**Molecular Clock Analysis of Caninae Species and Ecological Inference of their Divergence**

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**Introduction**

Caninae is one of three subfamilies within the family Canidae. The other two subfamilies, Hesperocyoninae (living from about 30 to 10 mya) and Borophaginae (living from about 36 to 2.5 mya), are all now extinct. The family Canidae is within the order Carnivora and suborder Caniformia, also known as Canoidea. This suborder includes other “dog-like” Carnivorans such as seals, raccoons, and bears. Caniformia’s sister suborder is Feliformia, consisting of the “cat-like” Carnivorans.

The subfamily Caninae is broken into three main groups: true dogs, true foxes, and the genus *Urocyon*. This division is mostly based on a maximum parsimony tree constructed from about 15 kb total of selected exons and introns (1). The most basal of the three is *Urocyon,* which has 3 species. The extant true foxes division is made up of 3 genera and 14 species. The extant true dogs division consists of 10 genera and 24 species. Of the 10 genera, 2 are extinct: *Cynotherium* (1 species) and *Dusicyon* (2 species). This does not include the numerous subspecies that exist for many of these species. The prehistoric records show that there are 49 extinct Caninae species, with 20 of them in the genus *Canis* (2).

Table 1.

|  |  |  |
| --- | --- | --- |
| **Fossil Species** | **Estimated Age (mya)** | **Relation to Extant Species** |
| *Canis lepophagus* | 8 | Ancestor of *C. Lupus* and *C. Latrans* |
| *Canis cedazoensis* | 1.05 | Descendant of *C. lepophagus*, ancestor of Golden Jackal |
| *Canis apolloniensis* | 1.1 | Ancestor of *C. Lupus* |
| *Canis dirus* | 0.067 | Ancestor of *C. Lupus* |
| *Canis (Xenocyon) falconeri* | 1.75 | Ancestor of *Cuon alpinus* and *Lycaon pictus* |
| *Vulpes riffautae* | 7 | Ancestor of *Vulpes* |
| *Vulpes qiuzhudingi* | 4.34 | Ancestor of *Vulpes lagopus* |
| *Vulpes stenognathus* | 2 | Ancestor of *Vulpes Vulpes* |
| *Nyctereutes donnezani* | 6.2 | Ancestor of *N. procyonoides* |
| *Eucyon davisi* | 8.3 | Ancestor of *Canis* |
| *Leptocyon vulpinus* | 18.2 | Ancestor of *Canis* and *Vulpes* |

**Methods**

NCBI was used to see what mitochondrial genes are available for multiple Caninae species. Many options for genes were available for the same 18 species. A lot of articles reference the same phylogeny published in 1997 that was based off of three cytochrome encoding genes: cytochrome b (COB), cytochrome c oxidase subunit I (COX1), and cytochrome c oxidase subunit II (COX2) (3). Since cytochrome c oxidase subunit III (COX3) was also available for the same species, it was included in the analysis in addition to the previously established three.

After these sequences were aligned, RaxML was used to construct two new phylogenetic trees with the parameters shown in Figure 1 and 2.



Figure 1. Executing code for obtaining the best maximum likelihood tree for the nucleotide alignment. Final LogLikelihood: -20320.864.

Based on the resulting tree (Figure 3), 11 fossil record species were chosen (Table 1). Those with known age estimates and direct ancestral relationships with the 18 extant species were used.

Through BEAST v2.5.2, these fossil species were incorporated into the sequence data and used to make a tree with a molecular clock. Since their DNA sequence is unknown, it is inputted into the Nexus file as a string of question marks. For all species, their estimated age is appended to their name (0 for the extant species). For the origin time, the age of *Leptocyon vulpinus* is used since this is an ancestor of both *Canis* and *Vulpes* genera. The estimated age range is 20.43 to 15.97 mya (4). The average of this range is used: 18.2 mya. The rest of the parameters were changed based on Dr Tracy Heath’s BEAST v2 Tutorial (5). After running the analysis twice (chain lengths of 5,000,000 and 8,000,000 instead of the suggested 2,000,000) the output files were imported into Tracer v1.7.1. Here, the kernel density estimate (KDE) (Figure 4) and the marginal density distribution of the turnover (Figure 5) can be compared for the two runs independent runs and prior.

LogCombiner was then used to combine the first and second runs with 20% burn-in and 10,000 resample states at lower frequency. This combined tree was then imported into TreeAnnotator for a Maximum clade credibility tree using median heights. The summary file was then opened and viewed using FigTree v1.4.4 (Figure 6).

The estimated ages were compared to that of established publications and the corresponding geological era, periods, or epochs. Ecological factors that could have stimulated some of the distinct divergences were investigated. Anatomical differences between sister taxa were compared to each other and to the local geography. Prey abundance and potential competitors for mutual resources are also considered.

**Results**

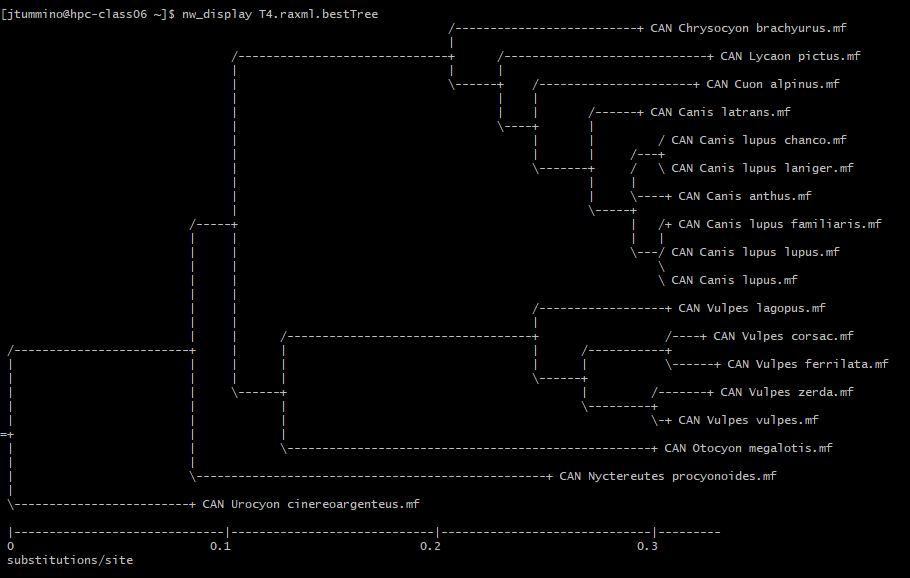


Figure 3. Best maximum likelihood tree for nucleotide sequence alignment.

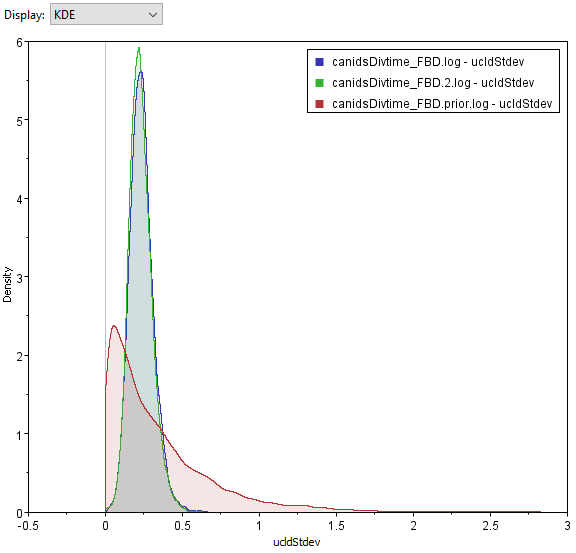


Figure 4. KDE of the marginal density of UCLD standard deviation of the two runs and the prior.

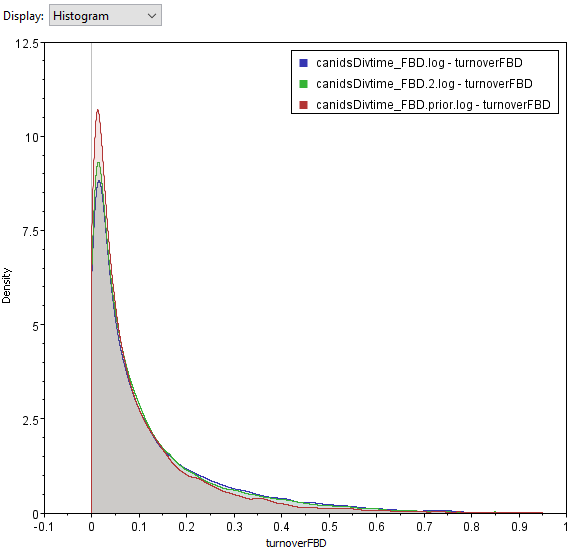


Figure 5. Histogram of the marginal density of the turnover of the two runs and the prior.

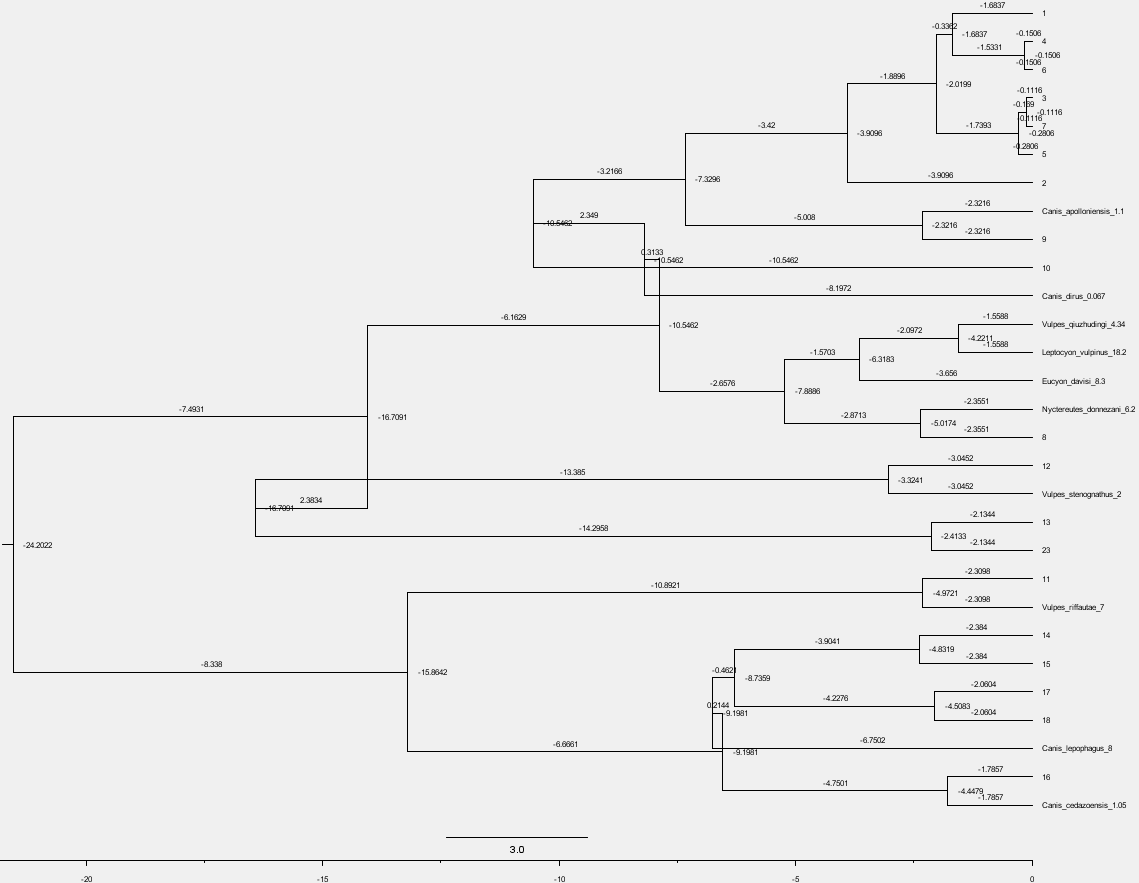


Figure 6. FigTree display of the combined tree summary for 29 taxa and age estimates on the bottom axis.

**Discussion**

**References**

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