazella (Table 9.2).

The chromosomes of G. gazella were found to be 2n=34/35 (female/male) with a fundamental number of 62. Banded karyotypes of the different subspecies of G. gazella appeared similar (Figures 9.1 and 9.2) to the G-banded karyotype of that species published by Kingswood and Kumamoto (1988). Autosomes consist of 12 pairs of meta-submetacentric chromosomes, one pair of submetacentric chromosomes with a very short p arm, and three pairs of acrocentric chromosomes. Females have two large submetacentric X chromosomes. Males have one X, one acrocentric Y (called Y1) and a second acrocentric (called Y2, but actually the autosomal homologue to the distal portion of the long arm of the X). G- and R-banding patterns of the additional autosome (Y2) and of the distal portion of the long arm of the X chromosome appear identical (Figures 9.1 and 9.2). The short arm of the X chromosome and the Y1 chromosome are entirely heterochromatic.
Figure 9.1 TG karyotype of a female *Gazella gazella farasani* (2n = 34).

Discussion

Comparison of the G-banding patterns of the X chromosomes from *G. gazella* with other gazelle species indicates that the autosome involved in X-translocation is the same as in *G. soemmeringi* (Benirschke et al., 1984), *G. dama* (Arroyo Nombela et al., 1990) and *G. subgutturosa* (Kingswood and Kumamoto, 1988; Vassart et al., 1993). It is difficult to number the chromosome pairs in gazelles because previous cytogenetic studies have used different numbering systems. For example, Benirschke et al. (1984) found that pair 14 of *G. soemmeringi* was involved in the X-autosome translocation, but according to Arroyo Nombela et al., (1990) pair 14 of *G. dama* was different and
was involved in a Y-autosome translocation. Standardization of karyotypes, as has been done for domestic species, should be established for wild species for which data are available.

Figure 9.2 RBG karyotype of a male Gazella gazella cora (2n = 35)

The difference in fundamental number (FN) between G. gazella (FN = 62) and G. subgutturosa (FN = 60) may be due to the short arm in pair 13 of G. gazella. These arms are difficult to see on banded chromosomes but are easily observed on non-differentially stained karyotypes of G. gazella. Based on C-banding analyses (Figure 9.3), these short arms are not heterochromatic. The fundamental number for other species in the family Bovidae is usually 58 to 62 (Wurster and Benirschke, 1968).
Except for *G. g. erlangeri*, levels of genetic variability derived from our samples of *Gazella gazella* are similar to those found in natural populations of a number of artiodactyls (for reviews see Baccus et al., 1983; Vassart et al., 1991). The mean heterozygosity for 184 species of mammals was $4.1 \pm 3.5\%$ (Nevo et al., 1984). This value compares to a mean heterozygosity of 5% in *G. g. gazella* and 3.6% in *G. s. marica*. Despite the different origins of the samples, the absence of genetic variability in *G. g. erlangeri* is of concern from a conservation standpoint. This finding is consistent with results found in 19 loci from blood samples of 15 individuals (Vassart et al., 1994) and 23 (Vassart, unpublished data) individuals of the same species. It is likely that the null polymorphism
and heterozygosity values found in *G. g. erlangeri* are the consequences of a genetic bottleneck. Similar results have been reported in two other species of ungulates, *Dama dama* (Pemberton and Smith, 1985) and *Capra ibex ibex* (Stüwe and Scribner, 1989). However, Ryman *et al.* (1990) have shown that taxa which are initially found to be monomorphic can be found to be polymorphic when more loci or more individuals are studied.

As expected, genetic distances showed that the different subspecies of *Gazella gazella* were more closely related to each other than *Gazella gazella* is to *Gazella subgutturosa*. Among ungulates, cervids are the group which has been most studied by means of protein electrophoresis. It is clear that there is much variation in genetic distances within and between species of cervids, and it is very difficult to correlate specific values with specific taxonomic levels (Linnel and Cross, 1991). Variation can be due in part to differences in techniques: for example how many and which loci are examined. Nei's genetic distances between subspecies have been reported to be 0.013 in *Rupicapra rupicapra* (Pemberton *et al.*, 1989), 0.0182 in *Cervus elaphus* (Gyllensten *et al.*, 1983), and 0.174 in *Rangifer tarandus* (Baccus *et al.*, 1983). Genetic distances between the species *G. gazella* and *G. subgutturosa* are similar to the subspecific differences found in *Rangifer tarandus*. Distances between the subspecies of *G. gazella* are lower, and with the karyological results, indicate that these subspecies probably diverged recently. If their population numbers do not drop to critically low levels, we suggest that they may be recognized and managed as distinct evolutionary significant units (*sensu* Ryder, 1986) for conservation programmes. Should their conservation situation worsen, their apparent genetic similarity makes it possible to consider collectively managing all subspecies of *G. gazella* as a means of preserving the species.

Acknowledgements

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References


10. Systematics of *Gazella subgutturosa*:
Implications for Conservation in the Arabian Peninsula

Steven C. Kingswood, Marc Vassart and Douglas Williamson

Abstract: Systematics is the branch of biology that studies the diversity of life; thus, it is intrinsically linked with conservation efforts to preserve biological diversity. The endangered status of *Gazella subgutturosa marica* prompted a review of the systematics of *G. subgutturosa* in order to assist in providing effective conservation measures for this taxon. Morphological and chromosomal data support delineation of *G. subgutturosa* from other gazelles of the Arabian Peninsula and *G. s. marica* from *G. s. subgutturosa*. Protein electrophoresis shows that *G. subgutturosa* is well differentiated from other species of gazelles, but how *G. s. subgutturosa* and *G. s. marica* can be distinguished has not been determined. The following recommendations are made for the conservation of *G. s. marica*: (1) continue to protect and maintain existing wild populations; (2) preserve additional genetic diversity by maintaining the existing captive populations in Saudi Arabia and the United States; (3) determine the genetic characteristics of wild populations of *G. s. marica* and *G. s. subgutturosa* through continued chromosomal and molecular studies; and (4) include individuals representing all three cytotypes of *G. s. marica* in reintroduction projects in Saudi Arabia; ideally, specimens should be free from introgression of *G. s. subgutturosa*, as determined through biochemical studies.

Keywords: *Gazella subgutturosa*, taxonomy, systematics, genetics, threatened species, wildlife management.

Introduction

The goitred gazelle *Gazella subgutturosa* inhabits desert and sub-desert steppes from the Arabian Peninsula to northern China and Mongolia (Harrison and Bates, 1991; Heptner et al., 1988). Four subspecies are recognized by Groves (1969, 1985): the Arabian sand gazelle *G. s. marica* from the Arabian Peninsula; the Persian gazelle *G. s. subgutturosa* from Syria, Iraq, eastern Turkey, eastern Transcaucasia in Azerbaijan, Iran, Pakistan, Afghanistan, Turkmenia, and Kazakhstan; the Xinjiang goitred gazelle *G. s. yarkandensis* from the Tarim Basin in Xinjiang, China; and the Mongolian goitred gazelle *G. s. hillieriana* from the Qaidam Basin in China to the Gobi Desert in Mongolia. Intergrades of *G. s. subgutturosa* and *G. s. marica* occur from Kurdistan to the lower Tigris-Euphrates valley of Iraq (Groves and Harrison, 1967). Populations of *G. subgutturosa*, notably *G. s. marica*, have declined throughout their range due to hunting and overgrazing by domestic livestock (Thouless et al., 1991; East, 1992). *G. s. marica*, one of nine threatened gazelle taxa (IUCN, 1990), is considered endangered by the IUCN (the World Conservation Union).

Taxonomy, traditionally based on phenotypic relationships, has been a major tenet in defining the biological diversity conservationists seek to preserve. In defining genotypes, cytogenetics and molecular genetics provide additional measures of biological diversity that must be considered when establishing conservation priorities. However, because many of the techniques in
cellular and molecular biology require fresh tissue samples, there have been few studies to investigate the genetics of natural populations of large mammals. For many species, the only genetic information available is from captive specimens whose geographic origin is largely unknown. The purposes of this paper are to review the systematics of *G. subgutturosa*, including data from chromosomal and electrophoretic studies, to discuss the conservation implications and limitations of these data, and to incorporate this information into a conservation strategy for *G. s. marica*.

**Systematics**

Four recognized species of gazelles inhabit the Arabian Peninsula; *G. gazella*, *G. bilkis*, *G. saudiya* (*G. dorcas saudiya* of Harrison and Bates, 1991), and *G. subgutturosa* (Harrison and Bates, 1991; Grubb, 1993). Putatively, there are two additional peninsular species; *G. arabica* and *G. dorcas* (Grubb, 1993; Williamson and Tatwany, this volume). According to Groves (1983) the taxonomic relationships of the Arabian gazelles are not clear, with the exception of *G. subgutturosa*. Based on analyses of skull measurements, Groves and Harrison (1967) and Groves (1969) were able to distinguish *G. s. subgutturosa* and *G. s. marica*. Multivariate analyses of skull measurements clearly established the position of *G. s. marica* among the gazelles of the Arabian Peninsula (Rostron, 1972; Groves, 1989). Although *G. s. yarkandensis* and *G. s. hillieriana* are phenotypically distinguishable from one another and from *G. s. subgutturosa* and *G. s. marica* (Groves, 1969 and 1985), they have not been analyzed morphometrically.

*G. subgutturosa* is chromosomally distinguishable from the other species of Arabian gazelles that have been studied (see Table 7.1, Kingswood and Kumamoto, this volume). Chromosomes of *G. subgutturosa* were originally reported as 2n = 30 in females and 2n = 31 in males (Wurster, 1972; Effron et al., 1976; Hsu and Benirschke, 1977). The difference in diploid number between females and males is due to an autosome-to-X chromosome translocation. Females do not have the unpaired autosome (i.e. a chromosome other than a sex chromosome) found in males because both autosomal elements of a pair are translocated (fused) to the X chromosomes. Although identified as Persian gazelles, *G. s. subgutturosa*, the origin of the animals sampled in these three studies is not precisely known. The animals karyotyped by Effron et al. (1976) and Hsu and Benirschke (1977) were in the collection of the Zoological Society of San Diego. This group was founded by goitred gazelles from Teheran Zoo, Iran, but included one individual of possible central Asian origin (Carter, 1991). Assuming the Persian gazelles that were karyotyped originated in Iran and/or Soviet central Asia, they would have been *G. s. subgutturosa*. Orlov (see Shi, 1987) also reported the chromosomes of *G. subgutturosa* to be 2n = 30/31. Presumably these animals were from Soviet Asia or China.

Two additional karyotypes were documented in the North American captive population of *G. s. marica* (Benirschke and Kumamoto, 1987; Kingswood and Kumamoto, 1988) founded by animals wild-caught in eastern Jordan (Kingswood, 1991). Recently, captive animals in Saudi Arabia and Qatar have also been found to have these karyotypes (Vassart et al., 1993). In addition to the autosome-to-X chromosome translocation, a Robertsonian translocation involving two autosomal pairs causes the diploid number to range from 30 to 32 in females and 31 to 33 in males (Figure 10.1). This translocation involves a putative fusion of the centromeres of two acrocentric chromosomal pairs. Chromosomally, animals can be translocation homozygous, translocation heterozygous, or non-translocation homozygous. In translocation homozygotes (2n = 30/31, females/males), both chromosomal elements of each acrocentric pair fuse to form one metacentric
pair. Only one chromosomal element of each acrocentric pair fuses in translocation heterozygotes (2n = 31/32), resulting in one metacentric element and leaving one acrocentric element of each pair unchanged. Neither element of each acrocentric pair fuses in non-translocation homozygotes (2n = 32/33).

Figure 10.1 G-banded karyotype of a male goitred gazelle (2n = 32), with the autosome-to-X chromosome translocation and heterozygous for the 14/15 Robertsonian translocation. Acrocentric chromosomes 14 and 15 are shown flanking their metacentric homologue to illustrate banding homology between chromosomal arms. The unfused autosome 16 is shown next to its translocated homologue at the lower end of the X chromosome. Inset shows the two X chromosomes from a female goitred gazelle karyotype. In all goitred gazelles, females do not have the unpaired autosome found in males because both autosomal elements of a pair are translocated (fused) to the X chromosomes. In G. s. marica, the homozygous form of the Robertsonian translocation (2n = 30/31, females/males) involves the fusion of both chromosomes of pairs 14 and 15. The translocation heterozygous form (2n = 31/32) involves the fusion of only one chromosome each of pairs 14 and 15. In non-translocation homozygotes (2n = 32/33), chromosomal pairs 14 and 15 are not fused.

Existence of the autosome-to-X chromosome translocation and the Robertsonian translocation in G. s. marica is inferred from G- and R-banding analyses. G- and R-banding are techniques of differentially staining chromosomes. The staining results in distinct patterns of bands on each chromosome that can be compared to the patterns on other chromosomes. Identical banding patterns indicate that the chromosomes, or portions thereof, are homologous, having identical
structures in terms of visible morphology. Thus, banding analyses allow the identification of translocations and other types of chromosomal rearrangements through the identification of the portion of a chromosome that is homologous to a portion of another chromosome.

Studies of non-differentially stained chromosomes (i.e. chromosomes not treated by banding techniques) in captive G. s. marica at Thumamah, Saudi Arabia, indicated similar variation in diploid number, presumed to be the result of a Robertsonian translocation (Granjon et al., 1991). These individuals are believed to have originated from animals wild-caught in different regions of Saudi Arabia, but precise locations are unknown. Under the assumption that pure G. s. marica are non-translocation homozygotes, Granjon et al. (1991) suggested that introgression of G. s. subgutturosa might explain the occurrence of translocation heterozygotes in the captive population of G. s. marica at Thumamah. However, translocation heterozygotes are present in the North American captive population of G. s. marica, founded by stock wild-caught in eastern Jordan (Kingswood, 1991), indicating that the translocation occurs naturally. Putative translocation heterozygotes and both homozygous forms have recently been found in wild-caught animals from the Al-Khunfah region in northern Saudi Arabia (Williamson, Flavell, and Badri, unpublished data). These data do not support the hypothesis that captive stocks of G. s. marica at Thumamah have experienced introgression of G. s. subgutturosa. However, biochemical studies are necessary to unequivocally rule out introgression. Results of the chromosomal studies of G. subgutturosa are summarized in Table 10.1.

The need for biochemical systematics research to delineate all taxa of Arabian gazelles, including G. s. subgutturosa versus G. s. marica, was indicated by Durand et al. (1989). Biochemical systematics based on protein electrophoresis indicate that G. subgutturosa clusters with four subspecies of G. gazella; erlangeri, gazella, cora, and farasani (Vassart et al., 1994). This similarity conflicts with the placement of G. subgutturosa in the subgenus Trachelocele (Ellerman and Morrison-Scott, 1951). However when haemoglobin data are considered, G. subgutturosa is found to be characterized by a unique pattern which distinguishes it from G. gazella (Vassart et al., 1994). Isozymic data from blood samples of 30 captive G. s. marica in Saudi Arabia indicated that 15% of the 20 loci studied were polymorphic and mean heterozygosity was 0.017 (Granjon et al., 1991). When only 16 of the 20 loci are considered, these values become 18.75% and 0.021 (Vassart et al., 1994). Analyses of tissue samples from five G. s. marica indicated 16.7% of 24 loci were polymorphic and mean heterozygosity was 0.036 (Vassart et al., 1994). These values are similar to those found in natural populations of artiodactyls (see Baccus et al., 1983; Vassart et al., 1991, and references therein).

Conservation implications

In seeking to preserve biological diversity, conservationists must be able to recognize the diversity that is present in natural populations of organisms. Systematic analysis of biological diversity should include phenotypic (morphological) and genotypic (cytogenetic and molecular genetic) measures. Among the gazelles of the Arabian Peninsula, the systematics of G. subgutturosa are probably the most well-defined. Morphological, chromosomal, and molecular data sets are consistent in distinguishing the goitred gazelle from the other species of Arabian gazelles. Recognition of G. s. marica as a distinct subspecies of G. subgutturosa is warranted on the basis of skull measurements and karyotypes divergent from those of G. s. subgutturosa. Molecular affinities and differences
between these two taxa have not been documented, and should be established, particularly considering the endangered status of G. s. marica.

Chromosomal differences between G. s. subgutturosa (2n = 30/31) and G. s. marica (2n = 30-32/31-33) are congruent with morphological differences between the subspecies. However, the limitations of the existing karyotypic data must be recognized in formulating decisions on the management of G. s. marica. Presently, the cytogenetics of G. subgutturosa are based largely on the karyotypes of captive specimens whose precise geographical origins are unknown. This is the case for all specimens of G. s. subgutturosa that have been studied to date (Table 10.1).

Table 10.1 Percent occurrence of the three Robertsonian translocation cytotypes in both captive and wild populations of the goitred gazelle. F/M - females/males, 30/31 - 2n=30/31, 31/32 - 2n=31/32, 32/33 - 2n=32/33.

<table>
<thead>
<tr>
<th>Subspecies</th>
<th>Cytotype (F/M)</th>
<th>30/31</th>
<th>31/32</th>
<th>32/33</th>
<th>ORIGIN</th>
<th>REFERENCE</th>
</tr>
</thead>
<tbody>
<tr>
<td>subgutturosa</td>
<td>3</td>
<td>100</td>
<td>0</td>
<td>0</td>
<td>?</td>
<td>Wurster, 1972</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>100</td>
<td>0</td>
<td>0</td>
<td>Iran?</td>
<td>Effron et al., 1976</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>100</td>
<td>0</td>
<td>0</td>
<td>Iran?</td>
<td>Hsu and Benirschke, 1977</td>
</tr>
<tr>
<td></td>
<td>9</td>
<td>100</td>
<td>0</td>
<td>0</td>
<td>Iran?</td>
<td>Benirschke and Kumamoto, 1987, Kingswood and Kumamoto, 1988</td>
</tr>
<tr>
<td></td>
<td>2?</td>
<td>100</td>
<td>0</td>
<td>0</td>
<td>USSR/China?</td>
<td>Orlov et al. (see Shi, 1987)</td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>100</td>
<td>0</td>
<td>0</td>
<td>Iran?</td>
<td>Kingswood and Kumamoto, unpubl. data</td>
</tr>
<tr>
<td>TOTAL</td>
<td>27</td>
<td>100</td>
<td>0</td>
<td>0</td>
<td></td>
<td></td>
</tr>
<tr>
<td>marica (origin known)</td>
<td>71</td>
<td>39.4</td>
<td>43.7</td>
<td>16.9</td>
<td>Jordan</td>
<td>Benirschke and Kumamoto, 1987, Kingswood and Kumamoto, 1988</td>
</tr>
<tr>
<td></td>
<td>35</td>
<td>8.6</td>
<td>60</td>
<td>31.4</td>
<td>Jordan</td>
<td>Kingswood and Kumamoto, unpubl. data</td>
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<tr>
<td></td>
<td>22</td>
<td>18.2</td>
<td>45.4</td>
<td>36.4</td>
<td>S. Saudi Arabia</td>
<td>Vassart et al., 1994</td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>12.5</td>
<td>62.5</td>
<td>25</td>
<td>N. Saudi Arabia</td>
<td>Williamson et al., in prep.</td>
</tr>
<tr>
<td>136</td>
<td>27</td>
<td>49</td>
<td>24</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>marica (origin unknown)</td>
<td>115</td>
<td>3.5</td>
<td>28.7</td>
<td>67.8</td>
<td>Saudi Arabia?</td>
<td>Granjon et al., 1991, Vassart et al., 1994</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>50</td>
<td>50</td>
<td>50</td>
<td>Qatar?</td>
<td>Williamson et al., in prep.</td>
</tr>
<tr>
<td>119</td>
<td>3.4</td>
<td>29</td>
<td>67</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>TOTAL</td>
<td>255</td>
<td>16</td>
<td>40</td>
<td>44</td>
<td></td>
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</tr>
</tbody>
</table>

Granjon et al. (1991) pointed out the possibility that the Robertsonian heterozygosity observed in Saudi Arabian captive populations may be due to hybridization in captivity between G. s. marica and G. s. subgutturosa. The presence of heterozygotes in wild populations and the North American captive population (the latter known to have been founded by individuals from eastern Jordan) indicates that the Robertsonian rearrangement occurs naturally in G. s. marica. In this case, however, chromosomal data can not address the question of whether hybridization between G. s. marica and G. s. subgutturosa has occurred in Saudi Arabian captive populations.
Although a Robertsonian translocation and autosome-to-X chromosome translocation are known to occur naturally in *G. s. marica*, the question of whether or not these chromosomal rearrangements cause fertility problems is relevant to the captive management of this gazelle. Translocation heterozygosity is known to reduce fertility in certain mammals, notably humans, mice, and cattle (reviewed by Dyrendahl and Gustavsson, 1979; De Boer and De Jong, 1989; Speed, 1989). For most species, however, there are too few empirical data, particularly from wild populations, to determine the effects of chromosomal rearrangements on reproduction. Chromosomal pairing and segregation studies during meiosis can help to determine the effects of chromosomal heterozygosity on fertility because homologous chromosomes must pair and then segregate for normal gametogenesis to continue. Rearranged chromosomes may disrupt homology to the point that gametogenesis is also disrupted.

Studies of gametogenesis in six male *G. s. marica* (three with 2n = 31, three with 2n = 32) indicated normal chromosomal pairing and segregation, suggesting that heterozygotes have normal fertility (Kingswood, 1992). Evidence of normal fertility in *G. s. marica* heterozygotes is consistent with the prevalence of Robertsonian and sex-chromosome translocations in gazelles (Kingswood and Kumamoto, 1994). This suggests that the translocations are karyotypically adaptive; an example of what White (1973) termed "karyotypic orthoselection". Whether or not chromosomal rearrangements in gazelles have selective value to their karyotypes is a question that can only be addressed theoretically. However, the fact that observed frequencies of the three cytotypes in *G. s. marica* (Table 10.1) do not differ from Hardy-Weinberg expectations indicates that there is an absence of selection for any one of the three karyotypes.

This review of the systematics of *G. subgutturosa* has demonstrated the unique biological characteristics of this species. Recognition that *G. s. marica* is morphologically and genetically distinct from *G. s. subgutturosa* reinforces the need for conservation efforts directed specifically towards the preservation of *G. s. marica*. Continued protection of wild populations is extremely important. The importance of existing captive populations must also be recognized as they may represent diversity that has since been lost in the wild through population declines. Based on this review of the systematics of *G. subgutturosa*, the following management and research recommendations are suggested for the conservation of *G. s. marica*:

1) Continue to protect and maintain existing wild populations.

2) Preserve additional genetic diversity by maintaining the existing captive populations in Saudi Arabia and the United States. Maintaining these captive populations serves to protect against the possibility of continued declines in wild populations. Ideally, captive populations should be genetically pure and represented by founders of known geographic origin. The U. S. population, of eastern Jordanian origin, is highly inbred, and the introduction of new founder stock from northern Saudi Arabia is recommended. Chromosomal translocations found in both captive populations are believed to be of natural origin and do not appear to confer a reproductive disadvantage to heterozygotes. Because observed frequencies of the three cytotypes indicate that there is an absence of selection for any one of the three karyotypes, all three karyotypic forms should continue to be maintained through random mating. However, it would be useful to continue monitoring the inheritance of the translocation through cytogenetic and pedigree analyses.
3) Establish the genetic characteristics of wild populations of *G. s. marica* and *G. s. subgutturosa*, particularly of those reported in the Rub al Khali (Saudi Arabia), Iran, and the zone of intergradation in Iraq, through continued chromosomal banding and molecular studies. Identification of biochemical characteristics unique to either subspecies is important in order to screen captive *G. s. marica* for evidence of introgression of *G. s. subgutturosa*.

4) In keeping with the draft guidelines of the IUCN / SSC Re-introduction Specialist Group (Anon., 1992), individuals selected for re-introduction should be of the same taxonomic unit and, ideally, closely related genetically to those which were extirpated. All three cytotypes of *G. s. marica* should be considered suitable for re-introduction projects in Saudi Arabia. Animals selected for re-introduction projects aimed at restoring populations of *G. s. marica* should ideally be free of *G. s. subgutturosa* introgression, as determined through biochemical studies.

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References


11. Bilkis gazelle in Yemen - status and taxonomic relationships

Arnaud Greth, Douglas Williamson, Colin Groves, Georg Schwede and Marc Vassart


Abstract: The Bilkis gazelle Gazella bilkis was described in 1985 from material collected in Yemen in 1951. No new information about the species has been forthcoming since then and the animal's current status is uncertain in two respects. Firstly, it is difficult to establish the taxonomic relationship between G. bilkis and a possible subspecies of the Arabian gazelle Gazella gazella erlangeri which also occurs in the south-west Arabian peninsula. Secondly, uncontrolled hunting and the general lack of conservation measures in Yemen mean that, if it does still survive, its continued existence is far from assured. Systematic field surveys and taxonomic research are urgently needed to clarify the status of this animal and implement a global conservation action plan.

Keywords: Gazella bilkis, Gazella gazella erlangeri, conservation, taxonomy, Yemen, Arabian peninsula.

Introduction

Given the rate at which tropical forests are being destroyed, it is relatively easy to understand how cryptic rainforest invertebrates with minuscule ranges can become extinct without being known to science, but it is startling to realize that a similar fate could befall the Bilkis gazelle Gazella bilkis, a medium-sized antelope from the Arabian peninsula.

Bilkis gazelle was first described by Groves and Lay in (1985) from museum specimens collected in Yemen in 1951 and named in honour of the Queen of Sheba. No further material or information has been forthcoming since 1951 and there is none known in captivity. To fully comprehend the problems regarding G. bilkis, an overview of other gazelle taxa in the Arabian peninsula is necessary. The taxonomic issue is confused by the presence of another poorly understood gazelle in the same region G. gazella erlangeri, which is believed to be a subspecies of the mountain gazelle.

In 1987, Ryder emphasized the "urgent need for conservation action" for some gazelle species. The situation has recently improved in the north of the Arabian peninsula for the sand gazelle G. subgutturosa marica and the mountain gazelle G. g. gazella (Thouless et al., 1991). But at least three other subspecies of G. gazella as well as Bilkis gazelle are still in jeopardy. Because information on all the gazelles is either very scarce or non-existent, it is very difficult to plan conservation measures. Priority should, therefore be given to taxonomic studies and field surveys in order to formulate and initiate a conservation strategy, as well as immediate remedial action.

This paper presents all available information on Bilkis gazelle and emphasizes the urgency of undertaking field surveys and taxonomic research to clarify its status and facilitate its conservation.
G. bilkis and the dark forms of G. gazella in the southern Arabian peninsula

- **Taxonomy:** The taxonomy of the genus *Gazella* is considered to be one of the most equivocal among mammal groups (Groves and Harrison, 1967). The classification was modified recently, changing the status of some taxa from subspecies to species (Groves, 1969; Furley et al., 1988), but taxonomic relationships between and within a number of species are still unclear.

Groves and Lay (1985) described *G. bilkis* from five specimens (skins and skulls) deposited in the Field Museum of Natural History in Chicago by Dr. H. Hoogstraal in 1951, and one skull presented to the Natural History Museum, London, by W.T. Blanford in 1869. According to these authors, a number of features of the skull, including the shape of the horns (straight with 12-15 rings in the male, long with clearly developed rings in the female), and the morphology of teeth, nasal and premaxillary bones clearly differentiated *bilkis* from other species of gazelles. The colour patterns were also distinct: the body was very dark with paler fur on the flanks, haunches or legs; there was a very thick flank stripe, black and conspicuous in the field, and a white line on the inside of the thigh continuing down the shank. As a diagnostic feature, the bilkis gazelle is the darkest species of the genus.

At least three other species of gazelles, *G. subgutturosa*, *G. saudiya* and *G. gazella* (Groves and Harrison, 1967) were widely distributed throughout the Arabian peninsula. They will be discussed here briefly to make a clear distinction between the two taxa with which we are mainly concerned. The Arabian sand gazelle *G. subgutturosa marica* cannot be mistaken for any other species, being very pale in color and living in sandy areas (Groves, 1989). The so-called "Arabian dorcas" gazelle, *G. saudiya*, probably either on the verge of extinction or already extinct in the wild, is small and sandy-brown in colour with long, straight horns in both sexes (Groves, 1989). Increasingly, it has been suggested that this gazelle is a distinct species, unrelated to African dorcas gazelles (Groves, 1989); recent cytogenetic studies strongly corroborate this (Rebholz et al., 1991), but it is still under investigation.

The situation of the mountain gazelle *G. gazella* is more complicated, because four subspecies occur in the south of the Arabian peninsula. One subspecies, *G. g. cora*, which is reported to be sympatric with *G. bilkis* (Groves, 1989), can be distinguished from it by the paler coat, as well as by many skull characteristics (Groves and Lay, 1985). A second subspecies, *G. g. farasani* (Thouless and Al Bassri, 1991) is restricted to the coral archipelago of Farasan, 30 km north of the Yemen border in the Red Sea. A third subspecies, *G. g. muscatensis*, with a pronounced dark grey coat (Groves, 1989), is restricted to the coastal strip of northern Oman (Figure 11.1).

The fourth subspecies *G. g. erlangeri* (Groves et al., in press) is more controversial from a taxonomic point of view and its differentiation from *G. bilkis* is still unclear. It can be distinguished from *G. g. cora* by its small size and its dark colour. Described by Neumann (1906) as *G. arabica erlangeri* from Lahej, north of Aden, based on a colored plate (pl. 59) in Sclater and Thomas (1898), and recently resurrected as *G. g. erlangeri* (Groves et al., in press), this taxon is possibly sympatric with *G. bilkis*; two specimens from Ma'bar, Yemen (14°46'N, 44°21'E), in the Field Museum of Natural History, Chicago, recorded by Groves and Lay (1985) as *G. g. cora*, are more likely to be *G. g. erlangeri*. Although Groves and Lay (1985) proposed that these two taxa are not conspecific because of probable sympatry and different morphological patterns, scientific evidence is still too weak to classify them as two distinct taxa. Cytogenetics and molecular techniques are necessary to clarify the picture.
Figure 11.1 Presumed range of the different subspecies of G. gazella (solid square = G. g. farasani) and of G. bilkis (solid triangles).

Chromosome studies of G. g. cora and G. g. erlangeri have shown that both subspecies have 34 chromosomes in females and 35 chromosomes in males. These numbers are identical to the ones found in G. g. gazella (Wahrman et al., 1973), confirming that these two taxa should be considered as subspecies of G. gazella. Blood allozyme studies on 18 loci from 16 G. g. gazella, seven G. g. cora, 15 G. g. erlangeri and five G. g. farasani also showed that all these taxa are closely-related (Vassart et al., 1994).

G. gazella has a large phenotypic variability and some subspecies in Israel and Iran have not yet been described (Karami and Groves, 1992; Mendelsohn et al., in press). Special attention should be paid to the taxonomy of this species to allow a clear distinction of taxonomic units and to adopt the appropriate conservation measures.

- Biological data: There is almost no information available on the biology and distribution of G. bilkis. All the specimens collected in 1951 came from the mountainous area of Ta'izz (13°35'N, 44°02'E), 200 km south of Sa'ana. Localities include El Hauban in Wadi Maleh, Usaifira and Jabal Zarba (Groves and Lay, 1985; Harrison and Bates, 1991). They were either solitary or in small groups on euphorbia-covered slopes, which were separated from cultivated areas by hills (Sanborn and Hoogstraal, 1953). No other biological data or photographs have been published. A limited
survey was carried out in February 1992 by A.G. in the mountains (Jebel Sabir, Jebel Samah) between Ta'izz and Al Thurbah, 50 km to the south. Neither gazelles nor signs of their presence were found. Photographs of gazelles were shown to at least 100 local people in all the villages visited. All replied that gazelles had not been seen in the area for several decades.

It has been suggested that *G. bilkis* is endemic to Yemen (Groves and Lay, 1985), but no systematic field survey of its range has ever been conducted, and, considering the biogeography of the Asir mountain range and the regional distribution of other mammal species, such as *G. g. cora*, it is possible that it occurred or even still exists in Saudi Arabia, at least in the south (Groves, 1989).

No known captive population of *G. bilkis* exists in the world. Chester and Marwell zoos in the UK maintain small groups of gazelles, which may include some individuals descended from *G. g. cora* and *G. g. erlangeri* hybridized with *G. bilkis*. A small group (identified from photographs by C.G.) was kept in Qatar in Sheik Al-Thani’s collection (Al Wabra, near Shahaniyah) but they all died without issue.

There is almost no information available for *G. g. erlangeri*. According to local bedouins, two forms of gazelles occur in the Asir mountains in the south-west of Saudi Arabia and the nearby coastal plain, the Tihama (M. Shobrak, pers. comm.). One, called “idmi” is light brown in colour and is almost certainly *G. g. cora*. The other one, smaller and darker, is probably *G. g. erlangeri* (Groves et al., in press). There have been no recent sightings of this form. Specimens in the Natural History Museum, London, and in the Field Museum of Natural History, Chicago, have been collected near Aden or Ta’izz (Yemen) and near Taif (Saudi Arabia). One farmer reported that in 1992 he regularly hunted small gazelles having “the color of volcanic stones” near Lahej. This information corresponds with Neumann’s (1906) description of gazelles caught in the same area. Animal dealers from Saudi Arabia or bedouins say that these gazelles are still often caught in Yemen, in the area between Najran and Sa’dah, near the border of Yemen and Saudi Arabia.

While no captive population of *G. g. erlangeri* exists outside the Middle-East, this gazelle can still be found in reasonable numbers in private collections, particularly in Saudi Arabia. Their docile disposition makes them popular as pets, and *G. g. erlangeri* is one of the most common gazelle species in the numerous private collections in the Kingdom. The illegal trade in these animals, which probably come from Yemen or from southern Saudi Arabia, indicates that this subspecies still occurs somewhere in good numbers in the wild. In 1991, a herd of 25 gazelles was found in a pet shop in Jeddah, called “Beautiful Creatures”. According to the owner, the animals came from a location near Aden. Since then, other groups have been seen regularly in this shop. In 1987 a small captive herd was created at the National Wildlife Research Center (NWRC) with three individuals (one male, two females) given by the Emir of Najran. They are reported to be from an area in Yemen, close to the Saudi border. The herd was transferred to the King Khalid Wildlife Research Center (KKWRC) near Riyadh in January 1992. Nineteen individuals (11 males, eight females) were exchanged with private collections and added to the KKWRC herd during 1992.

**Conservation status**

The rich biological diversity and high level of endemism in the south-west Arabian peninsula contrasts with the lack of information on its natural history and conservation importance. A few ornithological expeditions have visited North Yemen since 1965 (Cornwallis and Porter, 1982) but
none reported sightings of Bilkis gazelles and R.F. Porter (pers. comm.) saw no gazelles at all during six expeditions in North Yemen between 1979 and 1987.

The complete failure to locate Bilkis gazelles in the wild and the absence of conservation measures in Yemen indicate that if it survives at all its situation is desperate (unless *G. bilkis* and *G. g. erlangeri* are proved to be conspecific). Automatic rifles are widely available in Yemen and wildlife is generally overhunted. During the visit of A.G. to Yemen in February 1992, some Yemeni people reported that relatives or farmers still regularly hunted gazelles in some places, such as the Lahej region and Saham wadi, near Hoddeida. Moreover, the recent economic development of reunified Yemen following the discovery of oil is intensifying habitat degradation and causing a decline in wildlife.

**Questionnaire about dark forms of gazelles in Yemen**

To clarify the taxonomic relationships between *G. bilkis* and *G. g. erlangeri* and to collect biological information on these two taxa, a questionnaire and a set of color prints of the *G. g. erlangeri* herd kept at the NWRC was sent out to 25 people (10 antelope specialists, three Yemeni wildlife professionals, four people from the zoo community, three people in charge of conservation organizations in the Middle-East and five others including ornithologists involved in surveys in Yemen). A note was also published in the "Bulletin of the Ornithological Society of the Middle East" (Greth, 1991) and in "Gnusletter", which is published by the IUCN/SSC Antelope Specialist Group.

Of the 15 responses obtained, 10 said they had no information. Of the five positive responses, two experts identified the gazelles on the prints as *G. g. ssp.*, one as *G. g. gazella*, one as *G. bilkis* (for some of the pictures) and one as a mixed herd of *G. gazella* and *G. bilkis*. The phenotypic appearance of the NWRC herd is quite homogeneous. Even though the photographs sent for the inquiry were perhaps not of ideal quality for taxonomic identification, the contradictory answers obtained emphasize the taxonomic problems.

**Proposals and Recommendations**

- **Taxonomic research**: A joint effort should be made by geneticists, scientists involved in gazelle taxonomy, field researchers and zoo managers to apply modern genetic techniques on all available samples of the taxa discussed here. Allozyme and cytogenetic studies should provide valuable information. The best method may be the comparison of mitochondrial DNA, because the differentiation of the genome of the taxa concerned is probably relatively recent. This study should of course include *G. bilkis* and the different subspecies of *G. gazella*, with particular attention being given to *G. g. erlangeri* and *G. g. muscatensis*.

As a step towards this, Saudi Arabia’s National Commission for Wildlife Conservation and Development (NCWCD) has initiated an innovative research project in collaboration with the University of California, La Jolla, San Diego, as well as other institutions. The main aim of this study is to clarify the taxonomic status of *G. bilkis* and *G. g. erlangeri* (and other taxa), by comparing DNA sequences in the hair of living specimens with the type specimens. If it is possible to extract DNA from the hair of museum specimens several decades old, this study might help to determine relations between *G. g. erlangeri* and *G. bilkis*.

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- **Conservation action:** International conservation funds are needed urgently for a preliminary survey in Yemen. If *G. bilkis* or/and *G. g. erlangeri* is/are discovered, an ecological study should be conducted to define its/their distribution, habitat requirements, population status and the major threats. For both taxa, these studies should be concluded with a population and habitat viability analysis. It is also important to recall that the situation of *G. g. cora* is precarious in the Asir mountains and the coastal plains of the Tihama in Saudi Arabia (Thouless *et al.*, 1991). Appropriate conservation measures should be urgently taken by implementing protected areas and enforcing hunting laws.

Although *in situ* conservation must remain the priority, the implementation of a captive-breeding programme in co-operation with the international zoo community and the concerned IUCN/SSC Specialist Groups should be considered for all relevant taxa. Individuals of non-viable populations could be captured to serve as founder stock.

All these activities should lead to the formulation of an integrated conservation action plan for the different gazelle taxa within two years, based on collaboration between regional governments and different international conservation institutions.

Assuming that Bilkis gazelle still survives, its situation must be very precarious. To avoid a re-run of Operation Oryx, which in 1962 saved the last Arabian oryx by drastic and expensive measures, urgent steps need to be taken to study the dark forms of gazelle in Yemen and Saudi Arabia to provide a basis for planning their conservation.

**Acknowledgements**

The authors acknowledge with great respect and appreciation the work done by all the staff of the NCWCD for the conservation of gazelle species in the Arabian peninsula, and particularly H.R.H. Prince Saud Al Faisal, who initiated all these efforts, and Prof. A. Abuzinada, Secretary General of the NCWCD, who manages the day to day activities of this organization. T. Abaigar, R.H. Daly, R. Estes, J. Kingdon, C. Magin, H. Mendelsson, J. Newby and R. Porter helped us to gather information about the Bilkis gazelle. J.F. Asmodé, J. Dolan, J. Grainger, L. Granjon, A.R. Khoja, N. Lindsay, F. Rietkerk, and M. Shobrak gave useful information or comments on the early draft and helped finalize the proposals.

**References**


12. Genetics of Saudi dorcas gazelle: Which is the real thing?

Wilhelmus Rebholz, Douglas Williamson, Bill Flavell, Osama Mohammed and Faris Al-Timimi

Abstract: Karyotypes of what is believed to be Saudi gazelle Gazella saudiya are presented and compared with dorcas gazelle Gazella dorcas, because several authors think they belong to the same species. The Saudi gazelle are originally from Al Areen Wildlife Park (Bahrain) and Al Ain Zoo and Aquarium (United Arab Emirates), and are currently at King Khalid Wildlife Research Centre (KKWRC). Saudi gazelle have karyotypes distinctly different from dorcas gazelle from Africa, but the karyotypes of Saudi gazelle resemble those of the Indian gazelle Gazella bennelli. DNA sequencing data of cytochrome b also strongly support the idea that Saudi gazelle are different from dorcas gazelle, but closely related to Indian gazelle. It is possible that the Saudi gazelle are hybrids between different populations or subspecies of Indian gazelle, since their karyotypes closely resemble each other. However, more animals need to be studied to confirm this. Despite the confusion about the Saudi gazelle, dorcas gazelle once were part of the Arabian fauna. Since some animals caught in south-west Saudi Arabia have typical dorcas gazelle karyotypes and their DNA sequences are similar to dorcas gazelle from Africa they must be the Saudi dorcas gazelle Gazella dorcas ssp., as mentioned in several publications. The results presented here indicate that it is essential for Saudi dorcas gazelle and Saudi gazelle to be bred in separate captive breeding programmes.

Keywords: Gazella saudiya, cytochrome b, cytogenetics, DNA sequencing, gazelles, mitochondrial DNA, systematics, taxonomy.

Introduction

The taxonomy of the Antilopinae is still controversial, and as a result many publications use different classifications (Alados, 1986/1987; Benirschke and Kumamoto, 1988; Corbet and Hill, 1980; Groves, 1969, 1985, 1989; Grzimek, 1968; Haltenorth and Diller, 1980; Honacki et al., 1982; O'Regan, 1984; Spinage, 1986; Walther et al., 1983). See Groves (1969) for a historical review. Descriptions of pelage coloration and measurements of skulls and bones are common features used as a basis for classification. In gazelles these features often overlap, leading to different classifications and it is often not clear how species and subspecies are related. Classification of the five genera in the Antilopinae other than Gazella (Antidorcas, Antilope, Ammodorcas, Litocranius, and Procapra) is straightforward. However, classification within the genus Gazella is very difficult, slight differences between species being obscured by considerable geographical variation within species.

Since the first morphological study by Groves and Harrison (1967) on Saudi gazelle Gazella saudiya, they have been considered to be the Arabian subspecies of dorcas gazelle Gazella dorcas ssp. Basically, most or even all morphological data on Saudi gazelle have been collected from skins and skulls in the collection of the British Museum of Natural History (BMNH) in London (see Figure
12.1 for collection and sighting locations). While Groves and Harrison (1967) concluded that Saudi gazelle, Indian gazelle *Gazella bennetti* and dorcas gazelle all belong to one species, Gentry (1971) argued that Saudi gazelle is conspecific and "maybe even conspecific" with dorcas gazelle and Indian gazelle. Groves' (1969) idea that the Saudi gazelle is a subspecies of dorcas gazelle has been widely accepted by several authors (Corbet, 1978; Walther et al., 1983; Nader, 1989; Kingdon, 1990; Harrison and Bates, 1991). However, Groves (1985) himself later raised the question whether Saudi gazelle belonged to dorcas gazelle or not, because "it is so different from other (dorcas) races". A few years later the Saudi gazelle was elevated to specific status (Groves, 1988), while a year after that (Groves, 1989) he seemed to accept again that it belonged to dorcas gazelle. Another morphological study on several dorcas gazelle subspecies, including Saudi gazelle from the BMNH (Alados, 1986/1987), argued that the Saudi gazelle is closely related to *Gazella dorcas neglecta* of the Western Sahara, and that the relatedness of these two groups could be due to the parallel evolution of animals in desert conditions. However, recently Saudi gazelle were reclassified as being different from dorcas gazelle, using morphological data (Furley et al., 1988; Groves, 1988) and cytogenetic data (Rebholz et al., 1991).

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**Figure 12.1** Shaded triangles represent locations where Saudi gazelle specimens have been sighted or collected (information from Thouless et al., 1991). The shaded area is where the founders of the captive population of Saudi dorcas gazelle were captured (Faris Al-Timimi, pers. comm.).
Genetic research can clarify the taxonomic status of taxa which have been difficult to classify (Benirschke, 1977; Furley et al., 1988). The techniques used here are karyotyping, which involves comparison of chromosomes, and DNA sequencing of the mitochondrial cytochrome b gene. The number of chromosomes is relatively characteristic for each species, and banding techniques enable identification of individual chromosomes, which is useful for comparing chromosomes within and between species. Mitochondrial DNA is a fast "evolutionary clock" (several times faster than most nuclear DNA) and is therefore valuable for estimating evolutionary relationships between species and subspecies (Irwin et al., 1991). There is a difference between mitochondrial genes, although each gene evolves at a constant rate. However, during analysis one should be aware of the different types of error in the data (Harley and Vassart, this volume). For closely related taxa one should analyze a relatively large amount of sequence data to minimize stochastic error. For very divergent taxa, successive mutations and parallel mutations at a single base pair site can cause problems (transitions can be saturated), so only transversions should be looked at. When one is confident that only single changes are detected (changes take place at a linear rate in time) the data can be used to estimate the time of divergence of species from their common ancestor. The cytochrome b gene evolves at a linear rate between approximately 5 and 10 million years (Irwin et al., 1991), and therefore is useful to detect evolutionary relationships in the Antilopinae. Comparison of cytochrome b sequences reveals phylogenetic distances between the various genera of the Antilopinae and between species, respectively. The combination of different genetic techniques (karyotyping and DNA sequencing) using identical samples gives the taxonomic results a solid basis (Ryder and Chemnick, 1990). Many gazelle species are threatened with extinction (Ryder, 1987; IUCN, 1990), which makes it important to clarify the taxonomic status of animals which will be used as founders for captive breeding programmes.

![Figure 12.2 Dorcas gazelle Gazella dorcas isabella from Africa female A76 (2n=30), KKWRC.](image-url)
Material and methods

Blood samples of seven Saudi gazelles *Gazella saudiya* (four males and three females), four Saudi dorcas gazelles *Gazella dorcas* ssp. (two males and two females), and two dorcas gazelles from Africa *Gazella dorcas isabella* (one male and one female) were used to set up lymphocyte cultures. Lymphocyte cultures were carried out as described by Belterman and De Boer (1984). Pokeweed mitogen proved to be a better mitogen for gazelle lymphocytes than phytohaemagglutinin. Only Giemsa stained chromosomes were used for the karyotypes. Blood and skin samples were used for DNA extraction. The mitochondrial cytochrome *b* gene was amplified from this DNA using the PCR (polymerase chain reaction) technique, and the PCR product was then sequenced in both directions. Kocher's universal primers H 15149 and L 14724 were used for both PCR and sequencing, using standard protocols (Irwin et al., 1991). Approximately 300 base pairs were used for sequence analysis for all studied species. The Saudi dorcas gazelle are from the Al Wabra collection in Qatar, and their ancestors were caught from the wild in south-west Saudi Arabia (see Figure 12.1 for capture location). The Saudi gazelle and dorcas gazelle from Africa are kept at KKWRC, and were sent there by Al Areen Wildlife Park in Bahrain and Al Ain Zoo and Aquarium in the United Arab Emirates. It is not clear from which location in the wild their ancestors came.

![Figure 12.3 Saudi dorcas gazelle *Gazella dorcas* ssp., male 578 (2n=31), Al Wabra, Qatar.](image)

Cytogenetic results

The typical karyotype of a dorcas gazelle from Africa *Gazella dorcas isabella* consists of 28 metacentric autosomes and two subtelocentric X-chromosomes for females or one X-chromosome plus two Y-chromosomes for males (Figure 12.2). One Y-chromosome is metacentric, the other is subtelocentric. The two Y-chromosomes are a common feature in gazelle karyotypes. The Saudi
dorcas gazelles *Gazella dorcas* ssp. sampled in Al Wabra all have karyotypes identical to the African representatives of dorcas gazelle (compare Figures 12.2 and 12.3).

Figure 12.4 Saudi gazelle *Gazella saudiya*, female D4 (2n=47), KKWRC. Reprinted from Rebholz et al. (1991).

The submetacentric X-chromosomes of the Saudi gazelle (Figures 12.4 and 12.5) are double the size of the largest autosomes, probably caused by an X-autosome translocation, which is very common in gazelle. Autosome numbers of the seven Saudi gazelles studied vary between 45 and 50, which represents considerable variation within a species (Table 12.1). However, recently we discovered a female Saudi gazelle from Al Areen Wildlife Park with 51 autosomes (Kumamoto and Rebholz, unpublished data), which brings the range of autosomes between 45 and 51. Not only do autosome numbers vary between Saudi gazelles, their karyotypes also differ. Variation of metacentric chromosomes is very conspicuous. Their numbers vary between 10 and 13 and some seem to be single (see Figures 12.4 and 12.5). The other autosomal chromosomes are subtelo-centric and their numbers vary from 32 to 39 (see Table 12.1). Some paired chromosomes do not seem to be homologous pairs (arrow in Figure 12.4), but this is difficult to prove in these unbanded karyotypes. Data from banded chromosome descriptions are not available yet, so it is not known which chromosomes are involved in translocations. More individuals of Saudi gazelle need sampling to study the extent of the variation in this species.
Figure 12.5 Saudi gazelle *Gazella saudiya*, male D3 (2n=51), KKWR. Reprinted from Rebholz et al. (1991).

Table 12.1 Autosome counts of Saudi Gazelles.

<table>
<thead>
<tr>
<th></th>
<th>Al Areen Wildlife Park animals</th>
<th>Al Ain Zoo and Aquarium animals</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>male (D1)</td>
<td>female (D5)</td>
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<tr>
<td></td>
<td>10 metacentrics + 38 subtelocentrics (48 autosomes)</td>
<td>10 metacentrics + 39 subtelocentrics (49 autosomes)</td>
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<tr>
<td></td>
<td>male (D3)</td>
<td>female (D6)</td>
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<tr>
<td></td>
<td>12 metacentrics + 35 subtelocentrics (47 autosomes)</td>
<td>12 metacentrics + 36 subtelocentrics (48 autosomes)</td>
</tr>
<tr>
<td></td>
<td>female (D4)</td>
<td>male (D7)</td>
</tr>
<tr>
<td></td>
<td>13 metacentrics + 32 subtelocentrics (45 autosomes)</td>
<td>10 metacentrics + 38 subtelocentrics (50 autosomes)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>male (D8)</td>
</tr>
<tr>
<td></td>
<td></td>
<td>10 metacentrics + 39 subtelocentrics (49 autosomes)</td>
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</table>

DNA Sequencing results

The overall percentage sequence divergence between approximately 300 base pairs of the mitochondrial cytochrome *b* gene of several gazelle species is shown in Table 12.2. Transversions, transitions and nucleotide position in the codon are not taken into account. The cytochrome *b* gene showed 1.0 to 1.2% base pair differences between Saudi dorcas gazelle and three dorcas gazelle from Africa, whereas the dorcas gazelle from Africa all differ by 1.6% from each other (Table 12.2). Even allowing for stochastic error, all dorcas gazelle subspecies are very closely related, since they differ
by less than 2% from each other. However, Saudi gazelle is clearly more related to the two Indian gazelles (0.9 and 1.3%) than to the dorcas gazelle subspecies (4.5 to 5.9%). The 4.5 to 5.9% difference between dorcas gazelle and Saudi gazelle is consistent with values typically found between mammalian species. The gerenuk *Litocranius walleri* is used for comparison with gazelle species, to show the divergence between different genera. The gerenuk differs by from 7.6% to 12.2% from all gazelle species so far examined, which is greater than the differences between any of twenty gazelle taxa studied so far (Rebholz, unpublished data).

**Table 12.2** Percentages of sequence divergence between several antelope species, based on approximately 300 base pairs of the mitochondrial cytochrome *b* gene. The gerenuk *Litocranius walleri* is included for comparison.

<table>
<thead>
<tr>
<th>Species</th>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
</tr>
</thead>
<tbody>
<tr>
<td>1   <em>Litocranius walleri</em></td>
<td>-</td>
<td></td>
<td></td>
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<tr>
<td>2   <em>Gazella saudiya</em></td>
<td>8.8</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>3   <em>G. bennetti fuscifrons</em></td>
<td>8.0</td>
<td>0.9</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>4   <em>G. bennetti shikarii</em></td>
<td>7.6</td>
<td>1.3</td>
<td>0.4</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>5   <em>G. cuvieri</em></td>
<td>10.6</td>
<td>2.9</td>
<td>2.0</td>
<td>3.1</td>
<td></td>
<td></td>
<td></td>
<td></td>
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<tr>
<td>6   <em>G. dorcas isabella</em></td>
<td>10.4</td>
<td>4.7</td>
<td>4.8</td>
<td>5.3</td>
<td>4.2</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>7   <em>G. dorcas neglecta</em></td>
<td>12.2</td>
<td>5.9</td>
<td>5.8</td>
<td>6.5</td>
<td>5.4</td>
<td>1.6</td>
<td>1.6</td>
<td>1.6</td>
</tr>
<tr>
<td>8   <em>G. dorcas pelzeln</em></td>
<td>9.8</td>
<td>4.5</td>
<td>4.9</td>
<td>5.4</td>
<td>5.1</td>
<td>1.6</td>
<td>1.6</td>
<td></td>
</tr>
<tr>
<td>9   <em>G. dorcas ssp.</em></td>
<td>11.4</td>
<td>5.1</td>
<td>5.3</td>
<td>5.8</td>
<td>4.3</td>
<td>1.0</td>
<td>1.0</td>
<td>1.2</td>
</tr>
</tbody>
</table>

**Discussion**

Autosome numbers, shape and the characteristic subtelocentric X-chromosomes of the Saudi dorcas gazelle are identical to dorcas gazelle from Africa, suggesting strongly that the two groups are the same species. The subtelocentric X-chromosomes occur in dorcas gazelle only, whereas most other species have submetacentric X-chromosomes. Sequence data support the conclusion that the Saudi dorcas gazelle is a subspecies of dorcas gazelle.

The ancestors of the Saudi dorcas gazelle were caught in south-west Saudi Arabia which makes it very likely that they are the Arabian representative of the dorcas gazelle. Unfortunately, Saudi dorcas gazelle have not been sighted recently and are probably extinct in the wild.

On the basis of some morphological features, i.e. horn shape, Furley *et al.* (1988) suggested that Saudi gazelle should be separated from dorcas gazelle and should be grouped with Indian gazelle. Other morphological data clearly separate Saudi gazelle from Indian gazelle (Groves, this volume) which is in sharp contrast with the results presented here and with Furley's results.

It is obvious that the karyotypes of the Saudi gazelle are different from African and Saudi dorcas gazelle, which makes it very unlikely that the two belong to the same species or can even hybridize. Most obvious in Saudi gazelle is the variation in number of subtelocentrics, but other chromosomes also seem to be rearranged. However, karyotypes of Saudi gazelle are very similar to those of Indian gazelle (Furley *et al.*, 1988; Kumamoto and Rebholz, unpublished data), the only difference between them being that Saudi gazelle has 10 to 13 metacentric autosomes whereas the Indian gazelle has only eight. A similar sort of intraspecific karyotype variation is found in Soemmerring's gazelle (Benirschke *et al.*, 1984).
Cytochrome b sequence data confirm the karyotyping results: the Saudi gazelle is more closely related to Indian gazelle than to dorcas gazelle, and all dorcas gazelles are closely related to each other. Since dorcas gazelle subspecies show sequence divergences of between 1.0% and 1.6%, the sequence data strongly indicate that Saudi gazelle and Indian gazelle belong to the same species, but have separate subspecific status.

As is the case for the Saudi dorcas gazelle, Saudi gazelle in the wild have probably been hunted to extinction by now (Nader, 1987; Groves, 1989; Thouless et al., 1991), although in the early sixties "local hunters stated that it still occurred in fairly large numbers in the wastelands of southern Iraq, eastern Jordan and in restricted localities in northern Arabia" (Lewis et al., 1965). According to Gross (1987) there is a large herd of Saudi gazelle on an island off the coast of the Northern Emirates, but so far this information has not been verified.

Despite all the confusion about the Saudi gazelle and Saudi dorcas gazelle, the results presented here clearly show that they should be bred in separate captive breeding programmes. There is also clearly a need to take immediate action for organized breeding programmes, since both species are in only one collection (Saudi dorcas gazelle) or three collections (Saudi gazelle), which leaves them vulnerable to demographic catastrophes.

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We are indebted to Dr Marie Rodway and the reviewers for their comments on the manuscript and to Dr Frank Rietkerk, Dr Arnaud Greth, and Nick Lindsay for collecting the samples. We are also grateful to Terry Dennett for printing the photographs. We are grateful to the National Commission for Wildlife Conservation and Development (NCWCD), and Sheik Khalid Bin Mohamed Bin Ali Althani from Qatar for their support of this work and for the opportunity to sample their gazelles.

References


Chris Hillman

Abstract: The Antelope Specialist Group (ASG) of IUCN's Species Survival Commission (SSC) was established in 1978 with the priority of determining the conservation status and trend of antelope species. Since 1985 the information obtained has been compiled, and to date three volumes entitled "Global Survey and Regional Action Plans" have been produced covering sub-Saharan Africa. The fourth volume will cover North Africa and Asia.

Most country information is qualitative, underlining the urgent need for quantitative antelope data. Limited information on population dynamics indicates a downwards trend for many species, due to habitat loss, modification and commercial over-utilization for meat. Certain species are now in a critical state. A further limitation of the information concerns the taxonomy of certain groups, particularly the gazelle, duiker and hartebeest groups.

The ASG is primarily a scientific advisory group, highlighting the need for integration of action plans for all taxa for geographic and political areas; and identifying areas where conservation organizations should direct assistance. The onus is upon national governments to carry out specific aspects of action plans. At present limited information is available and species in need of attention have been identified; limited funds exist, but can rarely be directed efficiently at the needs of a species, without the integrated overall environmental management required.

Keywords: IUCN/SSC, ASG, global survey, action plan, conservation, antelope

Introduction

This paper attempts to outline the work and policy of the IUCN Species Survival Commission Antelope Specialist Group (IUCN/SSC ASG). The information presented relies heavily on the tremendous work put into the Antelope Specialist Group productions, collated and compiled by Dr Rod East. These represent much of what is known about antelope at the present time, and contain specific references and communicators' names and contacts from which the information was amassed. My own conservation knowledge and work experience is limited to East and north-east Africa and to antelope in general, but has evolved into concern for the overall environment and man's part in it. The paper also attempts to address the context of the present meeting with reference to gazelle and wildlife conservation in the Kingdom of Saudi Arabia.

Global antelope survey

The Antelope Specialist Group (ASG) was established in 1978, and held its first formal meeting in 1980. At this it was decided that the first priority for the group was the determination of the conservation status and population trends of all antelope species. Hence the Global Survey was instigated. Simple report forms were sent out initially to people in the field, and with experience from various antelope areas; however the main effort did not begin until 1985, when a volunteer - Dr Rod East of New Zealand, offered his services as compiler. Since that time the three current volumes of the ASG Global Antelope Survey and Action Plans have appeared (East, 1988; 1989; 1990). They
reflect the truly remarkable output of one man, and his extraordinary efficiency in eliciting and collating reports from antelope and other wildlife workers around the world. Part 4 should be out in the near future, after publication of the IUCN Antelope Red Data Book (East, pers. comm.).

A precursor to Volume 4 exists in the form of a paper presented recently by Rod East to the joint SSC Captive Breeding Specialist Group (CBSG) - ASG - AAZPA Antelope Taxon Advisory Group meeting, held at the Living Desert, Palm Desert, California in January 1992 (East, 1992a). This summarizes the information collated to date on the 23 species of antelope known from North Africa and Asia.

The goal of the ASG international conservation policy is "to ensure the long term survival of all antelope species by maintaining as many viable populations as possible of each species in as wide a range of its habitats as is practical" (East, 1988). This begs the question: "What is a species?" and hence the present very thorny and sometime controversial considerations over species and subspecies, probably nowhere more knotty than amongst the gazelle, duiker and hartebeest.

The three volumes produced cover three major regions of Africa - essentially East, Southern and West - and have each been treated on a political country case, ending with an overview of the antelope and general conservation status for the region, and finally action plans for each region. These plans have tended more to specific geographic locations within the region and their antelope populations. These locations are in the main existing protected areas such as National Parks.

The results of the survey to date have been more of a qualitative than quantitative nature. It has been possible to collate species lists for most countries, and to a greater or lesser extent determine their distribution and conservation status. The species/subspecies question comes up in every volume and in the main the criteria used have been based upon recognition by the International Commission of Zoological Nomenclature, with mention made of prominent subspecies as recognized in the area or country concerned. Quantitative data is limited to those protected areas and countries where wildlife conservation is well-established and sufficient expertise and resources have existed for some time. This is particularly true in some East and Southern African countries (Kenya, Tanzania, Uganda, Zimbabwe, South Africa, Botswana, Namibia).

It is evident that much more detailed information is required on antelope numbers and trends. These are best obtained from repeated aerial and/or ground censuses and nation-wide monitoring of all wildlife species. This is an expensive process, in terms of funds, personnel and time, and one which can be supported by few developing countries. Kenya established the Kenya Rangeland Ecological Monitoring Unit (KREMU) over a decade ago; Tanzania recently established the Tanzania Wildlife Conservation Monitoring Programme. Similar programmes exist in other African countries, usually operated by the national wildlife management authority. Elsewhere, subjective assessment of antelope numbers and trends have been made, usually by people with long-standing experience of the area concerned.

The survey stage of the process is not an end in itself; it is not a "stamp-collecting" exercise to accumulate all the academic knowledge possible on the existence of antelope species. It is an attempt to collate the relevant information and data required in order to plan for the long-term maintenance of components of the complex three-dimensional ecological processes on which the future of the earth, and thus mankind, depends. Antelope conservation is but a part of the overall environmental conservation strategy, taking full account of, and integrated with, human development needs (East, 1988).
The Global Antelope Survey and Action Plans are not a one-off exercise. Human development and natural evolution are dynamic processes, with change appearing all the time. The ASG regular publication "Gnusletter" includes updates on antelope information from various countries and workers, which in time will need to be incorporated into the Survey and Action Plans. At present the whole exercise is run and maintained by volunteers - two in particular - co-ordinator and compiler Rod East and the Chairman Dick Estes - supported by an army of volunteer correspondents in the field, including many of the people at the present Arabian Gazelle Workshop. It is evident that eventually professional full-time staff will be required to maintain the impetus, integrate new data with the old and update plans.

Action plans
Three parts have now been completed, Part 1 in 1988 (East and North-East Africa), Part 2 in 1989 (South and South-Central Africa), and Part 3 in 1990 (West and Central Africa). These cover the sub-Saharan region, leaving North Africa and the countries of Asia with Antelopes to be covered in Part 4 (North Africa and Asia), currently under preparation. Part 4 will be appropriate to the present deliberations, and will cover a vast area, but an area relatively poor in antelope compared with the areas of Africa covered in the first three parts, which probably contain 90% of all antelope species and populations (Estes, pers. comm.).

Priorities and strategy for antelope conservation action were established from the survey results, including the preparation of Regional Action Plans in the four regions covered. The responsibility for more specific action planning is considered to lie with the wildlife conservation authorities of the countries themselves, making use of the information and appropriate action plans in the Survey and Action Plans. While the Antelope Specialist Group does not have the resources to ensure that this happens, the onus is on the world conservation community to enable the integration and implementation of these group-specific Action Plans within any one country or region. If such integration and implementation is not carried out by the relevant national (e.g. NCWCD) and international conservation organizations, then the effort expended in collating and compiling the Action Plans will have been wasted, except as a historical documentation exercise. The SSC is currently engaged in an exercise to determine how best such integration of Specialist Groups' Action Plans can be carried out on a regional or country basis.

It is evident (East, 1988) that the long term survival of antelopes depends upon:
- The adequate protection and management of natural habitat in conservation areas (e.g. National Parks);
- The development of landuse disciplines that enable the co-existence of human and wildlife populations to the greatest degree possible;
- Greater public awareness of the need for and values of wildlife conservation, including utilization schemes.

The Regional Action Plans in each volume concentrate on specific areas and problems of antelope conservation within the region and countries covered, mainly concentrating on country-specific aspects and protected areas. In addition some general activities are suggested:
- Political and government action requires stimulation, including top-level approaches by the Director-General of the IUCN as opportunities present themselves;
National (central) government political action is required to stimulate field action. The National Conservation Strategy processes provide a framework for the implementation of Action Plans;

- Regional co-operation in antelope conservation is recommended, but probably limited to conservation areas in border zones and cross-border antelope species;
- Field action requires surveys of antelope status, and management of conservation areas;
- Captive breeding, which can provide insurance against extinction.

The strategies for antelope conservation include:

- Strict protection
- Tourism (including sport hunting)
- Sustained-yield utilization (e.g. farming, cropping, subsistence hunting)
- Multiple resource use
- Local participation in conservation planning
- Conservation education
- Sociological research
- Enlisting public support.

This is not the place in which to investigate and describe the actions proposed above. They are little different to those proposed by many other SSC Specialist Groups and conservation bodies around the world. There is an enormous literature on the various topics, not least on captive breeding as a means of ensuring both the continuity of a species, and the availability of a viable population for reintroduction. It is worth noting however, pertinent to the present workshop, the enormous costs involved in captive breeding and the maintenance of populations of larger animals such as antelope for prolonged periods in captivity (Conway, 1986), and also that captive breeding is no substitute for the maintenance of adequate areas of natural ecosystem with wild populations. Captive breeding can be a complement to integrated protected area conservation but must not be mistaken as the final solution. In situ conservation offers the most economically efficient and ecologically meaningful way of conserving antelope species and their ecosystems for the long-term future.

**Actions**

The primary aim of the SSC Specialist Group Action Plans is to recommend actions that preserve existing wild populations as the most ecologically efficient means of long-term self-sustaining conservation. Captive breeding and reintroductions are seen merely as stop-gap measures, providing an insurance policy against total extinction in the wild, towards the time when the re-establishment of a wild population is possible in the natural ecosystem.

There are severe constraints to the implementation of antelope conservation action plans, including limited financial resources and shortage of land for protected area conservation - as envisaged in the earlier conservation ethos of totally protected areas, which were thus isolated from reality.

There is now new acceptance that this was a limited vision of conservation based mainly upon the powerful commercial driving forces of Western tourism and recreation. It is almost impossible to achieve total "preservation" of significant land areas and their ecosystems, except in the
past colonial Africa and Asia, and even that possibility has now been eclipsed by events - not least human population growth in the less and least developed countries, and the aspirations for ever-improving living standards of human populations in the developed world. This is particularly the case in sub-Saharan Africa, the point being well made by East (1992b) "it is clear that Africa will change dramatically in the next century".

The role of the ASG has come to be seen as that of a scientific advisory group (East 1988; 1989; 1990). Components of this role include:

- Monitoring the status of antelope;
- Highlighting the problems of antelope conservation;
- Recommending practical solutions;
- Monitoring the success of attempts to integrate wildlife conservation and development;
- Identifying key areas where international assistance should give high priority.

The Bulawayo meeting of the ASG in 1987 further resolved that the ASG should establish three Regional Subgroups based upon the Action Plan framework (and presumably a fourth for North Africa and Asia), which would promote implementation of the Regional Antelope Action Plans by:

- Bringing priorities to the attention of the national conservation authorities;
- Recommending practical solutions, and providing technical help where requested;
- Continuing to monitor antelope status and providing updated information to the ASG data bank;
- Monitoring the success of attempts to conserve and utilize antelopes;
- Publicizing and obtaining funds for specific ASG projects.

Priority species then considered to be critically threatened were Hunter's hartebeest *Damaliscus hunteri*, and Swayne's hartebeest *Alcelaphus buselaphus swaynei* - a subspecies. It was proposed at the Bulawayo meeting that the ASG would actively pursue conservation assistance for these species where they occur (Kenya and Somalia, and Ethiopia respectively), but no progress was subsequently possible in this matter due to the local political situations, and the lack of ASG resources.

In addition it has been suggested that a Wildlife Management Advisory Group should be established to integrate Action Plans for all sub-Saharan Africa, and promote their implementation; and that more nationals who are actively involved in natural resource management should be involved in ASG activities in their own countries.

The ASG is entirely voluntary in its efforts and has no resources to implement the action plans it puts forward. Further, few countries where antelope exist can afford the luxury of putting plans into effect specifically for antelope species. Similar plans have been completed and forwarded to them by other SSC specialist groups, including Primates (Oates, 1986), Cetaceans (Perrin, 1989), Mustelids and Viverrids (Schreiber et al., 1989), Tortoises and Turtles (IUCN, 1989), Elephant and Rhino (Cumming et al., 1990), and Canids (Ginsberg et al., 1990).

There is an evident need for the integration of these plans with those of other and relevant SSC groups to establish overall regional and national conservation priorities and programmes. The National Conservation Strategy process is the most relevant framework, since in the end most conservation action is within a political national framework, rather than on a regional or continental
past colonial Africa and Asia, and even that possibility has now been eclipsed by events - not least human population growth in the less and least developed countries, and the aspirations for ever-improving living standards of human populations in the developed world. This is particularly the case in sub-Saharan Africa, the point being well made by East (1992b) "it is clear that Africa will change dramatically in the next century".

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There is an evident need for the integration of these plans with those of other and relevant SSC groups to establish overall regional and national conservation priorities and programmes. The National Conservation Strategy process is the most relevant framework, since in the end most conservation action is within a political national framework, rather than on a regional or continental
basis. The final compromise will provide for as many of the priorities as possible through coordinating species conservation priorities where they are common to a geographical area as far as is possible.

This suggestion is not unique to the ASG or even Africa. It is a concept that has been under consideration by the SSC for sometime, and continues to be developed and pursued - in the formation of SSC National Committees (S.N. Stuart, pers. comm.). "Successful implementation of Action Plans is most unlikely to occur where it relies heavily on the efforts of dedicated but over-committed volunteers who are remote from where the action is" (East, 1992c).

Relevance of the Action Plans to gazelle conservation in the Arabian peninsula

It is very evident from the contributions given to the present workshop that sterling work has been done in determining the genetic status of the various "forms" of gazelle currently under consideration in the Arabian peninsula. It is also clear however, that a very confused situation exists as to what comprises the subspecies and even the species represented, and that very little information exists or is being gathered from the wild populations remaining. One article (Magin, this volume) addresses the present survey of gazelle in the south of the Kingdom of Saudi Arabia, while another (Williamson and Tatwany, this volume) makes brief mention of some aerial and ground surveys. Conservation status of wild gazelle has been reported on in the recent past (Thouless et al., 1991), but the results of systematic surveys carried out in the wild have not been presented, neither have materials from wild individuals yet been accessed for genetic and taxonomic studies.

It is very clear from the various contributions that detailed genetic research has been carried out on gazelle taxonomy, but however, based almost entirely on captive animals in the Kingdom and Gulf states, and elsewhere. Clearly the provenance of these animals is very doubtful, with ample opportunity having existed in the past for hybridization to have occurred in the various collections (Habibi, 1992), and even in the introduction of gazelles to the Farasan Islands (Thouless and Al Bassri, 1991).

It is imperative that a programme for field conservation is initiated, as equally well-supported as the excellent genetic assessment of captive populations. The present survey in the wild between Taif and the Yemen border is only proposed to last for 6 months. In addition, every attempt should be made to collate existing information and material from the wild into a comprehensive data base, taking every opportunity to assess gazelle taxonomy from material from wild individuals.

The continued survival of gazelle and other wildlife in the Arabian peninsula will depend, as in other areas of the world, on successful field conservation management, integrated with other landuse disciplines. Considerable attention is presently being given in the Kingdom and other countries of the peninsula to captive breeding of animals that have, for the most part, been maintained in captivity from various uncertain origins.

In summary, the following are evidently required:

- A parallel well-supported field conservation programme, based upon the Protected Areas System Plan (Child and Grainger, 1990), and updated with more recent knowledge;
- Data and material of known provenance for taxonomy;
- Amalgamation of genetics data with ecological and behavioural data;
- Maintenance of areas for reintroduction in the wild;
• Studies of gazelle growth rates and development in captivity for the assessment of the
validity of morphological characters in taxonomic assessment;
• Integration of conservation and environmental management activities between the various
authorities concerned, on a national and regional basis, in order that environmental
conservation on the peninsula as a whole shall benefit and progress.

Conclusion
If we fulfill the ASG goal of conserving "as many populations as possible over as wide a range of
habitats as possible" then we will probably have covered much of the genetic variability within a
"species". The more attention we give to "subspecies" and "races", the more times we have to
subdivide the conservation dollar, and the more costly captive breeding becomes. It is more efficient
at this juncture to concentrate efforts to maintain what we have where we have it, as far as is possible,
while at the same time determining the taxonomic affiliations. In the long run, it is the conservation
of sufficient areas of ecosystems, as naturally complete as possible, that will ensure the survival of
genetic variability, biodiversity and species.

For as long as surveys and action plans continue to accumulate without any action
forthcoming, or in the case of the developing countries, the means to achieve the action being
proposed, they will continue to be looked upon as useful sources of information on various taxa, and
as ideals that cannot be achieved. The very high proportion of involvement by academic workers
outside the areas where the species exist, and/or by expatriates, also labels the plans as a form of
technical tourism, with limited relevance to real life in the developing world.

This is where national co-ordinating committees, based on the NCS process, could make the
greatest contribution in amalgamating all proposals for the conservation of various aspects of the
environment into a national plan. It is, sadly, far easier for example to fund the development and
management of the Senkelle Swayne's Hartebeest Sanctuary (54 km²) for example, than it is to deal
with Ethiopia's critical problems of human survival in the face of crippling environmental
degradation, civil war and famine - all of which stem from the failure of the global community
(including Ethiopia) to achieve an equitable sharing of natural resources and the development of
reasonable living standards globally. We in northern countries continue to commandeer more than
our fair share - 80% - of natural resources at bargain prices, despite the fact that we comprise such a
small proportion of the world's population - 20% (IUCN, 1980).

Until such time as we find a solution to human survival needs and the maintenance of critical
ecological processes, the management of protected areas in Africa and much of Asia, is doomed to a
cycle of burgeoning defensive wall construction, and failure. Recent events in Ethiopia illustrate
only too well the consequences of the removal, albeit briefly, of the defensive system presently
ensuring the survival of protected areas and their species. Within a few days three endangered large
mammal species - two of them antelope - had been brought to the verge of extinction (Hillman, 1991;
Tadesse et al., 1992). Similar tragedies can be expected elsewhere as the pressure on the
environment builds up in one of the scenarios visualized by East (1992b). The alternative scenario
(to that above) - of falling human population levels, improved living standards and the return of the
benefits of conservation to the people of the area - is plausible, but only at extreme costs in human
terms (famine, war and AIDS).
In contrast, consider the situation in Oman where local people are involved at all stages of the reintroduction of the Arabian oryx *Oryx leucoryx*, incorporating their traditional environmental conservation of the natural fauna and flora (Stanley Price, 1989). A similar situation existed here in Saudi Arabia with conservation of living natural resources in the traditional hema system, which it has been suggested should be re-instituted as a means of modern communal conservation (Child and Grainger, 1990).

We have to work towards the integration of our conservation requirements into the framework of daily life. Two simple antelope examples illustrate this necessity. The impala *Aepyceros melampus* demonstrably plays a part in the collection, modification, distribution, and eventual germination of *Acacia* seeds through ingesting them and their pods as a food source (Jarman, 1976). The same may be true for the gazelle under question at this workshop, which may play a significant role in tree propagation in the Arabian peninsula. As a second example, the presence of the mountain nyala *Tragelaphus buxtoni* in the high mountains of Ethiopia probably has some effect upon the electricity supply of the capital Addis Ababa, and of neighbouring Djibouti and Somalia, through its effect upon natural vegetation, water flow, dam water levels and siltation, and the production of vital local and exportable hydroelectricity.

No single component, for example a gazelle subspecies, or even all gazelle species, is in itself critically important - but all contribute to the overall ability of the environment to support life. Any simplification through species extinction and/or habitat loss, leads to the reduced capability of the earth's environment to support all other forms of life, including man himself.

The Global Antelope Survey and Action Plans cannot hope to solve these problems alone, but they are all part of an effort - co-ordinated to a degree - to address the situation. We must keep this in mind as we seek to decide what is a species and what a subspecies, and how much we can spend on captive breeding, in addition to habitat maintenance and humanitarian relief and development in the real world.

Why do we conserve? We each have our own reasons for being involved in wildlife and antelope conservation, but generally I believe we conserve to:

- Ensure sustainable ecological functionality, to withstand the inevitable further human increase and increased living standards without ecological collapse;
- Ensure the sustainable supply of natural resources for man's use;
- Maintain our heritage, for ethical reasons, and the moral right of all species to survive;
- Support human recreation and the associated tourism industry.

For our own credibility we need to ensure that all the above reasons are seen to be satisfied, and not just our own personal selfishness, or deep interest in one taxon, or simply because we enjoy it. Considerable attention has been paid to the initial taxonomic and catalogue stage of the Antelope Specialist Group work. Much more attention now needs to be paid to enabling the action proposed to occur, and obtaining detailed field data on antelope numbers, ecology and future survival in the wild.

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References


Protected Areas; workshop on the impact of civil conflict and war on protected areas; held at Caracas, Venezuela. 10 pp.


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Abstract: Nineteen different areas in south-west Saudi Arabia from which gazelle had been reported in the last five years (1988 - 1992) were visited between August and December 1992. Ground surveys were carried out on foot in the company of reliable local guides with an intimate knowledge of each area. Time spent on ground surveys varied from one half to eight days. Evidence of the continued presence of gazelle (faeces, tracks, sightings, reports) was obtained at 10 locations. All these populations were small: estimated population sizes ranged from five to 50. In eight of the remaining areas it appeared that gazelle had become locally extinct since the last report or visit by NCWCD biologists, while at one it was not clear whether gazelle had ever been present in the recent past. Thus populations currently appear to be becoming extinct at a truly alarming rate (eight out of 18, or 44% extinctions in the past five years).

Ninety seven gazelle observations were made, of which 10 were actual sightings. A total of 17 gazelles were seen in five different locations. Group size ranged from one to three (mean = 1.7, SD = 0.7). All observers identified the gazelles seen as Gazella gazella cora. In the five areas where gazelle spoor was found but no gazelle were seen, local people were unanimous that the taxon present was also G. g. cora. No evidence was found for the existence of G. g. erlangeri in the survey zone. The major current threat to gazelle populations is illegal hunting. Immediate and effective action by NCWCD is needed to protect those remnant gazelle populations which may be viable in the long term.

Keywords: Mountain gazelle, Gazella gazella cora, south-west Saudi Arabia, survey, population status, conservation recommendations.

Introduction

Many reports and publications have stressed the critical status of the small scattered populations of gazelle on the mainland of south-west Saudi Arabia (e.g. Child et al., 1989a,b; Thouless et al., 1991). Prior to the start of the survey, it was suspected that two taxa, both subspecies of the mountain gazelle or idmai Gazella gazella, might occur in this zone: namely Gazella gazella cora and Gazella gazella erlangeri. The overall status of G. g. cora is unclear. There may be a significant population of several thousand in the Jiddat al-Harasis region of Oman, but Daly (1993) states that its subspecific identity has not yet been firmly established. However, on a national level it is highly endangered in Saudi Arabia. No wild population of G. g. erlangeri has yet been discovered. Both these taxa are poorly represented in captivity.

The overall aim of this field project was thus to identify all significant mainland populations of gazelle in the south-west of Saudi Arabia, and where feasible outline appropriate conservation
measures for their protection. Three basic questions about the populations therefore needed to be answered: Where? What? and How many? (i.e. where are gazelle located, what taxon do they belong to, and how many of them are there). The survey zone covered the Asir / Sarawat mountains and Tihama coastal plain, from Taif and Jeddah southwards to the border with Yemen. This area is approximately 300,000 km² in extent (roughly the same size as Italy), and lies between latitudes 16.00 and 22.00°N, and longitudes 39.00 and 45.00°E.

Methods

The limited timetable of six months available for the survey was obviously insufficient to allow a systematic coverage of such a large area. Instead, attention was focused on those areas from which gazelles had previously been reported. A great deal of information on gazelle distribution in the survey zone was obtained through discussion with the staff and researchers of the National Commission for Wildlife Conservation and Development (NCWCD), the National Wildlife Research Center (NWRC), the King Khalid Wildlife Research Center (KKWRC), and by a literature search of scientific and technical reports. A total of 38 recent (i.e. from 1985 - 1992) reliable observations of gazelle or their signs (tracks, faeces, bedding sites, corpses, etc.) were identified. These were located in four main areas: Qilwah; Al Aqiq; Mahkshush; and scattered observations in the Tihama coastal plain from Al Lith south to Jizan.

In addition, around 10 areas were identified as potentially harbouring gazelle, based on communications received by the NCWCD from local people in response to appeals for information on wildlife distribution. Every effort was made during the survey to visit all the areas identified by the methods above, together with all new areas to which we became alerted during the course of fieldwork.

On most field trips an Arabic-speaking biologist / interpreter was provided by NCWCD, which enabled standardized interviews to be conducted with local residents in each survey area. Data obtained from these included the past and current distribution of gazelle, the taxon to which they belonged (as identified from photos and / or the wildlife poster produced by NCWCD), population estimates, and information on other wildlife species present. In addition, local opinion on the levels of illegal hunting and reasons for inferred population trends was canvassed - these data are analyzed and discussed by Magin and Greth (1994).

Contact with the relevant civil authorities was extremely important to the success of this project. During field trips, courtesy calls were always paid to the local Emarah (the headquarters of an Emirate) and frequently valuable help (information, guides, extra vehicles) was obtained from the Emirs and their staff. The guides obtained from the Emarahs proved particularly useful at putting local people at ease - since although hospitable the Bedu are by nature wary of strangers - thus persuading them to help answer our questions.

Each ground survey trip was undertaken with a local guide, who took us on foot and by car to the areas where he knew or suspected gazelle were present. Gazelle observations (visual sightings, presence of tracks or faeces, discovery of skulls or corpses) were recorded on standardized observation forms in the field, and were later entered into a Microsoft Word computer database which will be continued and updated by future workers. The database was also converted to a GIS format, enabling distribution maps to be output and compared with other species. Amongst the data noted for each observation were the date, place name, geographical co-ordinates (recorded using a
Sony IPS-360 Global Positioning System), habitat type and condition, and estimated distance to the nearest habitation. Full details of standardized observation forms and interview questionnaires are given in Magin and Greth (1992).

In regions where gazelle spoor was found at relatively low densities every sign (tracks and faecal pellet groups) was recorded. At higher densities tracks were ignored, except where they provided evidence that gazelles used areas where no faeces were found. Where gazelle spoor was very abundant (for example in the Tamarix woodland at Mahkshush), only those signs which helped to delimit the range of the gazelle were recorded. Observations of other fauna of significant conservation interest (e.g. wolf Canis lupus, striped hyaena Hyaena hyaena) were also noted.

Counts of gazelle faecal pellet groups were used as an index to compare gazelle density in different areas. Gazelle population sizes were "guessimated" from a combination of interviews with local people, subjective comparisons between areas and estimates of the total gazelle range in each area.

Results

During the first five months (August - December 1992) of the survey, 19 different areas from which gazelle were reported or suspected were visited (see Figure 14.1). Evidence of the continued presence of gazelle was found at 10 of these locations. In eight of the remaining areas it appeared that gazelle had become locally extinct since the last report or visit by NCWCD biologists, while in one, (Musfirah) because of a possible confusion between gazelle and Nubian ibex Capra ibex nubiana it could not be determined whether gazelle had ever been present in the recent past (Table 14.1).

Ninety seven gazelle observations were made, of which 10 were actual sightings. A total of 17 gazelle were seen, of which nine were seen by the author (seven corroborated by other witnesses i.e. Arnaud Greth, Nigel Brown and Bachar Al Abed) and eight by other members of the survey team (five by Abdullah Mutairi and three by Kevin Dunham and Faye Robinson together). Group size ranged from one to three (mean = 1.7, SD = 0.7). All observers considered that the gazelles seen were G. g. cora.

Most of the gazelle populations inhabited watershed areas of rocky hills dissected by small wadis, in which were no through routes and little human habitation. With the notable exception of Mahkshush the vegetation was remarkably similar in most areas. Typical tree species included Acacia tortilis, Acacia ehrenbergiana and Lycium shawii, while ground cover consisted mainly of Blepharis ciliaris, Indigofera spinosa, Tribulus, Fagonia and Heliotropium spp., with the grasses Aristida and Stipagrostis spp. At altitudes over approximately 1,000 m the woody species Acacia azak was found, while at lower elevations Commiphora spp. were common. All gazelle habitats examined shared the characteristic of being difficult terrain for motor vehicles, where off-road driving would be tortuously slow, and were accessible only by a limited number of tracks.

Conservation assessments of the 10 areas where the presence of gazelle was confirmed are given below.
Figure 14.1 Map of gazelle survey zone in south-west Saudi Arabia.
1. Mahkshush
The gazelle habitat consists of about 210 km² of low-lying coastal sand dunes, "subqha" salt flat and *Tamarix* woodland on the southern edge of the outwash fan of Wadi Hali. The population is thought to number around 50 head (Child *et al.*, 1989a; Thouless *et al.*, 1991; Magin, 1992b) and is therefore probably the largest remaining mainland population of mountain gazelle in the south-west of Saudi Arabia. There appears to be no direct conflict between gazelle conservation and human use in the core gazelle area: due to the highly saline soils and frequent flooding, the habitat is basically unusable for cultivation and only lightly grazed by livestock (camels, donkeys and cows). The surrounding higher zones are however heavily settled. The main threat to the population appears to come from illegal hunting. This is reported to occur mainly at night (since the gazelle in this area are almost totally nocturnal) using vehicles and/or rifles. Local people and members of the Coastguard are reportedly the main culprits. The population is therefore in great need of protection. The Mahkshush area has been recommended for gazetting as an SNR or Special Natural Reserve (Child *et al.*, 1989a; Child and Grainger, 1990), but no action has yet been taken. The appointment of one or two local "auxiliary" rangers (see Discussion) at Kiyad/Mahkshush/Sa'īdah would seem to be a necessary intermediate conservation step (Magin 1992a,b).

2. Habib Ben Ideeb
The village of Habib Ben Ideeb is situated some 30-40 km inland from Mahkshush at the edge of the Tihama foothills. Gazelle occupy an area perhaps some 500 km² in extent lying mainly to the north, south and east of the village. However, they are only present at very low densities, and the population is probably much smaller than at Mahkshush - perhaps 15-20 individuals. The habitat consists of rocky hills, undulating sandy plateaux with low dunes, and "harrats" or old lava flows. Gazelle seem to take refuge in those parts of the terrain which are inaccessible to motor vehicles, but most of the area is open and easily negotiable. There is some rain-fed cultivation of millet and sorghum on sandy areas, but most of the local people are settled in permanent villages and depend on livestock for their main livelihood. Illegal hunting, mainly by non-local people, appears to be the main threat. The area has been recommended for protection as an RUR or Resource Use Reserve by Rahmani and Shobrak (1992) mainly for the conservation of the Arabian bustard *Ardeotis arabs* but no action has yet been taken. From the point of view of gazelle conservation it would appear to be a low priority area: gazelle are only present at low densities and the area is large, easy to access and would therefore be difficult to police effectively (Magin 1992a).

3. Tibalah (Wadi Shirs)
In this region gazelle occupy an upland watershed area of rocky hills dissected by narrow wadis, interspersed with small undulating plateaux, estimated as some 120 km² in extent. In a 25 km² core area of the population range, gazelle densities are much higher than in the periphery. The total population is estimated as 15-40, but would undoubtedly increase rapidly with protection. Motorized access is restricted to several vehicle tracks passing along the narrow wadi beds. The area is used by nomadic Bedu pastoralists and their flocks, but livestock densities are relatively low. Illegal hunting by locals and outsiders is the main threat, which may be increased by the possible development of a mine some 10 km to the north. Prospects for protection are however good, if the Commission can
recruit several auxiliary rangers from among the local population, many of whom expressed enthusiasm for the conservation of "their" gazelle (Magin 1992a, 1992b).

Table 14.1 Summary details of gazelle areas visited between August and December, 1992.

<table>
<thead>
<tr>
<th>Area</th>
<th>Co-ordinates</th>
<th>Habitat / Altitude1</th>
<th>Population / Threats</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mahkshush</td>
<td>18°40'N 41°20'E</td>
<td>Sand dunes, subqha, Tamarix woodland; 0-30m</td>
<td>50; Hunting</td>
</tr>
<tr>
<td>Habib Ben Ideeb</td>
<td>18°41'N 41°37'E</td>
<td>Rocky hills, sandy plateaux; 100-800m</td>
<td>15-20; Hunting</td>
</tr>
<tr>
<td>Tibalah</td>
<td>20°03'N 42°05'E</td>
<td>Rocky hills; 1,500-1,800m</td>
<td>15-40; Hunting</td>
</tr>
<tr>
<td>Jabal Bahth</td>
<td>19°15'N 42°30'E</td>
<td>Rocky hills; 1,600-1,800m</td>
<td>&lt;50, in 5 small scattered populations; Hunting</td>
</tr>
<tr>
<td>Jabal Jandaf2</td>
<td>19°31'N 42°24'E</td>
<td>Rocky hills; 1,800m</td>
<td>5-10; Hunting</td>
</tr>
<tr>
<td>Wadi Iribidah</td>
<td>20°30'N 40°20'E</td>
<td>Rocky hills; 100-600m</td>
<td>&lt;20; Hunting</td>
</tr>
<tr>
<td>Jabal Ghurab</td>
<td>16°46'N 43°04'E</td>
<td>Rocky hills and low plateaux; 100-700m</td>
<td>10-20; Hunting, habitat loss</td>
</tr>
<tr>
<td>Jabal Marwan</td>
<td>19°47'N 41°07'E</td>
<td>Rocky hills; 150-600m</td>
<td>15-30; Hunting</td>
</tr>
<tr>
<td>Al Habda</td>
<td>17°38'N 42°41'E</td>
<td>Rocky hills; 300-800m</td>
<td>20?; Hunting, drought</td>
</tr>
<tr>
<td>Wadi That Al Qarn</td>
<td>17°46'N 42°27'E</td>
<td>Rocky hills; 100-500m</td>
<td>15-20; Hunting</td>
</tr>
<tr>
<td>Musfirah</td>
<td>18°31'N 42°27'E</td>
<td>Rocky hills, mountain scarp; 2,000m</td>
<td>0; Confusion between gazelle &amp; ibex?</td>
</tr>
<tr>
<td>Al Quz</td>
<td>17°10'N 42°22'E</td>
<td>Coastal dunes; 0-20m</td>
<td>0; Hunting</td>
</tr>
<tr>
<td>Khabat Al Doh</td>
<td>16°28'N 42°50'E</td>
<td>Coastal scrub; 0-50m</td>
<td>0-1; Hunting</td>
</tr>
<tr>
<td>Wadi Shair</td>
<td>20°19'N 41°48'E</td>
<td>Rocky hills; 1,300m</td>
<td>0; Hunting, disturbance</td>
</tr>
<tr>
<td>Jabal Al Shurafah</td>
<td>20°27'N 41°30'E</td>
<td>Rocky hills; 1,600m</td>
<td>0; Hunting, disturbance</td>
</tr>
<tr>
<td>Wadi Thurabah2</td>
<td>20°33'N 41°24'E</td>
<td>Rocky hills; 1,500-1,900m</td>
<td>0; Drought, hunting</td>
</tr>
<tr>
<td>Al Qusaiba</td>
<td>19°43'N 41°07'E</td>
<td>Rocky hills, sand dunes; 100m</td>
<td>0; Hunting</td>
</tr>
<tr>
<td>Qu'arshar</td>
<td>19°45'N 41°06'E</td>
<td>Low rocky plateau; 50-150m</td>
<td>0; Hunting</td>
</tr>
<tr>
<td>Jabal Nakrah</td>
<td>19°57'N 41°01'E</td>
<td>Rocky hills; 200-400m</td>
<td>0; Hunting, new settlement</td>
</tr>
</tbody>
</table>

1 = Altitudes given are approximate only.
2 = Wadi Thurabah is not a mis-spelling of Wadi Turubah, but a small side branch of the nearby Wadi Baydah.

4. Jabal Bahth
Gazelle are reported to occur in small numbers at five discrete locations (Wadi Meri, Wadi Hanif, another Wadi Hanif further south, Damm al Hammar, and Wadi Huwarah) along a ridge of high ground some 40 km long by 10 km wide situated between the two major wadis of Wadi Bishah and Wadi Tarj. The total number of gazelle in all five locations is estimated as less than 50. Only two of the populations were visited, since vehicle tracks were very rough to non-existent in this region and travel times were extremely slow. The major threat is illegal hunting, mainly by local people since the area is difficult to reach by car. The habitat is very similar to that at Tibalah (Wadi Shirs) but there is a much higher concentration of Bedu camps and livestock. Taken together with the dispersion of the populations this means that conservation measures would be costly and difficult to implement, and these populations should perhaps be accorded a low priority (Magin 1992a).
5. Jabal Jandaf
A small population of 5-10 gazelle persists on an undulating upland plateau to the west of Jabal Jandaf, perhaps 20 km² in area. The region is not heavily grazed, and only three Bedu camps were seen on the single access track, which passes along the bed of Wadi Al Fatha. The nearest was approximately 8 km from the gazelle area. The only threat is therefore believed to be from illegal hunting (Magin 1992b). The area may be included in the proposed Wadi Tarj protected area (Child and Grainger 1990) but no action has yet been taken. The recruitment of one of the local residents as a part-time guard would probably ensure the complete protection of this population.

6. Wadi Irbidah
Some gazelles are present at low density in a watershed region some 120 km² in extent 10 km to the west of Wadi Al Lith in the Tihama foothills. The population is unlikely to exceed 20 animals. The habitat consists of rocky hills dissected by small wadis. The surrounding area and major wadis are occupied by camps of Bedu pastoralists. The nearest camps are some distance (three to seven kilometres) from the gazelle area, but access by vehicle is relatively easy and it can be approached from a number of directions. In addition there are several through routes adjacent to the area, with a large amount of traffic. Illegal hunting, both by locals and outsiders, is apparently common, and is the major threat perceived. Many other areas of equal conservation value probably exist, and furthermore this particular area has the disadvantage of being difficult to police. It should therefore be regarded as a low conservation priority (Magin 1992a).

7. Jabal Ghurab
The gazelle habitat consists of low rocky hills and plateaux drained by densely vegetated wadis, situated on the Tihama plain near Jizan. The region experiences a higher rainfall than any of the other areas visited, and hence ground cover is dense, to the extent that in some places the habitat is reminiscent of African savannah. Several unusual plant species were present and common, e.g. *Adenium obesum*, *Delonix elata* and *Euphorbia ammak*. The gazelle area is approximately 10 km long by 4 km wide, bounded to the east and west by rain-fed cultivation and to the south by the workings of the Southern Province Cement Factory. To the north there may be no natural boundary since the chain of hills extends for approximately 30 km. Most habitations appear to be permanent, and are situated in the surrounding lowlands. Livestock are pastured in the region during the day. The gazelle population is estimated as numbering 10-20 animals, and is suffering from illegal hunting, including hunting with "saluki" dogs. A small part of the habitat has been lost to the cement factory workings. The highest densities of tracks and faeces, and indeed two gazelle themselves, were seen within one kilometre of the factory conveyor belt. The best possibility for protecting this population would be to enlist the co-operation of the factory authorities, and persuade them to engage a local man to exclude hunters from the area (Magin 1992b).

8. Jabal Marwan
A population estimated at 15-30 animals occupies a small area perhaps 30 km² at the base of the Tihama foothills in the vicinity of Jabal Marwan, near Qilwah. The habitat consists of well-vegetated rocky hills, supporting abundant cover of the grasses *Cenchrus* sp. and *Eleusine compressa*, drained by small wadis. Both permanent settlements and temporary Bedu camps are present near the gazelle
area. The major threat is from illegal hunting. The area is part of a much larger zone, Qilwah, which has been recommended for protection as a Natural Reserve / Biological Reserve (Child et al. 1989b, Child and Grainger 1990), but no action has yet been taken. Three other areas within the proposed Reserve - Al Qusaiba, Quarshar and Jabal Nakrah - where previous workers (Habibi and Al Basri 1988, Child et al. 1989b) had made gazelle observations were also visited. No signs of gazelle were found and local people interviewed were adamant that none remained. The best conservation option may not therefore be to gazette the entire area, but rather to employ one or two local auxiliary rangers to protect the known population and curtail illegal hunting (Magin 1993a).

9. Al Habda
A small population of gazelle, believed to number at most 20 animals, inhabits an area of rocky hills south-west of the village of Ar Rayth in the Tihama foothills. The density of the population is low, and the total gazelle range may perhaps be 10 km by five km (50 km²) in extent. The area has one small settlement, Al Habda, and several Bedu camps, but is not densely populated. The people rear livestock. The main threat is illegal hunting by outsiders, but locals also reported that the gazelle population had been adversely affected by recent droughts. Gazelle in this area are reputedly very mobile in response to rainfall, which would undoubtedly be a risky strategy in more densely-inhabited regions. Coupled with the low numbers of gazelle, this aspect of gazelle ecology would hinder conservation efforts. The area should therefore be accorded a low conservation priority (Magin, 1993a).

10. Wadi That Al Qarn
Some 30 km to the north-west of the village of Al Fatihah in the Tihama, this is reportedly the best gazelle area within Asir National Park (ANP). Scattered evidence of gazelle was found in an area some 10 km by five km (50 km²). The habitat consisted of two ranges of rocky hills, separated by a plain several kilometres wide. At the time the area was visited in December 1992, vegetation was luxuriant following recent rains. There were thick stands of *Hyphaene thebaica* along major wadi beds. The region was occupied by scattered Bedu camps and attendant livestock, most of whom had reportedly installed since the rain. The major threat is from illegal hunting by outsiders. Until recently the Asir National Park employed a Conservation Officer, based in Al Fatihah, to enforce the Kingdom's anti-hunting laws. He very kindly acted as our guide to the area, and estimated that there were 15-20 gazelle in the region. Since his resignation these gazelle have received no protection. Policing the area would be quite difficult since it is relatively open and easy to access. Nevertheless, the Commission should co-operate with the ANP authorities to ensure that a replacement (or two) are appointed as quickly as possible, preferably from among the local population (Magin, 1993a).

Discussion
Gazelle populations appear to be becoming extinct at a truly alarming rate. A total of 18 areas believed to have harboured gazelles within the last five years were visited during this study. Evidence of their continued existence was only found at 10 sites, representing a population extinction rate of 44% in five years. The major cause of extinctions and threat to existing populations is undoubtedly illegal hunting.
A slight caveat is required to these results: it should be remembered that it is always much easier to prove the presence of a species than its absence, particularly in the case of a rare, shy species such as the mountain gazelle. Discovery of a single track can establish that gazelle persist, but many days of intensive fieldwork might be needed to confirm their disappearance. Due to the pressure of time, only a day or two were spent in each area. Further fieldwork at any of the eight locations at which gazelle are presumed extinct might reveal signs of continued gazelle presence, leading George Bernard gazelle to say that "reports of my death have been greatly exaggerated". However, in strong support of the extinction hypothesis, local people - who generally appear to have a very detailed knowledge of their local fauna - were interviewed at each of these eight locations, and were convinced that no gazelle remained.

The need for action is therefore urgent. Traditional conservation measures, i.e. the gazetting of protected areas, installation of fully equipped and trained rangers, construction of ranger posts etc., will take time to implement, and will probably be accomplished too late to save most of the gazelle populations. This already appears to have been the case for the gazelle populations near Al Aqiq, north of Al Bah. First reported by Habibi and Al Basri (1988), who recommended that conservation measures be taken, these populations would have been protected in the Wadi Jirshah protected area proposed by Child and Grainger (1990). Unfortunately no action was taken. In 1992 no traces of any gazelle could be found and the populations are presumed to be extinct (Magin, 1993a). The gazelle in the proposed Qilwah protected area may suffer the same fate before gazetting can be accomplished.

Instead, what is required is an immediate and innovative approach. The action suggested here does, however, oblige NCWCD to have a commitment to the conservation of wildlife outside as well as inside gazetted protected areas.

Saudi Arabia is fortunate in having strict legislation controlling hunting, and unfortunate in having practically no one responsible for enforcing it outside protected areas. Successful conservation of gazelle populations will require some sort of policing / surveillance to enforce anti-hunting laws. A great deal could be accomplished in co-operation with the local Emirs, who for the most part are educated men who support the preservation of Saudi Arabia's wildlife heritage, if the Commission were willing to pay local people full- or part-time salaries to act as "auxiliary rangers." Such auxiliary rangers would be responsible for warning any hunters to leave their area, and if that failed to deter them, reporting their presence to the local Emir, who could then use the armed forces at his disposal to arrest or request them to leave. NCWCD should also assume some responsibility for ensuring that suspected hunters are prosecuted, and the full penalties of the law enforced. A fuller discussion of the potential auxiliary ranger system covering the selection of personnel, their proposed duties, and the relationship envisioned between them, NCWCD, and the Emaralas is given by Magin (1993b).

Appointment of local auxiliary rangers should be on a "payment by results" basis. Positions should be temporary, not permanent. If the conservation situation of the gazelle population in a particular area has not improved by the end of a specified trial period, the scheme in that region could be discontinued. The selected areas would therefore need continual monitoring, which could be carried out by NCWCD staff. Methods of establishing whether gazelle populations were stable or increasing would include interviews with local people, and fieldwork to estimate the densities of
tracks and faeces. While it is difficult to estimate absolute population numbers by the latter technique, it is relatively easy to ascertain relative changes in abundance, i.e. population trends.

The main advantages of auxiliary rangers as opposed to full-time rangers would be that as local residents they would in effect be on duty 24 hours a day; NCWCD would not need to provide them with any infrastructure or expensive equipment (e.g. houses, vehicles, radios); and they would undoubtedly have good links with the local community, many of whom would be members of their extended families. Auxiliary rangers could therefore be a cost-effective and efficient conservation weapon in the Commission's armoury. A similar system, using local people employed as "Community Game Guards" has been successfully operating in southern Africa for some time (Williamson, pers. comm.).

The success of such a scheme in Saudi Arabia would depend not only on the motivation of local people, but also on the willingness of the local Emir to act in cases of suspected hunting. Only where NCWCD is sure that both are present should the scheme be implemented. The initial impression obtained during this survey is that several areas containing gazelle populations which would benefit from protection do meet these criteria, and it is therefore recommended that NCWCD implement this system on a trial basis as soon as possible.

Conservation recommendations
Conservation measures are outlined below for six of the 10 gazelle populations visited: Mahkshush, Tibalah (Wadi Shirs), Jabal Jandaf, Jabal Ghurab, Jabal Marwan, and Wadi That Al Qarn. Criteria for selecting these populations include: estimated population size, range and potential for increase; willingness of local people / authorities to co-operate; and potential for successful policing.

1. **Mahkshush (south of Al Qunfidah)**
   - Gazette Mahkshush as a Special Natural Reserve (as recommended in Child and Grainger, 1990).
   - Build / rent ranger post at Kiyad.
   - Appoint minimum of two locally-recruited full-time rangers, or in interim period until gazetting is accomplished, two local auxiliary rangers.

2. **Tibalah (midway between Bishah and Al Baha)**
   - Make official contact with Emir of Tibalah.
   - Appoint two local auxiliary rangers from among population of Bedu nomads in Wadi Shirs.

3. **Jabal Jandaf (south-east of Al Baha)**
   - Make official contact with Emir of Tarj (sub-emirate of Bishah).
   - Appoint one local auxiliary ranger from among population of Bedu nomads from upper Wadi Al Fatha / Wadi Wuthahl.

4. **Jabal Ghurab (south-east of Abu Arish, Jizan Province)**
   - Make official contact with high-level management / board of directors of Southern Province Cement Factory, and with Emir of Ahad Al Massareha.
   - Persuade Southern Province Cement Factory to engage one or two local auxiliary rangers.

5. **Jabal Marwan (west of Qilwah)**
   - Make official contact with Emir of Biluswad (located in village of Al Rumayzah, sub-emirate of Qilwah).
• Appoint one local auxiliary ranger from among population adjacent to Jabal Marwan / in nearby Shi'b ash Shami.

6. Wadi That Al Qarn (north-east of Al Fatihah, south-west of Ad Darb)
• Make official contact with Asir National Park authority to persuade them to engage a new Conservation Officer to replace the one who recently resigned.
• Persuade ANP authorities to engage local auxiliary rangers and / or offer NCWCD support.

Acknowledgements
Thanks are due to all the people who have assisted in this survey, unfortunately too numerous to name, but comprising staff of NCWCD, NWRC, KKWRC, and many Emarahs, plus many voluntary and invaluable local guides. Particular thanks are due to Prof. Abdulaziz Abuzinada of NCWCD and Drs Georg Schwede and Arnaud Greth of NWRC for their unflagging interest and support.

References


Abstract: Exploitation of natural resources and overgrazing of natural vegetation have caused significant destruction and depletion of the renewable natural resources of Kuwait, thereby damaging the natural habitat of wild animals.

Realizing the intrinsic value of protected areas for conserving flora and fauna whilst allowing public recreation, in 1983 the Kuwait Government implemented measures to conserve its natural history by designating a 250 km² protected area, Kuwait National Park (also known as "Jal Az-Zor National Park") in the north-eastern region of Kuwait. The area has extensive boundary demarcation, a diversity of plant and animal species, interesting photographic features, good accessibility and is easy to protect.

In this paper, the area's biological, physical and social attributes and the protection measures enforced are discussed. A zoning plan with recommendations for reintroducing wildlife and plants in the park area is provided. Other areas (consisting of both marine and desert ecosystems) are suggested as future potential nature reserves. Finally, the current status of the desert ecosystem in the post-war period is highlighted.

Keywords: Kuwait, conservation, Kuwait ("Jal Az-Zor") National Park, protected areas, reintroduction programmes.

Introduction
The fauna and flora of Kuwait are subject to pressures from both man and his livestock. Human exploitation of vegetation for animal feed, fuel and recreation has caused significant destruction and depletion of the vegetation, thereby damaging the natural habitat of wild animals. In addition, overgrazing by domestic livestock has decreased species diversity, reduced vegetation growth and vigour, and caused soil erosion. Another significant factor is off-road use by vehicles, which has disturbed the vegetation and, in many cases, has resulted in irreversible adverse effects. The lack of a governmental or institutional framework for the protection and management of wild plants and animals in Kuwait has compounded the situation (Omar and Taha, 1981).

Realizing the intrinsic value of protected areas for conserving the country's flora and fauna while allowing public recreation, Kuwait Municipality designated areas in its Land-Use Master Plan for this purpose. This step was further pursued in 1981 and 1983 by requesting the Kuwait Institute for Scientific Research (KISR) to undertake two feasibility studies (phase I and II) in order to select the criteria for the establishment of protected areas in Kuwait. In accordance with the Land-Use Master Plan, KISR conducted research that resulted in the selection of a 250 km² area located in the north-east of Kuwait, and the identification of its ecological, biological, physical and social characteristics.

Detailed studies of the area showed extensive boundary demarcation, a high diversity of plants and animals, interesting photographic features, good accessibility and ease of protection.
Recommendations on park zoning, management and development were submitted to the Kuwait Municipality along with a proposed reintroduction programme for locally-extirpated plants and animal species (Omar et al., 1986a,b). The recommendations were considered by the Municipality Council and Kuwait National Park was designated as Kuwait's first protected area. Responsibility for the park's development and management was given to the Public Authority for Agriculture and Fish Resources (PAAFR). A 2 m high fence was erected by PAAFR to protect the area's boundaries. The Kuwait Municipality and PAAFR in collaboration with the Environment Protection Council (EPC) issued specific legislation to protect the park area.

In addition to the establishment of Kuwait's first national park, other areas potentially important for the conservation of wildlife, such as the islands of Kuwait, were recommended for protection by various government institutions.

Figure 15.1 Location of Kuwait ("Jal Az-Zor") National Park and potential future protected areas in Kuwait (modified from Omar et al. 1986a).
The purpose of this paper is to present a general description of the Kuwait ("Jal Az-Zor") National Park with emphasis on its physical, biological and social aspects and to outline the proposed plan for its management and use. The post-war status of the desert ecosystem is also highlighted, with emphasis on the impact of the war on the park, and remedies to restore renewable natural resources are proposed.

The physical characteristics of Kuwait ("Jal Az-Zor") National Park

The area of the designated park in the north-east of Kuwait includes a high diversity of plant and animal species, desert basins (playas), and is easily protected due to extensive boundary demarcation by natural features such as desert, valley, escarpment and sea. Vehicle access to the designated area is provided by two routes: a two-way surfaced road running from near Jahra town to Basra, Iraq and an 11 m wide two-way road between Jahra and the police station of Subiya point (Figure 15.1).

The area is generally flat with minor undulations. The most significant physical feature in the area is the Jal Az-Zor escarpment, which rises to a height of 150 m and runs parallel to the seashore. Five intersecting land forms have been identified: backslope, scarp, debris, coastal plain, and crest.

Drainage patterns generally run north-east in the form of numerous shallow wadis that dissect the debris slope. The pattern to the south is generally described as a series of wadis draining a limited catchment and falling abruptly to sea level. The most poorly drained areas are the coastal plain and some parts of the backslope. The entire surface of the Jal Az-Zor area is covered with sediments and rocks of sedimentary origin formed between the Miocene and Holocene periods.

Flora and fauna

- Flora: The coastal region is primarily covered with salt-marsh vegetation such as Zygophyllum qatarense, whereas the desert inland is occupied primarily by Rhanterium and Haloxylon steppes (Figure 15.2). It is estimated that the Rhanterium steppe occupies about 85% of the study area, followed by the Haloxylon steppe (10%) and the salt marshes (5%). A total of 39 plant species has been recorded in the salt-marsh region (coastal habitats) and 87 species from the inland area. In general, Halocnemon strobilaceum dominates near the shore, followed by Seidlitzia rosmarinus, Nitraria retusa, Z. qatarense and Schanginia aegyptiaca. Major plant species in the inland ecosystem vary according to the prevailing dominant plant community. On the Rhanterium steppe, major associations consist of Rhanterium epapposum, Stipagrostis plumosa, Moltkiospis ciliata, Asthenatherum forsskalii, Plantago sp. and Cutandia memphitica. Plants found in the Haloxylon steppe include Haloxylon salicornicum, Astragalus sp., Medicago sp., Schismus barbatus, and Cutandia memphitica.

Plant growth occurs mainly during January, February and March. Drought, particularly early in the growing season, usually causes poorer growth and lower plant vigour. Research on plant frequency and cover on the major plant steppes shows that both dominant and associated species are being depleted. While 57% of the species in the coastal plain are moderately to very abundant, 38% are rare and 5% are endangered. In the inland desert, however, 47% are between moderately and very abundant, 40% are considered rare and 13% are endangered.
Figure 15.2 Vegetation map of Kuwait ("Jal Az-Zor") National Park (from Omar et al. 1986a).

- **Fauna:** Since the State of Kuwait is situated at the edge of the great Arabian Desert, it is clear that the local fauna has close affinities with those of neighboring countries. The main vertebrate fauna of the park includes reptiles, birds and mammals (Tables 15.1 and 15.2).

The reptiles, such as the desert monitor, or "wirral" Varanus griseus, are mainly carnivorous, preferring live prey. The "dhub" or spiny-tailed lizards Uromastix spp. however, are the only herbivorous reptiles in Kuwait. These are the most visible reptiles, but other less easily-seen species are also present. The stone gecko Stenodactylus sleveni and agamid lizards Agama spp. are common. Snakes are widely-distributed but appear to be most common between the crest of Jal Az-Zor escarpment and Umm Ar-Rimmam. Burrowing reptiles are rarely seen, since they emerge mainly at
night when the humidity is high. The sand skink *Scincus scincus* and Jayakari's sand boa *Eryx jayakari* are found in the sand hummocks adjacent to water run-off areas. The Arabian worm lizard (*Diplometopon zarudnyi*) is probably the commonest subterranean reptile and may be found buried to a depth of several centimetres in the sand throughout the park.

Mammalian fauna is relatively numerous and predominantly nocturnal. The rodents generally prefer the sandy desert region with shrub cover under which they usually burrow. The Euphrates jerboa *Allactaga euphratica* and lesser jerboa *Jaculus jaculus* are found on the more open flat areas of stony desert. Red and fennec foxes (*Vulpes vulpes* and *Fennecus zerda*) have been seen in Umm Ar-Rimmam and Jal Az-Zor, and burrows were found in the deep gully of Jal Az-Zor and Umm Ar-Rimmam. Feral dog *Canis domesticus* packs range along the coastal stretches and are increasingly common.

Table 15.1 Selected mammals, reptiles and invertebrate species likely to be encountered within Kuwait ("Jal Az-Zor") National Park.

<table>
<thead>
<tr>
<th>Mammals</th>
<th>Reptiles</th>
<th>Invertebrates / Insects</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Gerbillus cheesmani</em></td>
<td><em>Uromastix microlepis</em></td>
<td><em>Androcionus crassicauda</em></td>
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<tr>
<td><em>Gerbillus dasyurus</em></td>
<td><em>Uromastix loricatus</em></td>
<td><em>Apistobuthus pterygocerus</em></td>
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<tr>
<td><em>Gerbillus nanus</em></td>
<td><em>Agama blanfordi</em></td>
<td><em>Compsobuthus arabicus</em></td>
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<tr>
<td><em>Meriones libycus</em></td>
<td><em>Agama pallida</em></td>
<td><em>Buthacus leptochelys</em></td>
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<tr>
<td><em>Meriones crassus</em></td>
<td><em>Phrynocephalus maculatus</em></td>
<td><em>Scolopendra sp.</em></td>
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<tr>
<td><em>Jaculus jaculus</em></td>
<td><em>Eremias brevirostris</em></td>
<td><em>Lycosa sp. narbonensis</em></td>
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<tr>
<td><em>Allactaga euphratica</em></td>
<td><em>Acanthodactylus schmidtii</em></td>
<td><em>Thanatus fabricii</em></td>
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<tr>
<td><em>Mus musculus</em></td>
<td><em>Acanthodactylus boskianus</em></td>
<td><em>Philodronus sp.</em></td>
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<tr>
<td><em>Hemiechinus auritus</em></td>
<td><em>Acanthodactylus scutellatus</em></td>
<td><em>Hyalomma sp.</em></td>
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<td><em>Parechinus aethiopicus</em></td>
<td><em>Acanthodactylus opheodurus</em></td>
<td><em>Porrellio evansi</em></td>
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<tr>
<td><em>Vulpes vulpes</em></td>
<td><em>Bunopus tuberculatus</em></td>
<td><em>Calosoma imbricatum</em></td>
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<tr>
<td><em>Canis domesticus</em></td>
<td><em>Stenodactylus sleveni</em></td>
<td><em>Calosoma olivieri</em></td>
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<td><em>Fennecus zerda</em></td>
<td><em>Scincus scincus</em></td>
<td><em>Gauropterus fligidus</em></td>
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<tr>
<td><em>Taphozous nudiventris</em></td>
<td><em>Diplometopon zarudnyi</em></td>
<td><em>Cardiophorus sp.</em></td>
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<tr>
<td><em>Asellia tridens</em></td>
<td><em>Varanus griseus</em></td>
<td><em>Cocinella septempunctata</em></td>
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<tr>
<td><em>Mellivora capensis</em></td>
<td><em>Eryx jayakari</em></td>
<td><em>Prionotheca coronata</em></td>
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<td><em>Lytorhyncus gaddi</em></td>
<td><em>Pimelia arabica</em></td>
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<td><em>Malpolon moilensis</em></td>
<td><em>Ocnera hispida</em></td>
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<td><em>Psammophis schokari</em></td>
<td><em>Akis elevata</em></td>
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<td></td>
<td><em>Coluber ventromaculatus</em></td>
<td><em>Scarabaeus rotundipennis</em></td>
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<td></td>
<td><em>Cerastes cerastes</em></td>
<td><em>Ammocleonus aschabadensis</em></td>
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<td></td>
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<td><em>Larinus sp. elegans</em></td>
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</tbody>
</table>

Of the 280 bird species recorded in Kuwait, among the most common terrestrial species seen in the park are crested larks *Galerida cristata*, shrikes *Lanius* spp., bee-eaters *Merops* spp., wagtails *Motacilla* spp., little owls *Athene noctua*, kestrels *Falco tinnunculus* and steppe eagles *Aquila rapax* (Table 15.2). The mud-flats play host to two sorts of migratory birds: autumn and spring passage migrants and winter visitors. Among the commonly seen coastal and mud-flat birds are: greater
flamingos *Phoenicopterus ruber*; herons (family Ardeidae); egrets *Egretta* spp.; cormorants (family Phalacrocoracidae); gulls and terns (family Laridae); ducks (family Anatidae); and crab plovers *Dromas ardeola* and numerous other waders (order Charadriiformes).

Table 15.2 Selected birds of Kuwait ("Jal Az-Zor") National Park.

<table>
<thead>
<tr>
<th>Species</th>
<th>English Name</th>
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<tbody>
<tr>
<td>Gallinula chloropus</td>
<td>Moorhen</td>
</tr>
<tr>
<td>Dromas ardeola</td>
<td>Crab Plover</td>
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<tr>
<td>Cursorius cursor</td>
<td>Cream-coloured Courser</td>
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<tr>
<td>Sterna caspia</td>
<td>Caspian Tern</td>
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<tr>
<td>Sterna hirundo</td>
<td>Common Tern</td>
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<tr>
<td>Sterna antillarica</td>
<td>Collared Dove</td>
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<tr>
<td>Athene noctua</td>
<td>Little Owl</td>
</tr>
<tr>
<td>Ammomanes deserti</td>
<td>Desert Lark</td>
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<tr>
<td>Alaeman alaudipes</td>
<td>Hoopoe Lark</td>
</tr>
<tr>
<td>Eremophilus lilopha</td>
<td>Temminck's Horned Lark</td>
</tr>
<tr>
<td>Corvus ruficolis</td>
<td>Brown-necked Raven</td>
</tr>
<tr>
<td>Passer domesticus</td>
<td>House Sparrow</td>
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<tr>
<td>Merops superciliosus</td>
<td>Blue-cheeked Bee-eater</td>
</tr>
<tr>
<td>Merops apiaster</td>
<td>European Bee-eater</td>
</tr>
<tr>
<td>Motacilla cinerea</td>
<td>Grey Wagtail</td>
</tr>
<tr>
<td>Motacilla alba</td>
<td>White Wagtail</td>
</tr>
<tr>
<td>Lanius minor</td>
<td>Lesser Grey Shrike</td>
</tr>
<tr>
<td>Lanius excubitor</td>
<td>Great Grey Shrike</td>
</tr>
<tr>
<td>Phoenicopterus ruber</td>
<td>Greater Flamingo</td>
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<tr>
<td>Egretta alba</td>
<td>Great White Egret</td>
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<tr>
<td>Egretta garzetta</td>
<td>Little Egret</td>
</tr>
<tr>
<td>Egretta garzetta</td>
<td>Western Reef Heron</td>
</tr>
<tr>
<td>Falco tinnunculus</td>
<td>Kestrel</td>
</tr>
<tr>
<td>Galerida cristata</td>
<td>Crested Lark</td>
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</tbody>
</table>

The invertebrates, especially the insects, are an ephemeral component of the community, the majority only appearing for a restricted period of each year. Grasshoppers (family Acrididae, order Orthoptera) are extremely common in March and April. Spiders are also well represented but few have been identified. Together with the grasshoppers, the bristle tails (Thysanura) and desert cockroaches (Orthoptera) probably form the basic food items for many of the desert predators. Scorpions (Scorpionidae) are also present.

**Social aspects**

Three groups of people are encountered in the park: nomads, who camp in the area for a long period of time; campers, who remain on-site for the spring season; and visitors, who spend from one to seven days during the spring holidays. Representatives of all three groups were interviewed, and
their views on camping and desert recreation as well as their interest in environmental protection and desert parks were evaluated. The nomadic population comprised only about 3% of the total sample number. Most users preferred mobile homes to nomadic tents or prefabs. A majority of the people who camped for recreation also engaged in physical activities such as walking, running, and ball sports. For evening entertainment, they watched television and listened to the radio. Electric generators were used to light camps and to supply electricity for appliances. Water tankers were the major means for getting water to camps, and food was usually cooked by gas stove. The preferred food to eat was fresh meat followed by canned food.

Most of the area users were married male Kuwaitis. The fact that a large number of Kuwaitis enjoy desert recreation demonstrates an avid local interest in the desert and its plants and animals.

Zoning plan
Different park functions and uses are identified in the Zoning Plan:

- Nature reserves (strict nature zone, managed nature zone and protected landscape);
- Recreation (park headquarters and visitor center, camping area, and hiking trails);
- Education and research.

Criteria for site selection were chosen taking into consideration the major zones: tidal mud-flat, Jal Az-Zor escarpment, backslope, Umm Ar-Rimmam depression, and shallow depressions. Each site was ranked using a Site Index. A map was prepared showing alternative functions of zones (Figure 15.3). At least three alternative areas were indicated for each function to give decision makers the opportunity to select the most appropriate site for each function.

Wildlife and vegetation reintroduction plan

- Introduction of suitable plants: Two locations within the park, with a total area of 3,100 ha, have been proposed for the reintroduction of plants. The larger site (2,300 ha) is situated in the south-west of the park, and the smaller site (800 ha) is near Talha in the north-west. The major problems for both areas under irrigation are root zone and tillage limitations and erosion hazards. Another problem is that only 1,400 m$^3$/day (about 310,000 gal/d) of underground water can safely be extracted under the "safe yield" strategy suggested for water utilization in the area (Omar et al., 1986b). If the only source of irrigation water is the underground aquifer and its limited replenishment from natural recharges, the potential for afforestation and "soft" landscaping is limited to 10 ha. The quality of the water is fair, varying between 1,000 and 10,000 ppm TDS and does not contain harmful levels of toxic minerals.

As the area for planting is rather limited and generally exhibits unfavorable growing conditions, it is suggested that planting (afforestation and soft landscaping) be limited to the hardy species that thrive best under these conditions. Twenty-eight tree species, 23 shrubs, and 5 ground cover plant species have been suggested as suitable for planting (Omar et al., 1986b).

- Reintroduction programme for wildlife: Six important habitats, vital for the successful reintroduction of wildlife have been recommended for immediate protection: coastal mud-flats, the
salt marshes and associated sand dunes, artificial oases (e.g. Kazma gardens), Jal Az-Zor escarpment and wadis, and the gravel sandy area.

Introduction and reintroduction of wildlife in the area can include either re-stocking the disappearing species of local fauna or reintroducing animal species that used to live in the region. Creation of artificial oasis inside the park boundaries with an abundance of water and trees will serve the purpose of conservation. An aviary should be established in this oasis to house the species of birds proposed for introduction or reintroduction. It is suggested that the following birds be released into the park: houbara bustard *Chlamydotis undulata* macqueeni, ostrich *Struthio camelus camelus*, chukar *Alectoris chukar*, and sandgrouse *Pterocles* spp.

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**Figure 15.3** Proposed management zoning scheme for Kuwait ("Jal Az-Zor") National Park (from Omar et al. 1986a).
Reintroduction of the following mammals was also recommended: rheem gazelle *Gazella subgutturosa marica*, Arabian oryx *Oryx leucoryx*, wild ass *Equus hemionus onager*, Cape hare *Lepus capensis*, and Arabian sand cat *Felis margarita harrisoni*.

It is recommended that wildlife is first reintroduced into isolated areas such as Failaka Island. When the animals and birds are fully adapted to the environmental conditions in the area and their population size increases, they can then be transferred to the open land in the National Park.

**Operational plan for the management and development of Kuwait ("Jal Az-Zor") National Park**

Under the auspices of the Range and Afforestation Department at PAAFR, funds were allocated for the erection of a 2m high wire fence along the park boundaries. Protection measures were also implemented by utilizing the manpower at four police stations in the park area. Continuous patrolling of the area and relocation of park users to areas outside the park boundaries were the main measures taken to protect the area. The erection of the fence was completed in early 1990, but the implementation plan for the establishment of the park ceased in August 1990 when the Gulf crisis started.

**Potential future protected areas in Kuwait**

A field reconnaissance survey was conducted to identify other sites in Kuwait that might be suitable as national parks. The survey was limited to areas delineated by the Kuwait Municipality in its Master Plan Second Review. Three desert regions were investigated and proposed as potential future protected areas: Al Batin in the south-west, Um-Niqa in the north-east, and Al-Khiran in the south-east of Kuwait (Figure 15.1). The islands of Kuwait (Kubbar, Qaru, Bobyan, Umm Al-Muradem and part of Failaka) were recommended as marine parks.

Exclosures for the protection of habitats and native plants were established at different localities in Kuwait. Since 1980, KISR has conducted research to monitor changes in the structure and species composition of range plants inside and outside the exclosures. Other areas for the conservation of native wildlife were also proposed by EPC and Kuwait University.

**Post-war status of the wildlife and vegetation**

In early March 1991, more than 700 Kuwaiti oil fields were set on fire by the Iraqi forces (Al-Besharah, 1992) causing catastrophic environmental pollution. Many articles cautioned that the wellhead fires and oil spills could cause serious environmental damage (Al-Satti, 1992; Blackwelder, 1991; Kuhn, 1991). Rice and Sheppard (1991) raised concerns about oil spill pollution on the marine environment because of the vulnerability of the Gulf ecosystem. Under these recently altered environmental conditions it could be expected that some changes in the desert ecosystem will have taken place.

A field reconnaissance survey in desert areas heavily contaminated with oil was conducted in August 1991 and October 1992. The dominant vegetation community in the area is *Cyperus conglomeratus* in association with *Cornulaca*. Field observation showed that crude oil flows and aerosol deposits (mist, soot and partially combusted oil) contaminated the plants and most of the soil in the area (Omar and Bartolome, 1992).
Many projects were initiated at KISR and EPC to study the impact of the crude oil on the flora and fauna of the contaminated areas. Preliminary results indicated low productivity of the vegetation and a high level of soil contamination. Birds, turtles, fishes and other animals were also casualties of the oil spills on land and at sea. Field studies are continuing and data on the long term impact of crude oil on the marine and desert ecosystems will soon be available.

In addition to environmental contamination, the park suffered a large amount of physical destruction such as the removal of the top soil by movement of tanks, artillery and other vehicles, and the breakage of existing fences (including the boundary fence). A further hazard is the presence of many mines, left behind by the departing Iraqis. Intensive efforts are presently being made by the military authorities to clean the desert and marine ecosystems.

**Summary and conclusions**

Realizing the intrinsic value of protected areas for conserving flora and fauna while allowing public recreation, the Kuwait Government took measures to conserve its natural heritage by designating and fencing large areas. The Kuwait ("Jal Az-Zor") National Park, established in 1983, is one example of this commitment. Other potential areas have been proposed and some are in the process of assessment and evaluation.

The Gulf War caused severe destruction and deterioration of terrestrial and marine habitats. The fences of the national park and other excluses were broken or destroyed by the Iraqi forces. Measures to reclaim soil and to rehabilitate and/or restore the natural habitats are being considered and undertaken by the authorities concerned.

**References**


Introduction
There has been considerable progress in gazelle conservation and taxonomy in the last five years in the Arabian peninsula. The taxonomic status of most of the taxa has been clarified and the implementation of the first conservation measures has allowed the recovery of some wild populations. However, there was a real need to summarize all the information gathered and to define the needs for the forthcoming years. During the NCWCD Workshop "Establishing priorities for gazelle conservation in the Arabian peninsula" the participants heard presentations on various aspects of gazelle conservation, including surveys, taxonomy, systematics and cytogenetics. Most presenters made their own individual recommendations at the close of their presentations. At the end of the Workshop, a round-table discussion was held between selected participants to discuss some of the issues raised and determine overall gazelle conservation priorities. This "Arabian Gazelle Working Group" consisted of the following participants (listed in alphabetical order):

Mr Mohammed N. Abu Zaid, Prof. Abdulaziz H. Abuzinada, Mr Mubarak Ali M. Al-Dosary, Dr Kevin Dunham, Dr Arnaud Greth, Dr Colin P. Groves, Dr Khushal Habibi, Prof. Eric Harley, Dr Chris Hillman, Mr Steve Kingswood, Dr Chris Magin, Dr Iyad Nader, Dr Samira Omar, Dr Wilhelmus Rebholz, Dr Georg Schwede, Dr Tommy Smith, Mr Mohammed Sulayem, Mr Hany Tatwany, Mr Mohammed Al Toum, Dr Marc Vassart, Mr Youssef Al Wetaid, Dr Douglas Williamson.

The meeting was chaired by Arnaud Greth, who directed the discussion by posing a series of questions to the Working Group. The questions and the discussion generated by each are summarized below. Speakers are identified by their initials (e.g. DW = Douglas Williamson). The Working Group finished by making a number of recommendations for conservation and research priorities for gazelle in the Arabian peninsula.

Discussion of the Arabian Gazelle Working Group

- AG: Why should taxonomic questions be raised in conservation and reintroduction programmes, and which ones should be answered?

DW: The goal of conservationists is to maintain biodiversity. Taxonomy is one (and possibly the best) index of biodiversity. Each case should be approached with an open mind.
CG: Taxonomy is the essential background information on which to base conservation decisions. The species should remain the main unit, compared to the subspecies.
IN: I agree with CG; species should be the conservation unit, but the subspecies should also be considered.
CH: The priority is to concentrate on the taxonomy of wild remnant populations, not on captive animals of doubtful origin.
AG: The best way to solve taxonomic questions is to prioritize in situ conservation, and conserve the local existing populations, when feasible.
DW: Taxonomy may also enable captive populations to make valuable contribution to conservation.
EH: Taxonomy should allow us to define conservation units from which breeding will give fertile offspring.
AG: These conservation units could also represent groups of animals that are reproducing without showing any inbreeding or outbreeding depression in the long-term.
DW: Some important conservation issues are not addressed by taxonomy, e.g. adaptation to the environment. It is also important to consider the distribution, the ecology and the behavior of the concerned taxon.
GS: Taxonomy must first give indications of local adaptations. Morphology and thus taxonomy reflect adaptation to a local environment.
MAZ: The problem is not only to answer why taxonomic questions should be raised in conservation but also when.
AG: This question should be raised during the early stages of any conservation project.

- AG: What is the conservation interest of subspecies?

DW: Many subspecies are really ecotypes (like the wild boar Sus scrofa in North Africa). But subspecies are often incorrectly identified.
IN: Subspecies must represent populations, not type specimens. Their description should be based on several aspects (e.g. morphology, genetics, physiology, behaviour, ...).
GS: Subspecies give indications of the geographical variability within a species.
AG: Subspecies also represent the evolutionary potential of new species.
TS: The species level is sometimes too restrictive. Certain conservation projects are directed to the subspecific level.
CG, GS, MAZ: A non-local subspecies should be reintroduced only if the local subspecies is completely extinct, as is the case for the ostrich (Struthio camelus) and the wild ass (Equus hemionus) in Saudi Arabia.
EH: The subspecies should be based on good genetic and biochemical evidence, aesthetic criteria and behavioral adaptations.
SK: Taxonomists must support conservation by providing the most complete taxonomic information available.
AG: What, if any, are the taxonomic differences between *G. g. gazella* and *G. g. cora*?

CG: *Gazella* is a larger subspecies, compactly built, with straighter horns in males (only slightly S shaped), a darker coat color, with a prominent flank-stripe. *Cora* is more reddish, longer limbed, the ears nearly reach the nostrils when laid forward and the horns are more S-shaped in the male. The coat color varies from pale sandy to dark brown. The side stripe is dark brown. There is even variation among individuals from the same locality.

DW: The side stripe can be variable. *Gazella* may not be the biggest subspecies.

CG: These morphological differences are based on museum specimens (30 *gazella* versus 15 *cora*), not on living specimens.

KH: There are ecological differences between *cora* and *gazella*. *Cora* can live on flatter, sandy areas. *Gazella* is always in mountainous areas. But their distribution also reflects past or present human disturbances.

MV: For the moment cytogenetic studies have not shown any difference between *gazella* from Palestine and *cora*. They have similar chromosomal banding patterns.

IN: You can not expect many chromosomal differences between subspecies.

EH: If you do find differences, it raises the question of whether a subspecies should be elevated to the rank of species.

MV: *Cora*, *erlangeri* and *gazella* are closer to each other than to *G. s. marica*, according to electrophoretic analysis. This confirms that the specific status for these three subspecies of *G. gazella* is correct. There is an appropriate amount of difference (genetic distance) between these taxa to confirm the subspecific level. But there are no fixed differences.

HT: We should not ignore the movements of animals by local people. The most illustrative example is the Farasan gazelle *G. g. farasani*, for which islanders have played a significant role by moving animals to the islands.

CG: Phenotypic and genotypic plasticity need to be investigated. Experimental rearing of gazelles in different environmental conditions should be conducted to evaluate the influence of the environment on the phenotype. Embryo-transplants would allow us to evaluate maternal effects.

KD: It seems we are in a situation where we are defining the subspecies of an individual by where it comes from.

DW: In Oman, some animals of doubtful origin have been released. They confiscated all the gazelles, put them in a large enclosure, and one day opened the doors. It is therefore possible that there are hybrids between species or subspecies in the wild populations. You can not be sure to find pure *cora* in Oman.

IN: We should make an effort to collect more animals directly from wild populations for genetic studies.

CG: We should visit systematically the localities given for specimens of *cora* at the British Natural History Museum.

EH: If we obtain perfect wild specimens of *cora* and *gazella*, and we found that there is no cytogenetic, allozyme or mitochondrial differences, would morphological differences between *cora* and *gazella be sufficient to justify their separation? That is the case for the king cheetah *Acinonyx jubatus*, which is very different morphologically, but is due genetically to a single gene point mutation.
WR: On a mitochondrial DNA basis, we found less than 4% difference between one specimen of *gazella* (from KKWRC) and two *cora* from Oman. This genetic distance could justify giving each taxon the status of a true species.

EH: There is only 5% difference between the chimpanzee *Pan troglodytes* and the human. This value would correspond to distances between genera.

MV, SK: This value should be confirmed by analyzing more samples.

EH: If the mitochondrial DNA results are confirmed, these two taxa should definitely be treated as different species.

GS: To confirm this result, the samples should be tested in different laboratories by different techniques.

AG: To summarize, there are obvious morphological and mitochondrial DNA differences. But the differences are minimal using cytogenetic and electrophoresis techniques... Strange results!

DW: We have to be sensible in our decisions because each subdivision will multiply the cost for conservation.

SK: Given the need to further clarify the morphological and genetic differences between *gazella* and *cora*, a standardized protocol for collecting samples should be established. However, data from captive populations may be meaningless if individuals representing different wild populations have been mixed in captivity.

CG: There are some captive breeding groups of *cora* at Al Ain Zoo and Aquarium in Abu Dhabi, as well as in Qatar.

CH: What is the point in discussing results from specimens of unknown source? We need to study all aspects of ecology and sample some individuals from wild populations.

TS: If wild specimens are needed, they can be live captured.

DW & AA: We need to establish captive populations of *cora*.

AG: The goal should be to establish a viable captive population that could be used for reintroduction.

- AG: Where would the founders of captive populations of *cora* come from?

CG: Non-viable wild populations could be sampled.

CM: We could also harvest from viable populations. The local people could give important help in catching the animals.

KH: We could obtain dramatic gazelle population increases by protection. First we should protect these populations, then we can capture specimens for captive-breeding.

- AG: How is it possible to define the historical distribution of *gazella* and *cora*, and particularly, the geographical limits?

DW: For *gazella*, very little historical data are available.

GS: Camera trapping could perhaps help identify the taxon present where gazelle populations still exist.
- AG: How can we assess the taxonomic status of KKWRC mountain gazelles?

EH: We first need to confirm the mitochondrial results of WR. We should base the separation into subspecies, first on genetic or cytogenetic evidence, second on morphological criteria if we do not find a natural polymorphism.

DW: Pelage and body size are two variables that are known to be extremely environmentally plastic.

KD: We have to raise these two points:
1) Are cora and gazella different?
2) Which subspecies do KKWRC / Hawtat Bani Tamim animals belong to? Then we can make a decision.

SK: Are there ecological differences between gazella and cora?

DW: We must not allow taxonomy to run conservation: taxonomy should remain a tool. We will never be sure what the historical distances were between the different gazelle subspecies. We would like to reintroduce mountain gazelles in other areas of Saudi Arabia, besides Hawtat.

- AG: Under which conditions should KKWRC mountain gazelles be reintroduced?

General agreement: For the moment, KKWRC mountain gazelles should only be reintroduced to areas where no natural population can be contaminated genetically and where the reintroduced population remains under control.

- AG: Should we consider G. g. farasani as a valid subspecies? Can we use this population as a reservoir for mainland gazelle reintroduction or should it be kept as an isolated population?

AG: The two hypotheses concerning the creation of this population are their introduction by local fishermen as a kind of primitive game-ranching or isolation from the mainland following the last Ice Age (15,000 years ago).

CG: Morphologically, this taxon is distinct from cora, but only differs from erlangeri in size. It could be interesting to create a captive population of farasani and to see how the morphotype will evolve under different environmental conditions.

AG: Morphologically, farasani seems very different from erlangeri, which is smaller and darker. In my opinion, farasani is more close to cora.

MV: On a cytogenetic and electrophoretic point of view, farasani and cora are identical.

DW: Apparently KH also thinks that farasani and cora are identical.

CH: A long-term study of farasani is needed.

CM: A computer simulation analysis would be interesting to estimate the probability of a population surviving in low numbers for 15,000 years without any introduction, to test the hypothesis of Thouless.

MS: Locals report repeated introductions of gazelles from the mainland.

WR: We only found a 0.7% difference between cora and farasani with mitochondrial DNA techniques. This represents a subspecific difference.

KH: The population of the Farasan Islands is now very close to 1,000 individuals.
CM & AG: We should not forget in situ conservation measures. Future management options could include the repopulation of other islands, and maybe the permission of controlled hunting. Some individuals could be reintroduced on the mainland, depending on the validity of the subspecies.

IN: We need to do further research on farasani, and assess the density of the population.

EH: Mitochondrial DNA would be an appropriate technique to judge the taxonomic validity of this subspecies.

- AG: Should G. g. erlangeri be considered as a valid subspecies?

CG: Skins of erlangeri and muscatensis are identical but the horns and skulls are different. The main characteristics of erlangeri are the small size, a very dark color, and straighter horns than cora.

AG: It is fundamentally necessary to determine its distribution as no wild population has ever been reported. Even though no evidence of erlangeri in Saudi Arabia has yet been found, the survey done by CM should be continued, and if possible, extended to Yemen. Mitochondrial DNA comparison with other taxa would also be interesting.

- AG: Should G. g. muscatensis be considered a valid subspecies?

CG: The horns are more open in muscatensis than in erlangeri, and the females have longer horns. They are probably close subspecies.

DW: A team should be sent to Oman to look at their cora and muscatensis.

- AG: How can we solve the taxonomic status of G. bilkis? Is it identical to G. g. erlangeri?

AG: This species is known from only five specimens. It may be extinct. Field surveys in Yemen are a high conservation priority.

KH: There may be one Bilkis gazelle in a German zoo.

AG: You should contact them. We are awaiting the results of mitochondrial DNA analysis on hairs from specimens of the Field Natural History Museum of Chicago. Unfortunately, D. Woodruff from the University of California, La Jolla, has not for the moment been successful in extracting DNA.

- AG: What are the taxonomic differences between G. s. marica and G. s. subgutturosa? Are they valid subspecies?

AG: I think that, after the presentations, everybody is agreed that marica and subgutturosa can be considered as valid subspecies (agreement of everybody).

DW: We can get some samples of Pakistani subgutturosa from Al Wabra, Qatar. During the NCWCD expedition in the Rub al Khali, 24 rheem skulls were collected. They have been measured and compared with the sand gazelle at Qassim. There were no real differences.
- AA: Could we reintroduce the KKWRC rheem anywhere in the Kingdom, and in 'Uruq Bani Ma'arid in particular?

KH: We should follow the guidelines for reintroduction.

AG: *Marica* should be considered appropriate for reintroduction anywhere within its historical range in Saudi Arabia, and especially in the south.

AA: We could ask the Omanis to provide us with some samples or some measurements.

HT: There is also the problem of the intergradation zone between *marica* and *subgutturosa*, which is not well documented.

SK: The putative intergradation zone existed primarily in Iraq and should not be a management concern for *marica* in Saudi Arabia.

AO: It would be interesting to analyze tissue samples from specimens at Al Areen, Bahrain.

SK: Individuals from wild populations should be genetically characterized as most data collected to date involves captive specimens of uncertain origin.

- AG: Was the "true" dorcas gazelle part of the fauna of Saudi Arabia?

CG: The "real" dorcas gazelles found by KKWRC in Al Wabra seem to be an indication if their location of origin (Saudi Arabia) is exact. There are 40 individuals in Al Wabra, Qatar, all originating from four founders. They have (30, 31) chromosomes (female, male). Now we should carefully differentiate the *G. saudiya* (that was before called the Saudi dorcas gazelle) from the true dorcas, *G. dorcas* spp.

AG: There is a publication mentioning bones of dorcas gazelles 6,000 years old found in Bedouin camps in the north of Saudi Arabia.

- AG: Does the "true" dorcas gazelle still exist in the wild?

DW: There are reports of "red gazelle" or "afri" in Al-Khunfah from the rangers. Substantiation of these reports should be given a high priority.

AA: We could ask the rangers to capture some of these gazelle.

- AG: How should the Saudi dorcas gazelle populations of Al Ain and Al Areen be considered?

DW: The populations of Al Ain and Al Areen are supposed to be *G. saudiya*.

AG: The number of chromosomes found by WR (around 50) could only be compared with the karyotype of *G. bennetti*. Could these two captive groups be hybrids from *bennetti* specimens or even be a subspecies of *bennetti*? This should be investigated.

WR: A large number should be sampled for karyotypes.

AG: Until we have solved the taxonomic relationships between *saudiya* and *dorcas*, we should suspend all reintroductions of other dorcas subspecies (*G. d. isabella* at KKWRC or *G. d. osiris* at NWRC).
- AG: What could the taxon called *G. arabica* be? Is it *G. g. farasani*?

CG: The only specimen (one skull) was found at the Farasan islands. I don't think it could be *farasani*. It is very different from any other gazelle. But I have no real answer to propose...

- AG: What are the main *in situ* conservation measures that should be adopted urgently?

DW: The NCWCD should take urgent steps to protect the gazelle populations "discovered" or "rediscovered" by CM. The protection should involve the local people.

TS: We should explore the possibility of employing people outside the network of Protected Areas.

CM: I would recommend the protection of the Tibalah area as a high priority.

- AG: What are the main *ex situ* conservation measures that should be adopted urgently?

AG: A viable population of *erlangeri* should be built up at KKWRC, based on the founders gathered by NWRC. It sounds sensible to collect individuals of the *cora* subspecies from wild populations for a captive breeding programme. We should try to obtain some individuals from the group of dorcas believed to originate from Saudi Arabia that are in Al Wabra.

**Recommendations / guidelines for gazelle conservation and research priorities**

The Arabian Gazelle Working Group recommend the following priorities for conservation and research in the Arabian peninsula for the next years.

*"In situ" recommendations:*

1) Survey all areas to determine the current status of gazelle populations; augment historical data with information from locals and ground and aerial surveys.

2) Protect relevant and significant areas (primarily with respect to gazelle, but considering all other environmental aspects that require conservation), not necessarily as totally protected areas, but including conservation integrated with other land use, and using local people to implement and participate in the conservation process; this recommendation is particularly valid for all the remnant populations in the Hejaz mountains.

3) Conduct field studies of the ecology, behavior and dynamics of wild gazelle populations, using radio-telemetry, among other techniques, over a reasonable period (to record any periodic temporal variation).

4) Monitor the status of known wild populations annually.

5) Obtain tissue samples from wild gazelle populations to determine their taxonomic status.

*"Ex situ" recommendations:*

1) Create and / or maintain minimum viable captive populations of the following threatened taxa: *Gazella gazella cora*, *G. g. erlangeri*, *G. subgutturosa marica*, *G. saudiya*, *G. dorcas* ssp. If possible, founders should be wild-caught and / or of known provenance.
2) Maintain existing captive populations of critical taxa involving specimens of doubtful provenance, until their origin is determined or wild-caught specimens become available.

3) Define and describe both extant and extinct gazelle taxa (species, subspecies) in the Arabian peninsula through inter-disciplinary analysis of data on morphology, distribution, ecology, behaviour and genetics; complete the analysis of mitochondrial genes, which seems to be an appropriate tool, on representative samples from each taxon.

4) Reduce captive populations of non-critical species.

5) Reintroduce threatened taxa into suitable areas of their historical range or into areas closest to their historical range when their original range is no longer and never could be "safe" for reintroduction. When the indigenous taxon (i.e., subspecies) is extinct, the most closely related taxon may be considered for reintroduction.

6) Use specimens from the present captive populations of questionable provenance for reintroduction only when no other suitable form is available or likely to become available in the near future.

Recommendations for individual taxa

Gazella gazella ssp.

1) Compare the mitochondrial DNA of G. gazella gazella (wild-caught specimens from Palestine) with G. gazella cora (wild-caught specimens from south-western Saudi Arabia).

2) Determine the taxonomic status of animals at KKWRC by comparison with these two populations.

3) With the same technique, determine the taxonomic status of the putative subspecies: erlangeri (KKWRC specimens), farasani (wild-caught specimens) and muscatensis (collaborate with Oman to sample wild-caught specimens).

4) Conduct a survey in Oman to assess the status of the subspecies muscatensis, and in Yemen to assess the status of the subspecies erlangeri.

Gazella bilkis

1) Conduct a survey in Yemen of all gazelle populations to assess the status of this species.

2) If not extinct, collect samples for comparison with G. g. erlangeri.

3) Continue attempts to extract DNA from museum specimens for comparison with the different subspecies of G. gazella.

Gazella subgutturosa

1) Compare, using cytogenetic, electrophoretic and mitochondrial DNA techniques, samples from native populations of G. s. subgutturosa (e.g. wild-caught specimens from Iran or captive specimens at Al Wabra, Qatar, that are originally from Pakistan) with:

   a) wild-caught specimens from northern Saudi Arabia (Harrat al-Harrah or Al-Khunfah protected areas) and from the southern Arabian peninsula (Oman and Yemen, if possible);

   b) captive specimens at KKWRC.
**Gazella dorcas**

1) Survey Al-Khunfah protected area and Al Hijr proposed protected area (No. 32 in the system plan) to determine the status of what locals refer to as the "red gazelle".

2) Create a captive population of *G. dorcas* putatively from the Arabian peninsula with specimens from Al Wabra (Qatar), for future reintroductions.

**Gazella saudiya**

1) Attempt to extract DNA from museum specimens (Natural History Museum, London) for comparison with captive specimens of putative *Gazella saudiya* at Al Areen Wildlife Park (Bahrain) and Al Ain Zoo and Aquarium (United Arab Emirates).

2) If the taxonomic status of these captive populations is confirmed, create a captive population with collaborative efforts between KKWRC, Al Ain Zoo and Aquarium and Al Areen Wildlife Park, for future reintroductions.

**Gazella arabica**

1) Attempt to extract DNA from museum specimens (Berlin Zoological Museum) for comparison with other gazelle species of the Arabian peninsula, and particularly *G. gazella farasani*. 


Male Farasan Island gazelle *Gazella gazella farasani*

Female Farasan Island gazelle *Gazella gazella farasani*
3 Male mountain gazelle (Thumamah) *Gazella gazella gazella*

4 Female mountain gazelle (Thumamah) *Gazella gazella gazella*
5 Male Erlanger’s mountain gazelle *Gazella gazella erlangeri*
6 Male Arabian sand gazelle (Thumamah) *Gazella subgutturosa marica*
Female Arabian sand gazelle (Thumamah) *Gazella subgutturosa marica*

Male (right) and female (left) Sudanese dorcas gazelle *Gazella dorcas isabella*