

Arabian Gazelles: Taxonomy and Phylogeography

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Introduction The phylogeny of the Arabian gazelles is generally not well understood (e.g., Groves 1996). Morphological traits were commonly used as a basis for classification leading to frequent misclassifications. Sister group relationships within the genus are only poorly resolved and there are still lively debates about the status of certain taxa (e.g., Wronski *et al.*, unpublished). The aim of this project is to characterize several Arabian, African and Asian gazelle species using molecular tools while including several taxonomically unclear “species”. First results are presented here.

Genetic divergence in Mountain gazelles

An analysis mitochondrial DNA data of Mountain gazelle's (Fig. 1) unraveled two reciprocally monophyletic genetic lineages within the presumed species *Gazella gazella*:

- 1) a northern clade from Galilee the Golan Heights and
- 2) a clade comprising all other ‘*G. gazella*’ from the Arabian Peninsula and the Arava Valley in the southern Negev (Fig. 2).



Figure 1 Mountain gazelle (*Gazella gazella*) held at King Khalid Wildlife Research Centre, Thumamah, Saudi Arabia. Photo: Hannes Lerp



Figure 4 Sand gazelle (“*Gazella subgutturosa marica*”) held at King Khalid Wildlife Research Centre, Thumamah, Saudi Arabia. Photo: Hannes Lerp

Taxonomic status of Sand gazelles

Analyses of mitochondrial data revealed polyphyly within Goitred gazelle (Fig. 3, *Gazella subgutturosa*), resulting in two distinct clades (Fig. 4):

- 1) on the Arabian Peninsula, Iraq, Jordan, Syria and Turkey (*Gazella marica*; Sand gazelle)
- 2) one genetically diverse larger clade from the rest of its Asian range (*Gazella subgutturosa*; Goitred gazelle)

The closest relative of the Sand gazelle is the Slender-horned gazelle (*G. leptoceros*).

In order to overcome the limitation of mitochondrial markers further investigations are needed not only including other (nuclear) markers but also morphological, behavioral, and life-history traits.

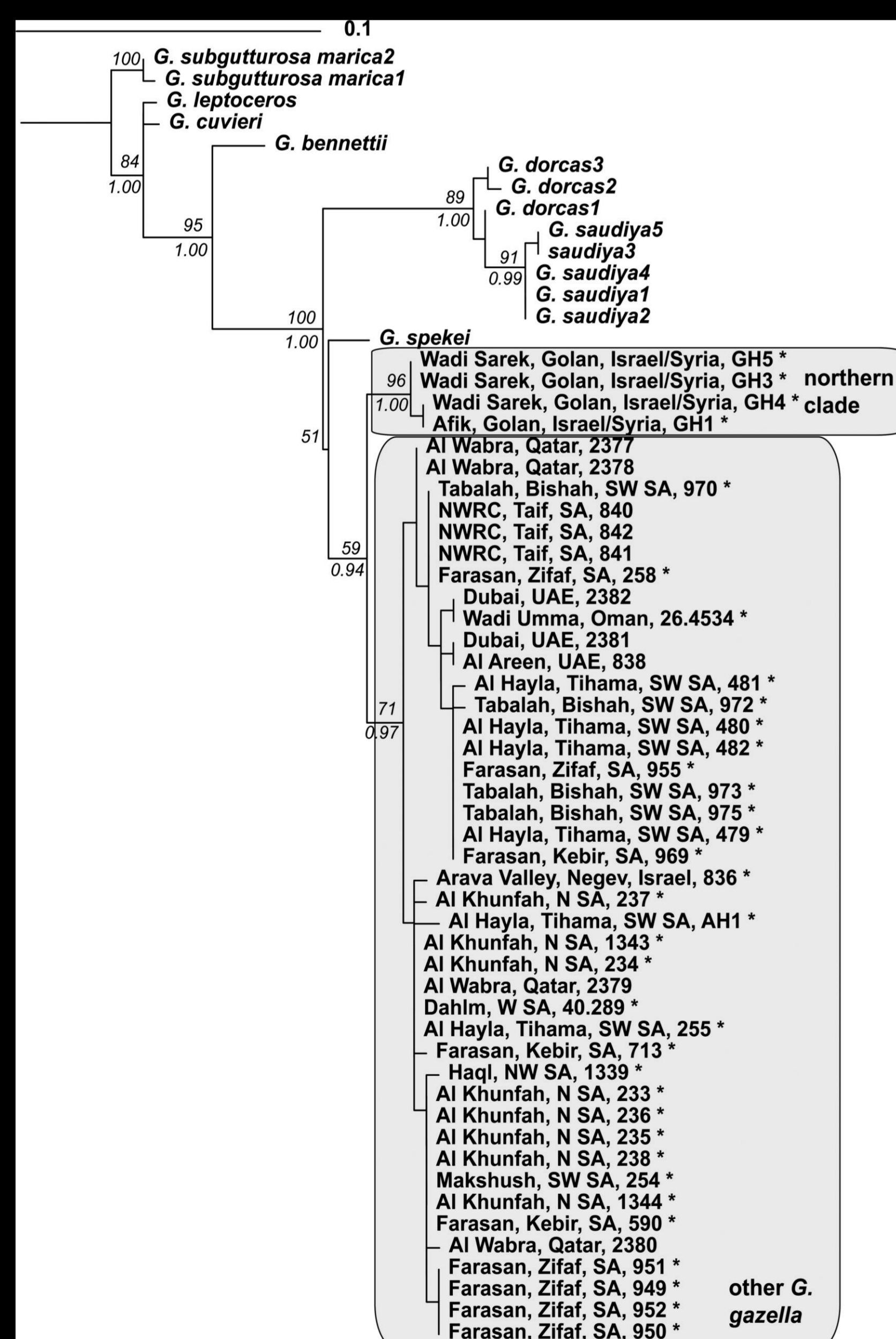


Figure 2 Maximum likelihood tree (cytochrome *b*). Individuals of wild origin are marked with an asterisk (*). Bootstrap support values (MLB > 50%) are above the branches, posterior probabilities from Bayesian inference (pp > 0.95) are given below the branches. Only support values for higher order clades are indicated. From Wronski *et al.* 2010.

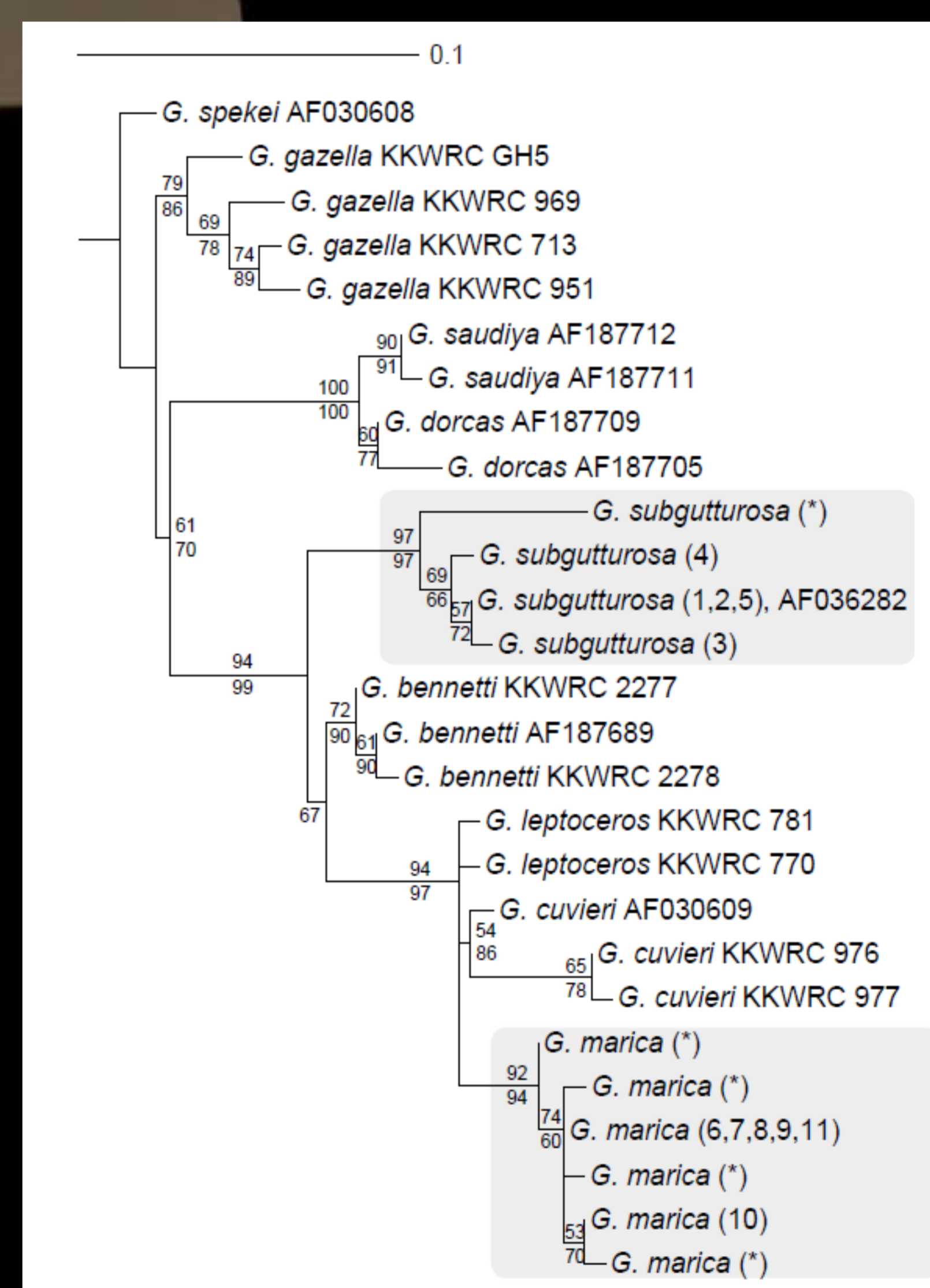


Figure 3 Maximum Likelihood tree (cytochrome *b*) with the GTR + Γ + I model. Likelihood Bootstrap-support (below) and Parsimony bootstrap support (above) were estimated from 1,000 replicates and are given at the branches. The numbers given in brackets corresponds with known provenances; asterisks indicate unknown provenance. For sequences obtained from GenBank the accession numbers are given; for sequences obtained from KKWRC, sample numbers are provided.

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References

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