S11 Comparison of Golden Jackal Sample to Jackals and Wolves

Carles Vilà[1], Robert K Wayne[2]

[1]***Estación Biológica de Doñana***
Department of Integrative Ecology
Sevilla, Spain

[2]***University of California, Los Angeles***
Department of Ecology and Evolutionary Biology
Los Angeles, California, United States of America

Recent reports have indicated that some North African golden jackals possess gray wolf-like mitochondrial DNA sequences [1,2]. The authors have suggested that those individuals may represent a previously undescribed gray wolf lineage present in North Africa, thus supporting previous claims based on the usual morphology and size of some canid specimens from this region [3]. Conceivably, the recent divergence estimated with *G-PhoCS* between golden jackals and gray wolves/dogs compared to previous estimates [4] could be due to a presence of wolf-like individuals in Israel rather than the more basal golden jackal lineage [5]. However, the mitochondrial DNA of the sequenced jackal was not wolf-like (unpublished results) and critically, analysis of previously published SNP data suggest Israeli golden jackals, including the specimen used in this paper, represent a lineage distinct from those in North Africa (Figure S11.1). Also, an analysis of 25 exonic sequences (16,180 bp) across a large panel of over 150 jackals from outside Africa did not indicate close proximity to the gray wolf / dog clade (Koepfli *et al.* unpublished data).

The divergence time of wolves and golden jackals has been estimated as about 1.5 million years from fossil data [4]. The molecular data presented here and results in preparation suggest a much more recent divergence time, indicating that fossil remains thought to be golden jackals are not directly ancestral to living forms. The difficult of deducing affinities of a generalized canid such as the golden jackal are exemplified by the problems in assigning recent specimens to one species or another [3].

Methods

Allele Sharing Distance/Neighbor Joining Tree Reconstruction
A subset of golden jackal samples from Kenya and Israel were previously genotyped using the Affymetrix Canine Mapping SNP Array 2.0 (127K SNPs) [6,7] and Illumina CanineHD array (170K SNPs), along with a number of other species in the *Canis* genus. To provide additional resolution and insight into the phylogenetic relationships of the African and Middle Eastern golden jackals with other canids, a neighbor-joining (NJ) tree based on allele-sharing distances was generated with a subset of SNPs from a panel of two Kenyan golden jackals, two Israeli golden jackals representing both mitochondrial haplotype clades (Cau-like and Clu-like), two ancient and two modern dog breeds, gray wolves from the Middle East, Asia, Europe and North America, Coyotes (*C. latrans*), Ethiopian wolves (*C. simensis*), and a Black-backed jackal (*C. adjustus*) and Side-striped
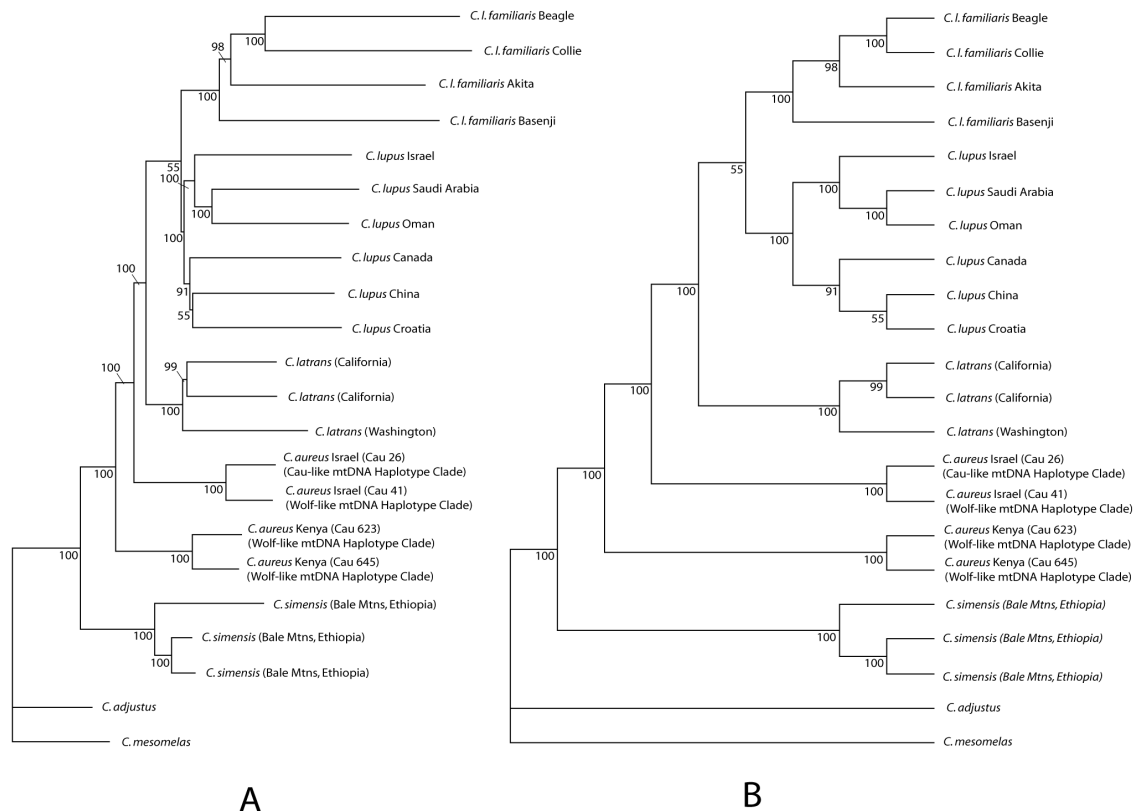
Figure S11.1. Neighbor-joining allele-sharing distance based phylogram (A) and cladogram (B) utilizing the 14,695 SNP dataset from canine SNP array assays. Bootstrap support based on 1,000 replicates is shown. Sample numbers and mtDNA haplotype clades for golden jackals are indicated for comparison with other analysis results.

jackal (*C. mesomelas*). We applied allele conversions to a subset of 14,695 nuclear SNPs distributed across the genome to generate a combined dataset, based on a comparative analysis of the 52,329 SNPs that overlap between the two different arrays (kindly provided by Suiyuan Zhang of NHGRI).

The allele-sharing distance was calculated as one minus the proportion of alleles shared for the 14,695 SNP panel, using the program MICROSAT [8] with 1,000 bootstrap replicates. Neighbor joining trees for each replicate of the resulting pairwise matrices of allele sharing distance were calculated using the program NEIGHBOR and a consensus tree was generated using the majority rule option in the program CONSENSE, both from the PHYLIP package [9]. The resulting tree was visualized as unrooted (Figure S11.1) using DENDROSCOPE [10].

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