

Research Article

Two reciprocally monophyletic mtDNA lineages elucidate the taxonomic status of Mountain gazelles (*Gazella gazella*)

TORSTEN WRONSKI^{1,2}, TIMOTHY WACHER^{1,2}, ROBERT L. HAMMOND^{1,2,3}, BRUCE WINNEY^{1,2,4}, KRIS J. HUNDERTMARK^{1,2,5}, MARK J. BLACKET^{1,2,6}, OSAMA B. MOHAMMED^{1,2}, BENITO FLORES^{1,2}, SAWSAN A. OMER^{1,2}, WILLIAM MACASERO^{1,2}, MARTIN PLATH⁷, RALPH TIEDEMANN⁸ & CHRISTOPH BLEIDORN⁹

¹Zoological Society of London, Conservation Programmes, Regent's Park, London NW1 4RY, UK

²King Khalid Wildlife Research Centre, National Commission for Wildlife Conservation and Development, P.O. Box 61681, Riyadh 11575, Kingdom of Saudi Arabia

³Current address: Department of Biological Sciences, University of Hull, Cottingham Road, Kingston upon Hull, Hull HU6 7RX, UK

⁴Current address: Department of Clinical Pharmacology, Old Road Campus Research Building, University of Oxford, Old Road Campus, Off Roosevelt Drive, Headington, Oxford OX3 7DQ, UK

⁵Current address: Institute of Arctic Biology and Department of Biology and Wildlife University of Alaska Fairbanks, Fairbanks, AK 99775, USA

⁶Current address: Department of Zoology, University of Melbourne, Parkville 3010, Australia

⁷Department of Ecology and Evolution, J.W. Goethe–University Frankfurt am Main, Siesmayerstrasse 70–72, 60323 Frankfurt am Main, Germany

⁸Institut für Biochemie/Biologie, Abteilung für Evolutionsbiologie/Spezielle Zoologie, Universität Potsdam, Karl-Liebknecht Str. 24–26, 14476 Potsdam, Germany

⁹Current address: Institute for Biology II, Molecular Evolution and Systematics of Animals, University of Leipzig, Talstr 33, 04103, Leipzig, Germany

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Mountain gazelles (*Gazella gazella*) rank among the most critically endangered mammals on the Arabian Peninsula. Past conservation efforts have been plagued by confusion about the phylogenetic relationship among various 'phenotypically discernable' populations, and even the question of species boundaries was far from being certain. This lack of knowledge has had a direct impact on conservation measures, especially *ex situ* breeding programmes, hampering the assignment of captive stocks to potential conservation units. Here, we provide a phylogenetic framework, based on the analysis of mtDNA sequences (360 bp cytochrome *b* and 213 bp Control Region) of 126 individuals collected from the wild throughout the Arabian Peninsula and from captive stocks. Our analyses revealed two reciprocally monophyletic genetic lineages within the presumed species *Gazella gazella*: one 'northern clade' on the Golan Heights (Israel/Syrian border) and one genetically diverse larger clade from the rest of the Arabian Peninsula including the Arava Valley (Negev, Israel). Applying the Strict Phylogenetic Species Concept (*sensu* Mishler & Theriot, 2000) allows assigning species status to these two major clades.

Key words: Arabian Peninsula, conservation units, captive breeding, *Gazella gazella*

Introduction

Conservation genetics has major implications for the conservation of biodiversity by clarifying taxonomic relationships (Avice, 1989), and determining populations or individuals for future reintroductions (Vogler & DeSalle, 1994). The identification of taxonomically appropriate populations of endangered species for captive breeding

and reintroduction programmes is fundamental to the success of those programmes. Gazelles are amongst the most taxonomically complex mammal groups (Groves, 1969, 1989, 1996, 1997), a fact that has hampered and complicated conservation efforts on these elegant and diminutive antelopes (Ryder, 1986, 1987; Hammond *et al.*, 2001). Classification of the genus *Gazella* in general and of *Gazella gazella* in particular has raised questions amongst taxonomists and has been subject to many revisions (e.g. Groves, 1967, 1996, 1997; Vassart *et al.*, 1994, 1995;

Correspondence to: Christoph Bleidorn. E-mail:bleidorn@uni-leipzig.de

Lorenzen *et al.*, 2008). Mountain gazelles (or 'Idmi'), most conveniently referred to as *G. gazella* spp., are associated with upland areas or zones of broken terrain on the Arabian Peninsula and the Levant. The species occurs from the eastern Mediterranean coastline of Lebanon and Syria, along the mountain chain through western Saudi Arabia, Yemen and Oman to the United Arab Emirates (Mallon & Kingswood, 2001). Like other large mammals of Saudi Arabia [e.g. Arabian oryx (*Oryx leucoryx*), Mallon & Kingswood, 2001; Spalton *et al.*, 2002], the number of Mountain gazelles has drastically declined during the past 50 years. Extensive hunting, rural development and population fragmentation are most frequently cited as the principal causes of decline (Thouless *et al.*, 1991; Magin & Greth, 1994; Mallon & Kingswood, 2001).

Mountain gazelles are known for their high level of phenotypic variation (Groves, 1989, 1996, 1997; Vassart *et al.*, 1996), which is mainly described from museum specimens and captive stocks of mostly unknown wild origin. Because many wild populations are now extirpated (Magin, 1996; Williamson & Tatwany, 1996; Thouless *et al.*, 1997; Mallon & Kingswood, 2001), the chance of correctly determining the origin of distinctive types is diminishing. Confusion about identity, even at full species level, has been a consistent topic in the literature on *G. gazella* for the last 20 years. Earlier classifications have included Bennett's gazelle (or 'Chinkara', *G. bennetti*), which is distributed from Iran to India, and Cuvier's gazelle (or 'Edmi', *G. cuvieri*) from North Africa as subspecies (Haltenorth & Diller, 1977; Roberts, 1977), but karyological data have shown these to be unrelated to *G. gazella* (Kumamoto & Bogart, 1984; Furley *et al.*, 1988).

By the time the National Commission for Wildlife Conservation and Development (NCWCD) in Saudi Arabia established priorities for conservation, there was doubt as to whether the known forms of Mountain gazelle represent one species with a surprising number of distinctive subspecies relative to the total range, or whether deeper species differences might be concealed within the variation. For example, at least four different taxa ('gazella', 'bilkis', 'arabica' and 'erlangeri') are referenced as full species and seven taxa are referred to as subspecies of Mountain gazelle in the literature of the past years (Greth *et al.*, 1996; Habibi *et al.*, 1997). This presents a serious practical problem for conservation managers undertaking *ex situ* captive-breeding programmes, namely when considering the question of whether the captive gazelles should be managed as one unit or up to four different species. The 1992 symposium *Establishing Priorities for Gazelle Conservation in the Arabian Peninsula* recommended at that time 'a case-by-case study for each threatened taxon' using a combination of range distribution data and traditional morphometrics supported by cytogenetics, protein electrophoresis and molecular genetic analyses (Greth *et al.*, 1996).

Twelve years later taxonomic uncertainties still block progress in conservation management of Mountain gazelles and related taxa (IUCN/SSC, 2001; Edmonds, 2002). In this study we contribute to the genetic identification of Mountain gazelles and to the development of a framework of probable conservation units (Ryder, 1986; Moritz, 1994; Vogler & DeSalle, 1994). Early studies on the cytochrome *b* gene showed a 0.0–1.7% base pair difference between most subspecies of *Gazella gazella*, but *G. gazella* from Israel (i.e. the subspecies *gazella*) differed from the other subspecies by 1.9–2.5% (Kingswood *et al.*, 1997; Rebholz & Harley, 1999). Phenotypically, these animals (*G. gazella gazella*) differ in colouration, size and skull morphometrics from other forms of *G. gazella* (Groves, 1969, 1996). Based on the analysis of mtDNA sequences of five individuals of '*G. gazella*' in the context of a phylogeny of the bovid subfamily Antilopinae, Rebholz & Harley (1999) suggested that two genetically distinct lineages (or even separate species) might exist: one from the Golan Heights (Israel/Syrian border) and one comprising animals from the rest of the Arabian Peninsula. In the present study, we investigated the taxonomic relationships between different lineages of '*G. gazella*' using a larger sample set of 126 samples.

The primary objective of our present study was to provide an in-depth analysis of the phylogenetic relationships among different *Gazella* spp. while focussing on genetic differentiation between '*G. gazella*' from the Levant and those from the Arabian Peninsula. To do so, we analysed mitochondrial markers (i.e. cytochrome *b* and the 'D-loop'/Control Region) of samples obtained from wild Mountain gazelle of known origin, from museum specimens, as well as from captive-breeding stocks (Fig. 1).

Materials and methods

DNA sampling

We obtained several DNA samples from skins in museum holdings that had been collected in the wild prior to the extirpation of the respective populations. All skin samples suitable for extraction of mtDNA were provided by the Harrison Zoological Museum, Sevenoaks, Kent, UK (HZM, 3 samples; Table 1, see supplementary material, which is available on the Supplementary content tab of the article's Informaworld page at http://www.informaworld.com/mpp/uploads/wronski_et_al_table_1supplementary_doc.pdf; Fig. 1).

Blood or tissue samples of putative Mountain gazelles were obtained from 48 captive individuals, i.e. King Khalid Wildlife Research Centre, Saudi Arabia (KKWRC, seven samples); National Wildlife Research Centre, Saudi Arabia (NWRRC, six samples); Al Wabra, Qatar (six samples); Al Areen, Bahrain (two samples); Chester Zoo (two

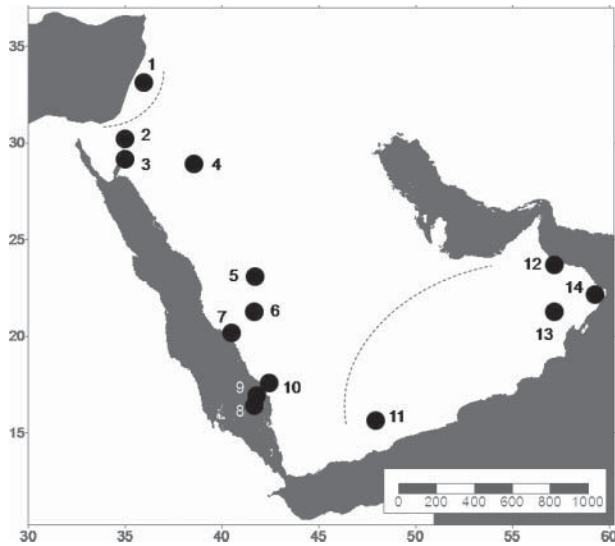


Fig. 1. Map of the Arabian Peninsula showing locations from which samples of wild specimens used to extract mtDNA (CR and *cyt b*) originated: (1) Avnei-Eitan, Eli-bar, Wadi Sarek, Afik in the Golan Heights, Israel/Syria; (2) Arava Valley, southern Negev, Israel; (3) Haql, Wadi Khulagb, north-western Saudi Arabia; (4) Al Khunfah Protected Area, northern Saudi Arabia; (5) Dahlm, western Saudi Arabia; (6) Tabalah, Bishah, south-western Saudi Arabia; (7) Makshush, south-western Saudi Arabia; (8) Farsan, Zifaf, Saudi Arabia; (9) Farasan, Kebir, Saudi Arabia; (10) Al Hayla, Tihama, south-western Saudi Arabia; (11) Yemen, near Saudi border (NWRC, Taif); (12) Wadi Umma, Oman; (13) Ghbaba, Oman; (14) Sier Hills, Muscat, Oman. The upper dotted line separates gazelles from the Golan Heights from the rest of the Arabian Peninsula.

samples), Dudley Zoo (one sample), Blackpool Zoo (one sample) and Bristol Zoo (one sample) in the UK, as well as from a number of private collections in Saudi Arabia and the UAE (22 samples; Table 1, see supplementary material).

Hair samples originating from wild Mountain gazelles were collected at several locations in Saudi Arabia (45 samples). Samples from animals of wild origin from Israel (Arava Valley, Negev, southern Israel and the Golan Heights, Israel/Syrian border) were provided by the Israel Nature Reserves Authority and obtained through the Institute of Zoology, London (IOZ, 19 samples). One sample was obtained from an unknown location in Jordan, probably from a captive population (Table 1, see supplementary material).

Sequences from other gazelle species (*G. bennetti*, *G. cuvieri*, *G. spekei*, *G. saudiya* and *G. leptoceros*) were obtained from GenBank (nine sequences, Rebholz & Harley, 1999; Hammond *et al.*, 2001). Two *G. subgutturosa marica* samples and three *G. dorcas* samples were obtained from animals that belong to captive groups held at KKWRC.

DNA extraction

For DNA extraction, hair samples and samples of sand particles coated in dried blood were placed in 250 μ l of a 5% suspension of Chelex (Bio-Rad) in 10 mM Tris-HCL (pH 8.0) and digested with proteinase K (20 μ l of 20 mg/ml) overnight at 55°C. After digestion the Chelex suspension was heated to 99°C for 5 minutes, to destroy any remaining proteinase K, and centrifuged briefly to pellet the Chelex particles. A volume of 5 μ l of the supernatant was used in PCR amplification reactions.

Small pieces of skin (approximately 4 mm²) from museum specimens were digested using a conventional Tris-HCL/ SDS/ proteinase K protocol but with the addition of Dithiothreitol (DTT) to a final concentration of 0.1 M. Extractions were performed using a conventional phenol/chloroform protocol (Ausubel *et al.*, 1995). DNA in aqueous solution was purified by centrifugation through a Prospin-Ultra micro-concentrator following the manufacturer's instructions (Life Science International).

From whole blood and tissue samples, DNA was extracted using a conventional proteinase K digestion, phenol/chloroform extraction and ethanol precipitation (Ausubel *et al.*, 1995). However, blood samples collected in sodium or lithium heparin often failed to give PCR products even though DNA concentration and quality was high, suggesting that heparin was inhibiting *Taq* polymerase activity (Beutler *et al.*, 1991). Washing blood samples (fresh or previously frozen) with isotonic saline or the use of heparinase buffer prior to digestion increased the likelihood of successful PCR amplification.

PCR amplification and sequencing

The 5' region of the cytochrome *b* gene was PCR-amplified using the versatile primers L14724 and H15149 (Kocher *et al.*, 1989; Irwin *et al.*, 1991). All reactions were performed in a 25 μ l reaction volume with 0.5 units of *Taq* polymerase (Bioline, UK), 1.5 mM MgCl₂, 40 μ M of each dNTP and 200 nM of each primer. Amplifications for all primers pairs were performed with a cycle profile of 95°C for 30 seconds, 50°C for 30 seconds and 75°C for 30 seconds. Amplification yields, particularly for template DNA derived from museum skins, were enhanced by the use of a manual 'hot start' protocol.

Prior to sequencing, excess primers and dNTPs were removed from the PCR products by treatment with Shrimp Alkaline Phosphatase and Exonuclease I (Amersham-Pharmacia Biotech). Double stranded PCR products were sequenced with a Thermosequenase-based cycle-sequencing kit using an end-labelled primer protocol (Amersham-Pharmacia Biotech). Both L14724 and H15149 were used as sequencing primers. Sequence reactions were run on standard Polyacrylamide sequencing gels and visualized by autoradiography. For museum samples,

each sample was amplified and sequenced from at least two separate DNA extractions. Autoradiographs were scored by eye, with each individual sequence read at least twice.

Sequences from the Control Region (CR) were determined by the direct sequencing of PCR products. The left domain (Saccone *et al.*, 1991), between the tRNA PRO and the conserved central domain were amplified using the primers Thrl (Kocher *et al.*, 1989) and one to two gazelle-specific primers, i.e. HH16397 or HH16168 (Arctander *et al.*, 1996). Amplified PCR products were cleaned prior to sequencing using protocols as described for cytochrome *b*.

All sequences have been submitted to NCBI GenBank and are deposited under the accession numbers GU384739–GU384870.

Data analysis

Amplification success varied largely among different types of samples, and was lowest when old/dried material was used. Consequently, we did not always yield sequences from both markers for each individual (Table 1, see supplementary material), and both data-sets were analysed separately. Both datasets (cytochrome *b* and CR) were aligned using MAFFT version 6 (Kato *et al.*, 2005) using the iterative refinement method E-INS-i. A χ^2 -test as implemented in PAUP 4.0b10 (Swofford, 2002) was used to test for compositional heterogeneity of base frequencies. Maximum likelihood (ML) analysis of the dataset was conducted using RAxML version 7.0.3 (Stamatakis, 2006), using GTR+GAMMA+P-Invar model parameters. GTR is the only available nucleotide substitution model in RAxML. In the case of cytochrome *b*, we partitioned the dataset in a way that model parameters were optimized for each codon position separately. Fifteen iterations were run for each dataset; we have chosen the analysis with the best likelihood value for presentation. Support values were estimated by 1000 bootstrap replicates.

We used MrModeltest (Nylander, 2004) to estimate the best fitting model for Bayesian inference for both datasets. Bayesian analysis was conducted with MrBayes 3.1.2 (Ronquist & Huelsenbeck, 2003) using the HKY + GAMMA model. Two independent runs, each with four Markov chains, were run in parallel for 1 million generations, with trees being sampled every 500 generations. Log-likelihood values per generation were plotted (Fig. 2) and manually inspected using Tracer 1.4 (available at <http://tree.bio.ed.ac.uk/software/tracer/>). We used several diagnostic tools to check for convergence of chains. These included the average standard of split frequencies (<5% was used to check if the chains converged, but see Theriot *et al.*, 2009), and cumulative posterior probability plots for each clade as supported by AWTY (Nylander *et al.*, 2008). Moreover, posterior probability estimates were compared between the two analyses using a scatter-

plot as generated by AWTY. All these diagnostics indicated that excluding the first 5% of generations as burn-in was sufficient for both datasets. Therefore, the first 101 trees were discarded and posterior probabilities were estimated as the frequency of clades in the sampled trees.

Average sequence distances between and within groups were calculated using MEGA 3.1 (Kumar *et al.*, 2004).

Results

Our final cytochrome *b* dataset included 60 Operational Taxonomic Units (OTUs) and 360 aligned nucleotide positions; the CR dataset included 87 OTUs and 213 aligned positions. No significant base heterogeneity was detected for either dataset.

Cytochrome *b*

The best tree based on cytochrome *b* sequences obtained from the ML analyses is depicted in Fig. 3. A tree with nearly the same branching order was recovered in the Bayesian analysis; slight differences in the topology were only found within the group including all ‘other *Gazella gazella*’ and in the *G. dorcas* clade. The tree is rooted with *G. subgutturosa marica*. A monophyletic clade including *G. bennetti*, *G. dorcas*, *G. saudiya*, *G. spekei* and individuals assigned to ‘*G. gazella*’ is well supported [ML bootstrap (MLB) = 95%, posterior probabilities (pp) = 1.0]. Within this group, *G. bennetti* branches off first, followed by *G. dorcas*/*G. saudiya*, and *G. spekei* (Ogaden and Somalia, except coast of northern Somalia) is genetically the closest to *G. gazella*, and is therefore recovered as the sister taxon to all *G. gazella* individuals (although with < 50% MLB). While *G. dorcas*/*G. saudiya* is well supported to be monophyletic (MLB = 89%, pp = 1.00), no significant bootstrap support for the monophyly of *G. gazella* was found (MLB = 59%, pp = 0.94). However, within the latter group two reciprocally monophyletic and well-supported sister groups were found. One of these two clades (‘northern clade’) includes all individuals from the Golan Heights (MLB = 96%, pp = 1.00), whereas all other *G. gazella* individuals from different geographical regions on the Arabian Peninsula (including the Arava Valley, southern Negev, Israel) cluster in a second clade (MLB = 71%, pp = 0.97). Internal relationships within the latter clade are only weakly resolved (MLB < 50%, pp < 0.95, Fig. 3) and differ between ML and Bayesian analyses.

Control Region

When analysing the Control Region (CR or D-loop) dataset, we concentrated exclusively on *G. gazella* individuals for two reasons: first, all individuals of *G. gazella* originating from the Arabian Peninsula were recovered as monophyletic

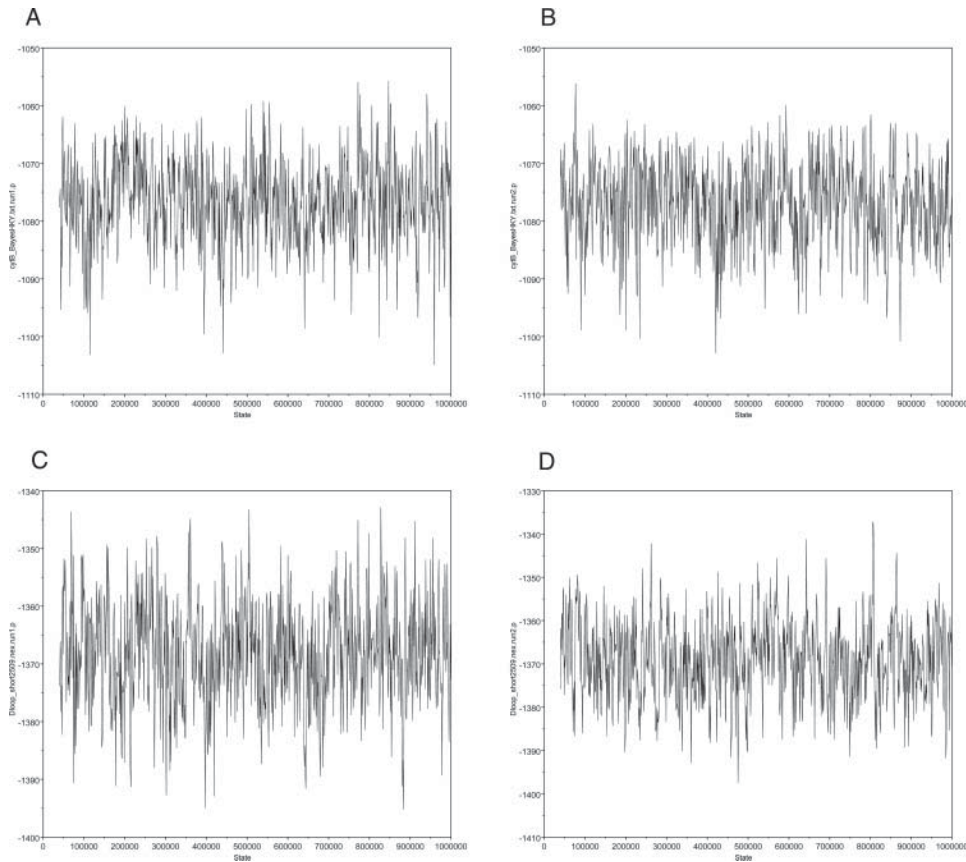


Fig. 2. Log-likelihood values plotted against the generation number (with a burn-in phase of 5%) generated with the software Tracer 1.4. (A) MCMC-run 1 for the cytochrome *b* dataset, (B) MCMC-run 2 for the cytochrome *b* dataset, (C) MCMC-run 1 for the CR dataset, (D) MCMC-run 2 for the CR dataset.

in the best ML tree of the cytochrome *b* analyses (although without bootstrap support). Second, CR sequences of all available potential outgroup taxa were too diverse for a reliable alignment when compared with the *G. gazella* sequences. Consistent with the results from the cytochrome *b* dataset, when rooting the tree with the clade comprising genetically distinct *G. gazella* from the Golan heights, ML analysis recovered two reciprocally monophyletic clades each with very strong support (MLB = 100%; Fig. 4). The same two main clades were recovered with Bayesian inference (pp values indicated in Fig. 4).

While the individuals of the ‘northern clade’ appear rather uniform and only four different haplotypes were distinguished, some differentiation can be seen in the clade containing all other *G. gazella* individuals, even though most clades receive only poor support. Calculation of average uncorrected p-distances yielded values of 0.089 within the ‘other *G. gazella*’ group and 0.024 within the ‘northern clade’. An average distance of 0.127 was calculated between these two clades.

Discussion

Our analyses of mitochondrial sequence divergence unravelled two well-supported reciprocally monophyletic genetic lineages within the presumed species *Gazella gazella*: one northern clade from the Golan Heights and a clade comprising all other ‘*G. gazella*’ from the Arabian Peninsula and the Arava Valley in the southern Negev (Fig. 1). This result is also corroborated by the fact that the average uncorrected p-distance between these two groups is considerably higher than average values within these groups. This finding is of immediate importance for the conservation management of Mountain gazelles, especially for captive breeding programmes (e.g. Wronski & Plath, 2010). Based on our current results, at least the ‘northern clade’ from the Golan Heights should be treated as a distinct management unit. Phenotypically, these animals (currently referred to ‘*G. gazella gazella*’) differ in colouration, size and skull morphometrics from other forms of ‘*G. gazella*’. ‘*G. gazella gazella*’ is the largest and darkest form with straight horns and is not as long-limbed as the main Peninsula form(s).

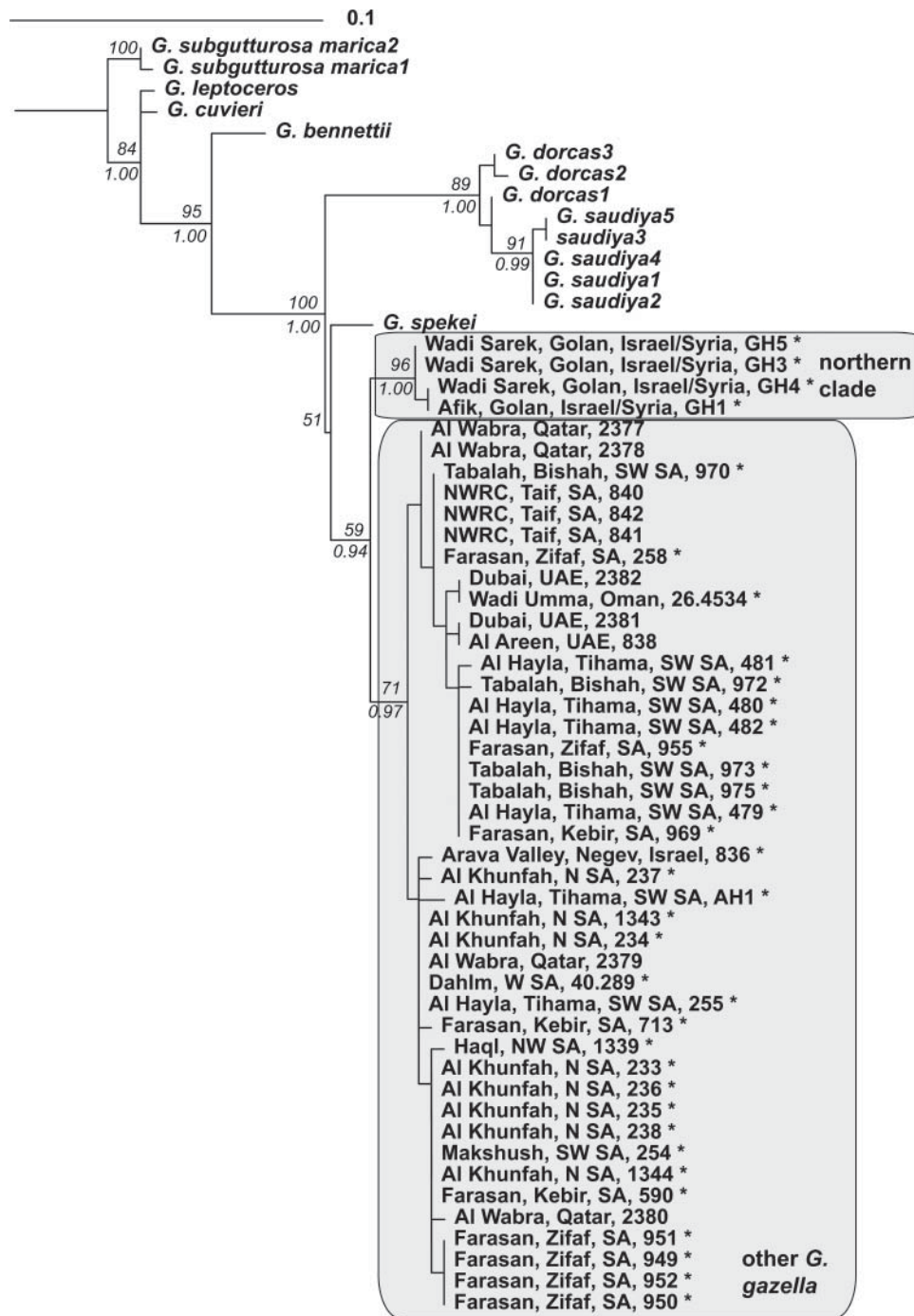


Fig. 3. Maximum likelihood tree of the cytochrome *b* dataset. Individuals of wild origin are marked with an asterisk (*). Bootstrap support values (MLB > 50%) are above the branches, posterior probabilities from Bayesian inference (pp > 0.95) are given below the branches. Only support values for higher order clades are indicated.

Female horns are much reduced, barely reaching 50% of the skull length, while male horns are not bowed outward to any extent, but horn tips tend to turn inwards (Groves, 1985, 1989). The skull is different in that the ascending branch

of the pre-maxilla almost never reaches the nasal, and nasal tips protrude further forward than the lateral prongs (Groves, 1989, 1997). Horns are less lyrate and wider across the base than in Arabian animals (Groves, 1969).



Fig. 4. Maximum likelihood tree of the Control Region dataset. Individuals of wild origin are marked with an asterisk (*). Bootstrap support values (MLB > 50%) are above the branches, posterior probabilities from Bayesian inference (pp > 0.95) are given below the branches. Only support values for higher order clades are indicated.

It remains unclear to date if this genetic structuring within '*G. gazella*' is due to prolonged allopatric separation, or if the observed differentiation is a consequence of local adaptation to divergent environmental conditions (ecological speciation: e.g. Crandall *et al.*, 2000; Nosil *et al.*, 2005; Radar *et al.*, 2005; Rundle & Nosil, 2005;

Räsänen & Hendry, 2008). For example, the separation between the Golan area and the rest of the Arabian Peninsula corresponds with the 50-mm precipitation isobar (Mendelssohn, 1974; Yom-Tov & Ilani, 1987). Thus, future studies will need to examine potential differentiation between the two major clades not only using molecular

markers, but also differentiation in morphological, behavioural, life-history and other traits will need to be examined, and an attempt should be made to link trait divergence to differences in ecology (e.g. Crandall *et al.*, 2000; Radar *et al.*, 2005; Moodley & Bruford, 2007; Plath *et al.*, 2007; Tobler *et al.*, 2008). Given the formerly contiguous distribution of Mountain gazelles along the mountain ranges and coastal areas of the Arabian Peninsula (Harrison & Bates, 1991; Thouless *et al.*, 1991; Wacher & Cunningham, pers. observ.), genetic differentiation reflecting local adaptation seems a more likely scenario than just allopatric divergence.

Taxonomic implications

The finding of two distinct genetic lineages of '*G. gazella*' has important implications for gazelle taxonomy. We are aware of the limitations of species delineations on the basis of mitochondrial markers only (e.g. Funk & Omland, 2003; Verkaar *et al.*, 2004; Nijman *et al.*, 2008), and the limited number of aligned nucleotide positions (213 bp control region, 360 bp cytochrome *b*) used in our analysis. Undoubtedly, more (nuclear) markers will be needed to further clarify the species status of the lineages described here. However, Zink & Barrowclough (2008) demonstrated for birds that mitochondrial markers proved to be robust indicators of population histories and species boundaries.

The pronounced genetic divergence between Mountain gazelles from the Golan Heights and the rest of the Arabian Peninsula suggests that the Golan gazelles are probably a separate species (see also Rebholz & Harley, 1999). With the present data at hand, the decision of whether or not these clades should be considered separate species completely relies on the species concept being applied. As we know that captive gazelles from different clades can interbreed, one could argue, according to the Biological Species Concept (*sensu* Mayr, 2000), that a single species exists, whereby the two clades might represent different subspecies. However, it is almost untestable if these clades indeed interbreed in nature. Applying the Strict Phylogenetic Species Concept (*sensu* Mishler & Theriot, 2000), the finding of two reciprocally monophyletic groups in both analyses (cytochrome *b* and CR) justifies the recognition of at least two species. This raises the question of how the two major species lineages of gazelles should be named. The nominate *G. gazella gazella* was originally described as *Antilope gazella* Buffon (1764) from the Levant.

If the Golan population is assigned species status (*G. gazella*), it raises taxonomic questions as to which species name can be assigned to the populations from the Arabian Peninsula. The two oldest names are *Antilope arabica* (Lichtenstein, 1827) and *A. cora* (Smith, 1827), but there are nomenclatural difficulties with both these names. If molecular evidence from the type material of *Gazella arabica* does not confirm a distinct species and the specimens group instead with the Peninsula clade of gazelles, then this

would be the appropriate name for all Mountain gazelles of the Arabian Peninsula.

In key recent publications (Harrison & Bates, 1991; Thouless *et al.*, 1991; Magin & Greth, 1994; Vassart *et al.*, 1994; Greth *et al.*, 1996; Groves, 1996, 1997), '*G. g. cora*' is used in reference to the general population of Mountain gazelles on the Arabian Peninsula following a recommendation by Groves (1996) based on rules of precedent (priority rule, International Code of Zoological Nomenclature, ICZN). Since the origin of the type material of *Antilope cora* (India: Smith, 1827; Persian Gulf, eastern Arabia: Smith, 1827 and Groves, 1983) is uncertain [the accounts in Smith (1827) indicate this by referring to a number of possible localities] the type locality of '*cora*' cannot finally be determined. The applicability of the name '*cora*' to animals of the Arabian Peninsula remains therefore highly questionable.

A special problem when considering the biogeography of gazelles on the Arabian Peninsula is the population found on the Farasan Islands. Investigations of phenotypes have established that typical 'modern' Farasan Mountain gazelles are distinguishable from both mainland populations and the type specimen of *G. arabica*, putatively collected at Farasan in the 19th century. The modern gazelles are consistently smaller with relatively wide spacing between the upper tooth rows (Groves, 1983; Thouless & Al Bassri, 1991). The coat colour is typically distinguished by a greyish body with a coppery wash to the hind neck and legs, although these features are not always apparent. Our analysis shows that the majority of Farasan gazelle samples form a tightly clustered group (Fig. 4). A second, divergent cluster was recovered from a minority of Farasan gazelle samples. This distinctive lineage could potentially represent the original Farasan haplotype of '*Gazella gazella farasani*'. The presence of two (or more) genetic lineages on the Farasan Islands is consistent with local history, which indicates that gazelles are moved regularly to and from the islands, but it is not clear if one of the lineages can be considered representative of a long-established island form, and, if so, which one? The status of '*G. gazella farasani*' should be reviewed cautiously considering the different hypotheses concerning the origin of this population. Molecular techniques based on nuclear markers should be applied on type and extant material to estimate the genetic distance between Farasan and mainland populations in more detail.

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