Phylogenetics project

Close relatives of the Arctic fox (*Vulpes lagopus*) among canines

Introduction

The research question is "what other member of the family *Canidae* is closest related to the Arctic fox (*Vulpes lagopus*)?" and therefore I have tried to select a few other *Vulpes* and a spread of other *Canidae* (Table 1). The outgroup is the Red panda (*Ailurus* fulgens) as both *Ailuridae* and *Canidae* families belong to the suborder *Caniformia*.

My expectation is that one of the *Vulpes* species will be closest related to the Artic fox while the rest of the species are further removed. Other morphologically fox-like species can be expected to be closer than the wolf-like ones. Out of the *Vulpes* species, I expect the red fox (*Vulpes vulpes*) to be the closest relative to the arctic fox as they share neighbouring habitats (i.e. live relatively close geographically) as well as many morphological traits.

For each species, a complete mitochondrial genome and the Cytochrome B gene were retrieved from RefSeq or GenBank, depending on availability.

Table 1: Species included in study.

Latin name	Common name	RefSeq/GenBank ID
Ingroup (*Caniformia -> Canidae*)		
Vulpes lagopus	Arctic fox	OR880609.1
Vulpes vulpes	Red fox	NC_008434.1
Vulpes ferrilata	Tibetan sand fox	NC_027935.1
Vulpes macrotis	Kit fox	PV090784.1
Urocyon cinereoargenteus	Gray fox	MW600068.1
Otocyon megalotis	Bat-eared fox	MW257223.1
Nyctereutes procyonoides	Common raccoon dog	NC_013700.1
Lycaon pictus	African hunting dog	NC_028427.1
Chrysocyon brachyurus	Maned wolf	NC_024172.1
Cuon alpinus	Dhole	NC_013445.1
Canis lupus lupus	Eurasian wolf	NC_009686.1
Canis aureus	Golden jackal	NC_067757.1
Outgroup (*Caniformia -> Ailuridae*)		
Ailurus fulgens	Red panda	NC_011124.1

Result

Sequences were aligned with MAFFT using the FFT-NS-1 (fast) algorithm. Tree reconstruction was then performed with IQ-TREE in MFP mode. Best-fit model according to Bayesian information criterion (BIC) was TIM2+F+I+G4 for the full mitochondrion and TPM2+F+I+G4 for Cytochrome B. Difference between these models lie in base substitution rates where TPM2 assumes the substitution rate for AC=AT, AG=CT, CG=GT are equal and remaining possible substitutions have equal base frequency. TIM2 assumes only AC=GT, AT=CG have equal frequency and remaining substitutions have unequal base frequency.

The reconstructed trees grouped roughly as expected, with species grouping within their respective Genus. In trees reconstructed with both full mitochondrial and Cytochrome B the closest relative to the Arctic fox was the Kit fox (Figure 1, teal highlight). Based on the full mitochondrial genome (Figure 1A) the closest related Genus to *Vulpes* was *Nyctereutes* containing the Common raccoon dog. The more wolf-like species were placed as a separate group equally related to all other fox-like species. For the tree based on Cytochrome B (Figure 1B), however, *Vulpes* was placed as equally related to all other *Canidae*, including wolf- and fox-like species. I find the full mitochondrial genome based tree more likely to give a true representation of the species relationship.
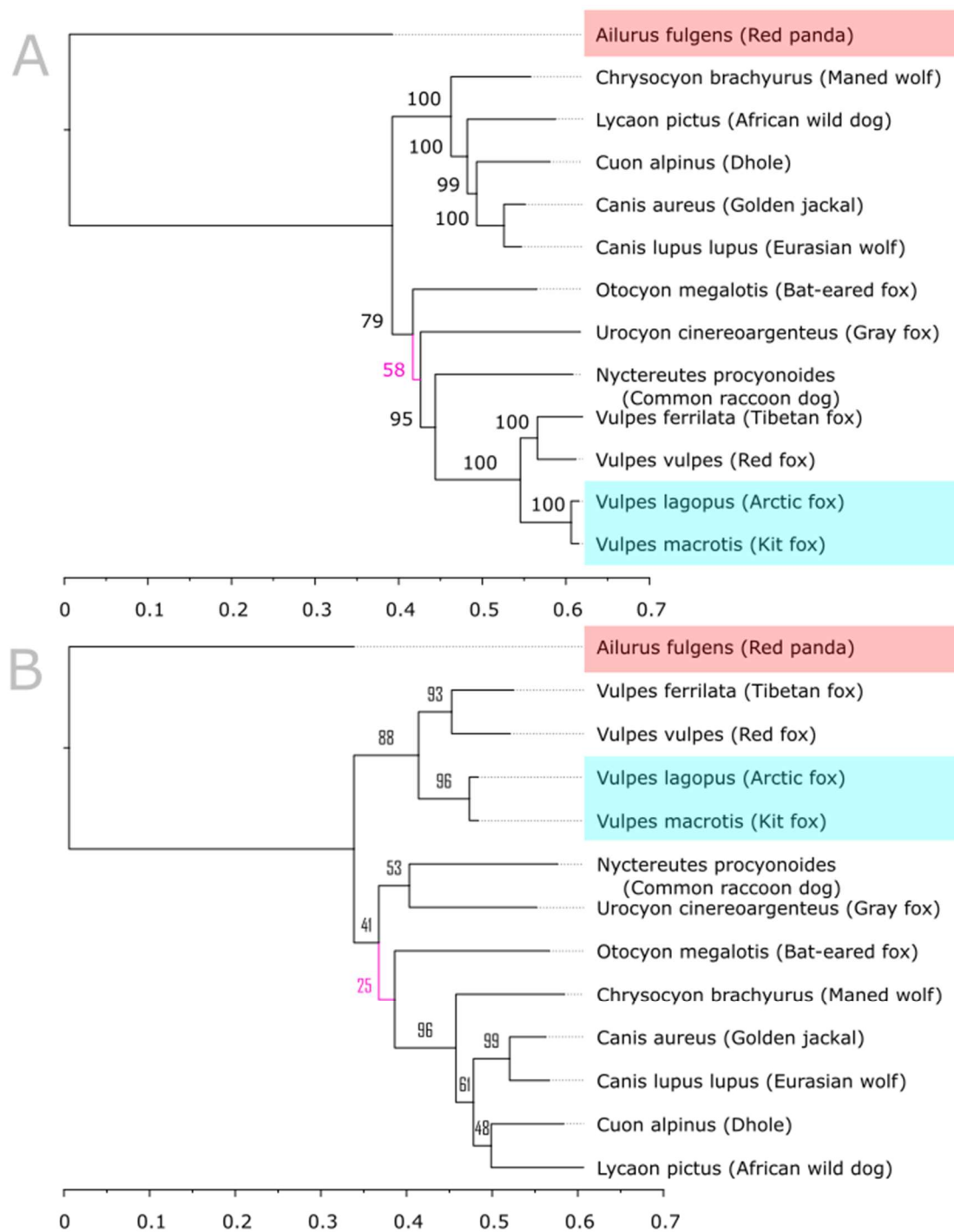
Figure 1: Phylogenetic trees reconstructed with IQ-TREE and sorted in decreasing order for complete mitochondrial genome (A) and Cytochrome B (B). Outgroup, *Ailurus fulgens* (Red panda), highlighted in red. Target species, *Vulpes lagopus* (Arctic fox), and closes relative, *Vulpes macrotis* (Kit fox), highlighted in teal. Least supported branch by bootstrap (1 000 iterations) in pink.