

Supplementary Information

Dark grey gazelles *Gazella* (Cetartiodactyla: Bovidae) in Arabia: Threatened species or domesticated pet?
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Table S1: Museum skin samples of putative *Gazella erlangeri* and putative *Gazella muscatensis* used in this study.

| Taxon | Museum | Catalogue No. | Origin | Collector | Year of collection |
|-----------------------|--------------------------------|----------------|-----------------|-----------|--------------------|
| <i>G. erlangeri</i> | Museum für Naturkunde, Berlin | ZMB_MAM_89578 | Lahadsch, Yemen | unknown | unknown |
| <i>G. erlangeri</i> | Natural History Museum, London | ZD 1896.12.4.1 | Aden, Yemen | Buxton | 1896 |
| <i>G. erlangeri</i> | Natural History Museum, London | ZD 1897.1.5.15 | Aden, Yemen | Brook | 1897 |
| <i>G. muscatensis</i> | Natural History Museum, London | ZD 1939.819 | Muscat, Oman | Maud | 1939 |
| <i>G. muscatensis</i> | Natural History Museum, London | ZD 1939.820 | Muscat, Oman | Maud | 1939 |

Table S2: Skull measurements taken in this study. Abbreviations correspond to those in Supplemental Fig. S4. See Bärmann et al. (2013).

| Abbr. | Description |
|-------|--|
| BPL | basi-palatal length – length of the palate along the midline |
| CBL | condylo-basal length |
| DFH | distance front to horns |
| DFO | distance front to orbit |
| DH | distance between horns pedicles |
| DOC | distance orbit to condyle (measured parallel to tooth row) |
| HBD | horn base distance (distance of the anterior-most parts of the pedicles) |
| HD1 | horn pedicle diameter 1 (medio-lateral) |
| HD2 | horn pedicle diameter 2 (antero-posterior) |
| HL1 | horn length, distance between the base of the horn sheath and the horn tip |
| HTD | horn tip distance |
| IB | inter-bullae distance |
| LF+P | length of frontal+parietal |
| LL | length of lacrimal (maximum length of facial part) |
| LP | length of parietal |
| MWH | maximum width of horns sheaths |
| OD | orbit diameter (parallel to tooth row) |
| OHB | occipital height, braincase complete |
| OHO | occipital height, occiput only (dorsal of foramen magnum) |
| WAO | width across orbits (maximum width of frontals) |
| WB | width of braincase |
| WBA | width of basioccipital anterior |
| WPP | width across paroccipital processes |
| ZW | zygomatic width (behind orbits) |

Table S3: Descriptive statistics of genetic variation at 11 microsatellite loci used in this study of *Gazella arabica* (North, East, Southwest) and putative *Gazella erlangeri*. The following are given for each locus: observed heterozygosity (H_O); expected heterozygosity (H_E); number of observed alleles (N_A); range of allele sizes (S); and allelic richness (A_r calculated with HP-rare; Kalinowski 2005). Significant deviations from HWE (i.e., heterozygote deficiency) indicated by asterisks, whereby * $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$.

| Locus | North ($N = 12$) | | | | East ($N = 14$) | | | | Southwest ($N = 22$) | | | | Putative <i>G. erlangeri</i> ($N = 14$) | | | | | | | |
|-----------|--------------------|-------------|-------|----------|-------------------|-------|-------------|-------|------------------------|-------|-------|-------------|---|----------|-------|-------|-------------|-------------|--------|-------|
| | N_A | S | H_O | H_E | A_r | N_A | S | H_O | H_E | A_r | N_A | S | H_O | H_E | A_r | N_A | S | H_O | H_E | A_r |
| BM302 | 5 | 134- 150 | 0.167 | 0.493*** | 3.49 | 3 | 138- 146 | 0.286 | 0.265 | 2.28 | 5 | 134- 148 | 0.091 | 0.482*** | 3.17 | 1 | 138 | Monomorphic | 1.00 | |
| BM415 | 6 | 126- 146 | 0.750 | 0.696 | 4.09 | 4 | 138- 144 | 0.385 | 0.443 | 2.80 | 8 | 124- 146 | 0.45 | 0.764*** | 4.77 | 1 | 142 | Monomorphic | 1.00 | |
| CSSM043 | 7 | 243- 263 | 0.800 | 0.837 | 5.69 | 9 | 255- 279 | 0.429 | 0.865*** | 6.22 | 10 | 247- 269 | 0.190 | 0.897*** | 6.79 | 4 | 269- 275 | 0.545 | 0.619 | 3.26 |
| TEXAN19 | 9 | 145- 167 | 0.667 | 0.833* | 6.18 | 6 | 143- 157 | 0.857 | 0.791 | 4.98 | 9 | 147- 169 | 0.591 | 0.873*** | 6.21 | 1 | 149 | Monomorphic | 1.00 | |
| BM4505 | 9 | 240- 286 | 0.444 | 0.856*** | 6.52 | 10 | 238- 300 | 0.714 | 0.894* | 6.77 | 14 | 240- 388 | 0.450 | 0.901*** | 7.23 | 5 | 244- 276 | 0.818 | 0.628 | 3.98 |
| SR-CRSP6 | 4 | 146- 158 | 0.545 | 0.697* | 3.45 | 5 | 154- 162 | 0.692 | 0.791 | 4.52 | 8 | 140- 160 | 0.611 | 0.848*** | 5.59 | 2 | 156- 158 | 0.692 | 0.507 | 2.00 |
| MCM38 | 6 | 103- 135 | 0.167 | 0.710*** | 4.46 | 8 | 111- 165 | 0.857 | 0.836 | 5.71 | 15 | 113- 165 | 0.700 | 0.914*** | 7.52 | 6 | 177- 187 | 0.462 | 0.790* | 4.60 |
| INRA40 | 7 | 186- 246 | 0.556 | 0.784 | 5.52 | 6 | 200- 220 | 0.375 | 0.742* | 4.75 | 14 | 188- 280 | 0.471 | 0.873*** | 7.11 | 2 | 224- 302 | 0.400 | 0.533 | 2.00 |
| OarFCB304 | 9 | 141- 181 | 0.545 | 0.844*** | 6.31 | 11 | 139- 171 | 0.571 | 0.886** | 6.76 | 14 | 141- 175 | 0.667 | 0.915*** | 7.46 | 4 | 151- 157 | 0.357 | 0.601* | 3.03 |
| RM088 | 2 | 113- 115 | 0.000 | 0.290** | 1.93 | 2 | 113- 115 | 0.429 | 0.423 | 1.99 | 3 | 113- 121 | 0.318 | 0.513* | 2.25 | 1 | 113 | Monomorphic | 1.00 | |
| TEXAN6 | 7 | 168- 194 | 0.500 | 0.739** | 4.80 | 7 | 168- 190 | 0.429 | 0.778*** | 5.20 | 11 | 156- 190 | 0.714 | 0.880* | 6.59 | 1 | 168 | Monomorphic | 1.00 | |

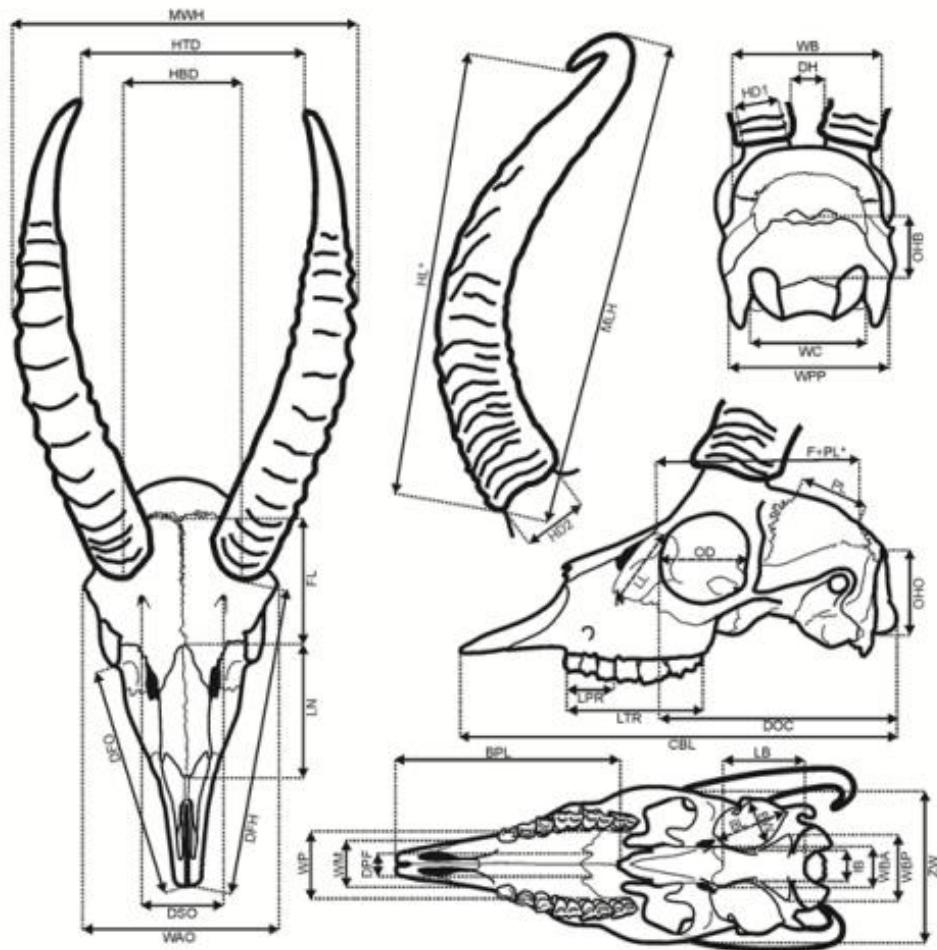


Figure S4: Skull measurements used in this study of putative *Gazella erlangeri* and *Gazella arabica*. Abbreviations correlate with descriptions in Supplemental Tab. S2. See Bärmann et al. (2013).

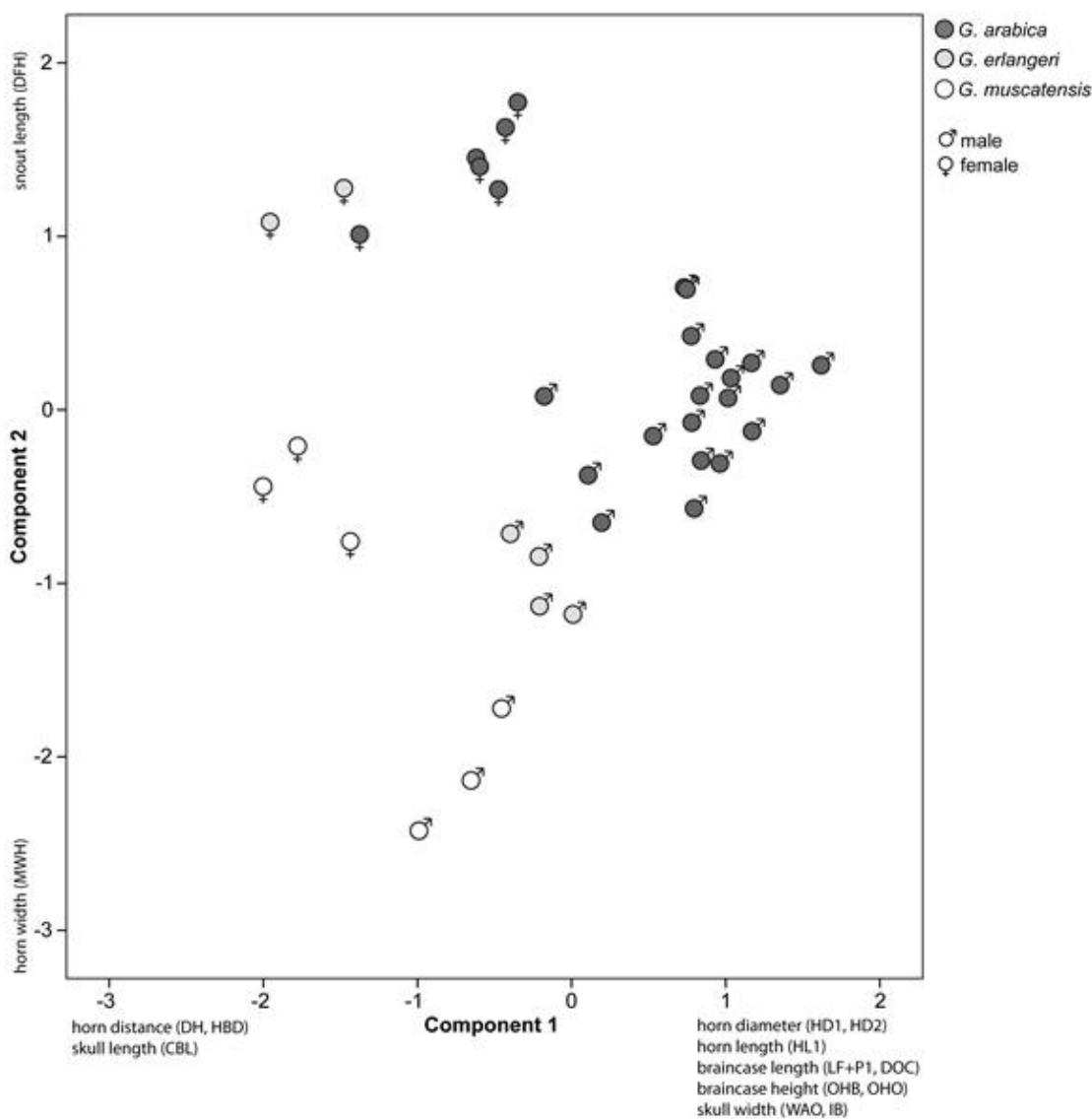


Figure S5: Principal component analysis of skulls of adult *Gazella arabica* ($N=24$), putative *Gazella erlangeri* ($N=7$), and putative *Gazella muscatensis* using 24 linear measurements. Component 1 mainly reflects differences in horn length and diameter, occipital height, braincase length, and skull width. Component 2 is mostly influenced by horn distance and width, as well as distance from snout tip to horn base.

References

- Bärmann E.V., Azanza B., Wronski T., Lerp H., Börner S., Erpenbeck D., Rössner G.E., Wörheide G., 2013a. A morphometric and genetic framework of the genus *Gazella* de Blainville, 1816 with special focus on Arabian and Levantine mountain gazelles. Zool. J. Linn. Soc. 169(3): 673–696.
- Kalinowski S.T., 2005. HP-rare 1.0: A computer program for performing rarefaction on measures of allelic richness. Mol. Ecol. Notes 5(1): 187–189.