

# Phylogenomics and Evolution of the Ursidae Family

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Fig 8. Red Panda (Ailurus fulgens)



Fig. 6. American Black Bear (Ursus americanus)

## Introduction:

Ursidae is a family of generally omnivorous mammals colloquially referred to as bears. The family consists of five genera: Ailuropoda (giant panda), Helarctos (sun bear), Melursus (sloth bear), Tremarctos (spectacled bear), and Ursus (black, brown, and polar bears) all of which are found in North and South America, Europe, Asia, and Africa (Kumar et al. 2017.) The phylogenetic relationship between Ursidae bears and the red panda (Ailurus fulgens) has been somewhat inconsistent and controversial. Previous phylogenetic analyses have placed the red panda within the families Ursidae (bears), Procyonidae (raccoons), Pinnepedia (seals), and Musteloidea (raccoons and weasels, skunks, and badgers) (Flynn et al. 2000.) Determining monophyly would elucidate the evolutionary relationship between Ursidae bears and the Red Panda. This analysis (i) tested the monophyly of the family Ursidae; and (ii) determined how the Red Panda fits within the evolutionary history of Ursidae as determined by phylogenomic mitochondrial data for the genes NADH dehydrogenase subunit 1 (ND1) and ATP synthase F0 subunit 6 (ATP6). The results in the phylogenomic analyses support the monophyly of the family Ursidae and provide strong evidence that, though the Red Panda shares a common ancestor with Ursidae bears, it is not monophyletic and should not be included in the family Ursidae.

## Objectives:

- To determine the relatedness among the 30 individual bear taxa.
- To determine if Ailurus fulgens obtained its common name (Red Panda) from similarities to the genes belonging to the Ursidae family or if it's simply based on phenotypic attributes.

## Methods:

- Mitochondrial gene sequences of the ATP6 and ND1 genes were taken from a sample of 31 species (30 Ursidae family and 1 Ailuridae family).
- Datasets were collected from the NCBI popset database.
- Collected datasets were aligned and combined using Sequence Matrix.
- Aligned datasets were then run through Phylogeny.fr to create the trees.
- FigTree was used to better visualize the phylogenetic trees.
- The three phylogenetic trees were then compared and analyzed to obtain our final conclusions.

## Results:

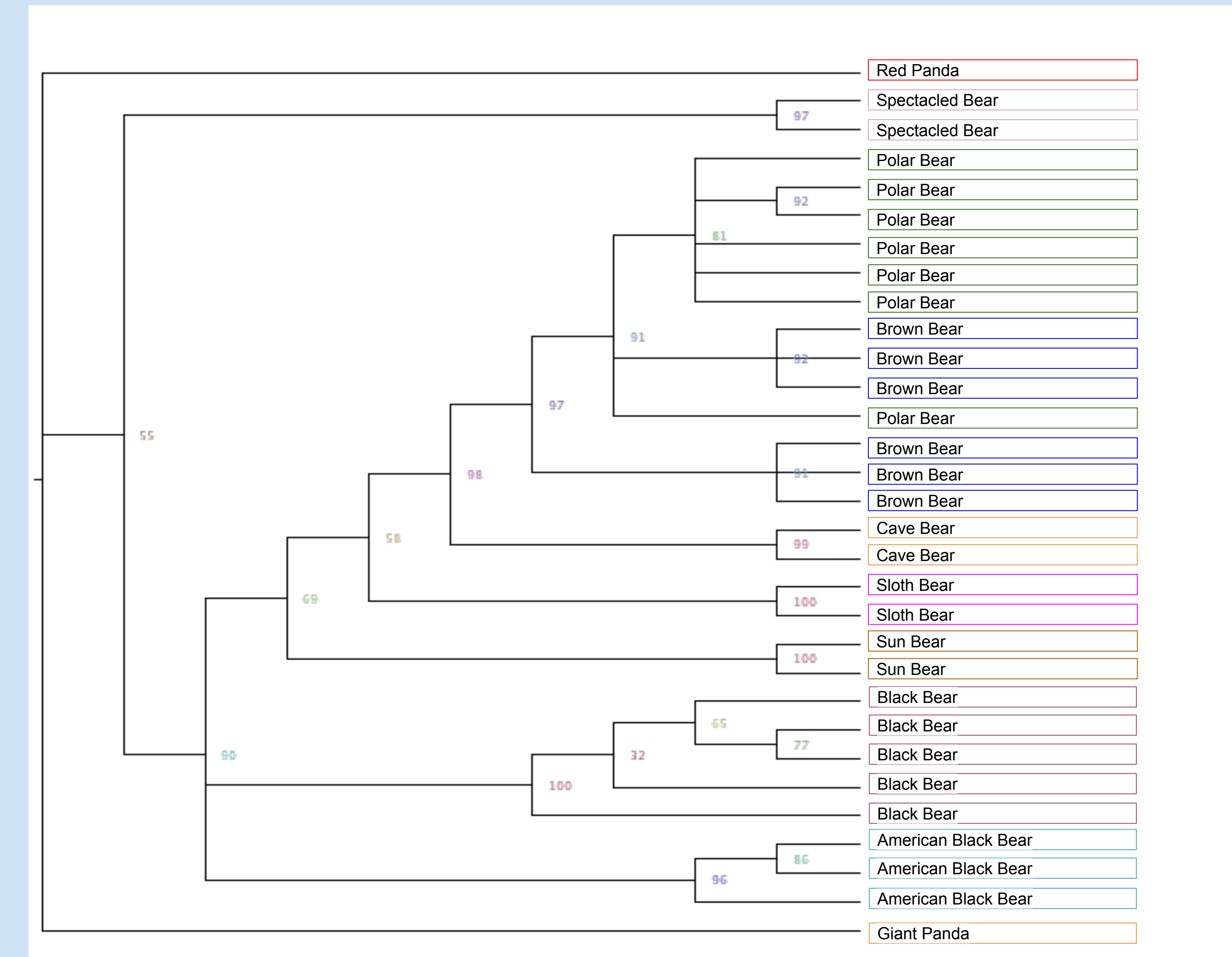


Fig. 2. Phylogeny of the ATP6 gene within family Ursidae.

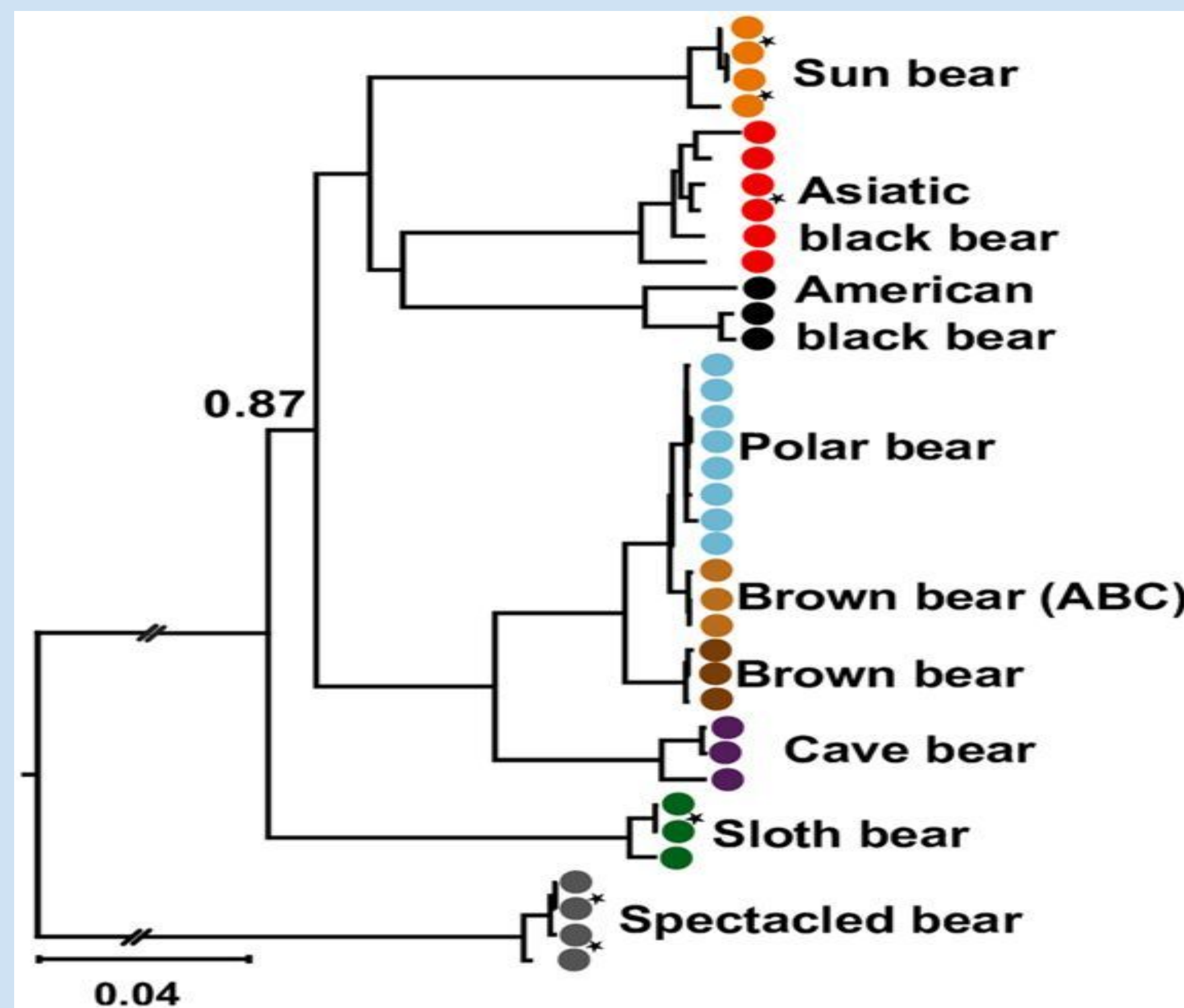


Fig. 1. A phylogenetic tree produced via molecular phylogenetic analysis of the whole mitochondrial genome of Ursidae species. Adapted from Kumar et al. 2017.



Fig. 14. Sloth Bear (Melursus ursinus)



Fig. 13. Sun Bear (Helarctos malayanus)



Fig. 7. The Spectacled Bear (Tremarctos ornatus)



Fig. 12 Cave Bear (Ursus spelaeus)



Fig. 9 Polar Bear (Ursus maritimus)



Fig. 10 Black Bear (Ursus thibetanus)



Fig. 5. Panda Bear (Ailuropoda melanoleuca)



Fig. 11 Brown Bear (Ursus arctos)

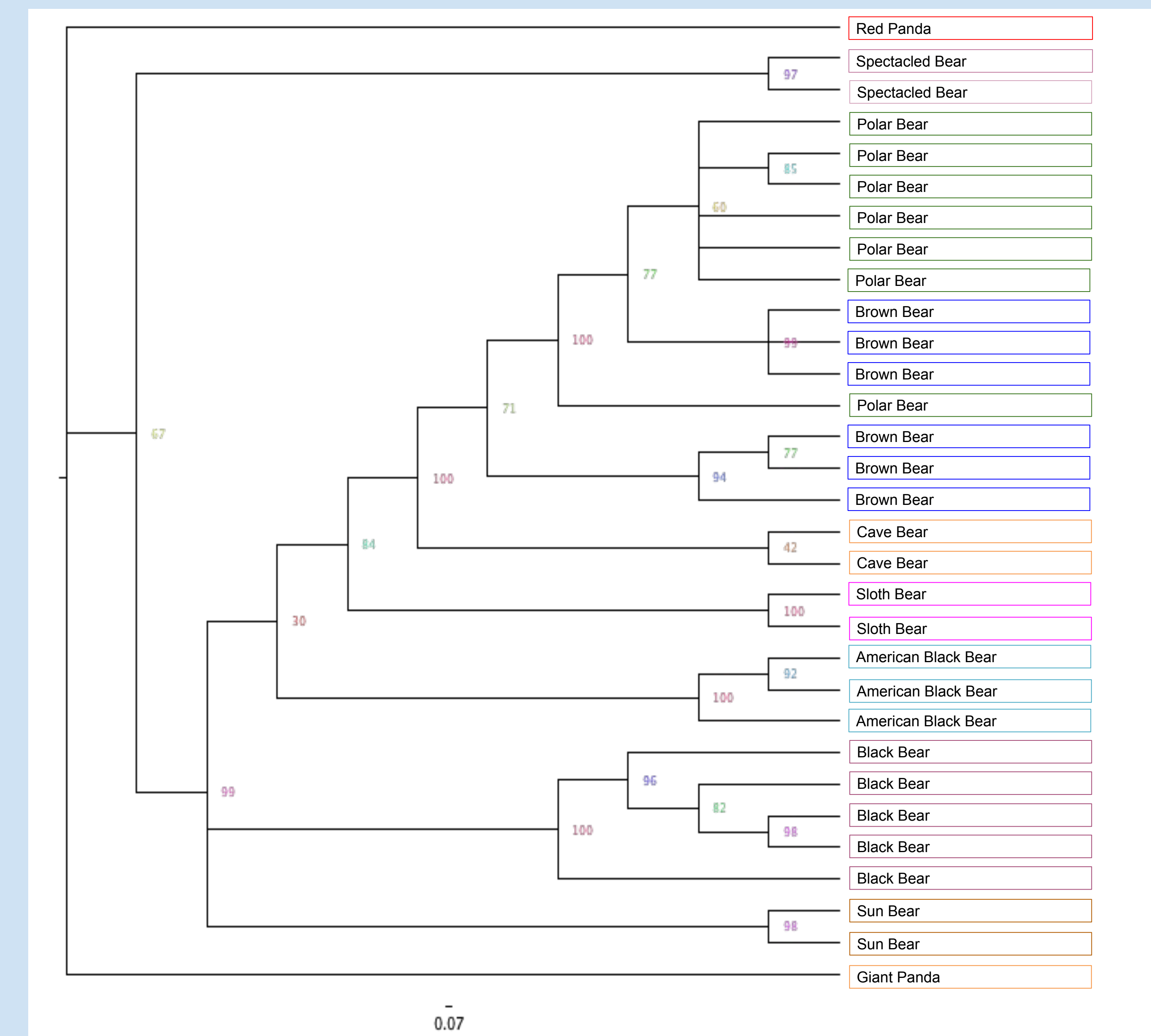


Fig. 3. Combined results from ND1 and ATP6 genes. These two combined genes show relatedness between the species. Our findings show that more genes are needed to increase the confidence numbers within the tree to determine the relatedness of all species.

## Conclusion:

The family Ursidae is shown to be monophyletic through molecular phylogenetic analysis of the ND1 and ATP6 genes and confirms previous analyses placing the red panda as an outgroup to Ursidae. This conclusion leads us to believe that, though Ursidae bears and the red panda share a common ancestor, they evolved through separate lineages and should be grouped separately. Future works should include phylogenetic analysis of whole genome data sets to further elucidate the relationship between the red panda and family Ursidae.

## Future Works:

- Gather more phylogenomic data for Ursidae.
- Generate trees again using different genomic data.
- Expanding the combined data set

## References:

- Flynn, J.J., Nedbal, M.A., Dragoo, J.W., & Honeycutt, R.L. (2000). Whence the red panda? *Molecular Phylogenetics and Evolution*. 17(2): 190-199.
- Kumar, V., Lammers, F., Bidon, T., Pfenninger, M., Kolter, L., Nilsson, M., & Janke, A. (2017). The evolutionary history of bears is characterized by gene flow across species. *Scientific Reports*, 7: 46487.

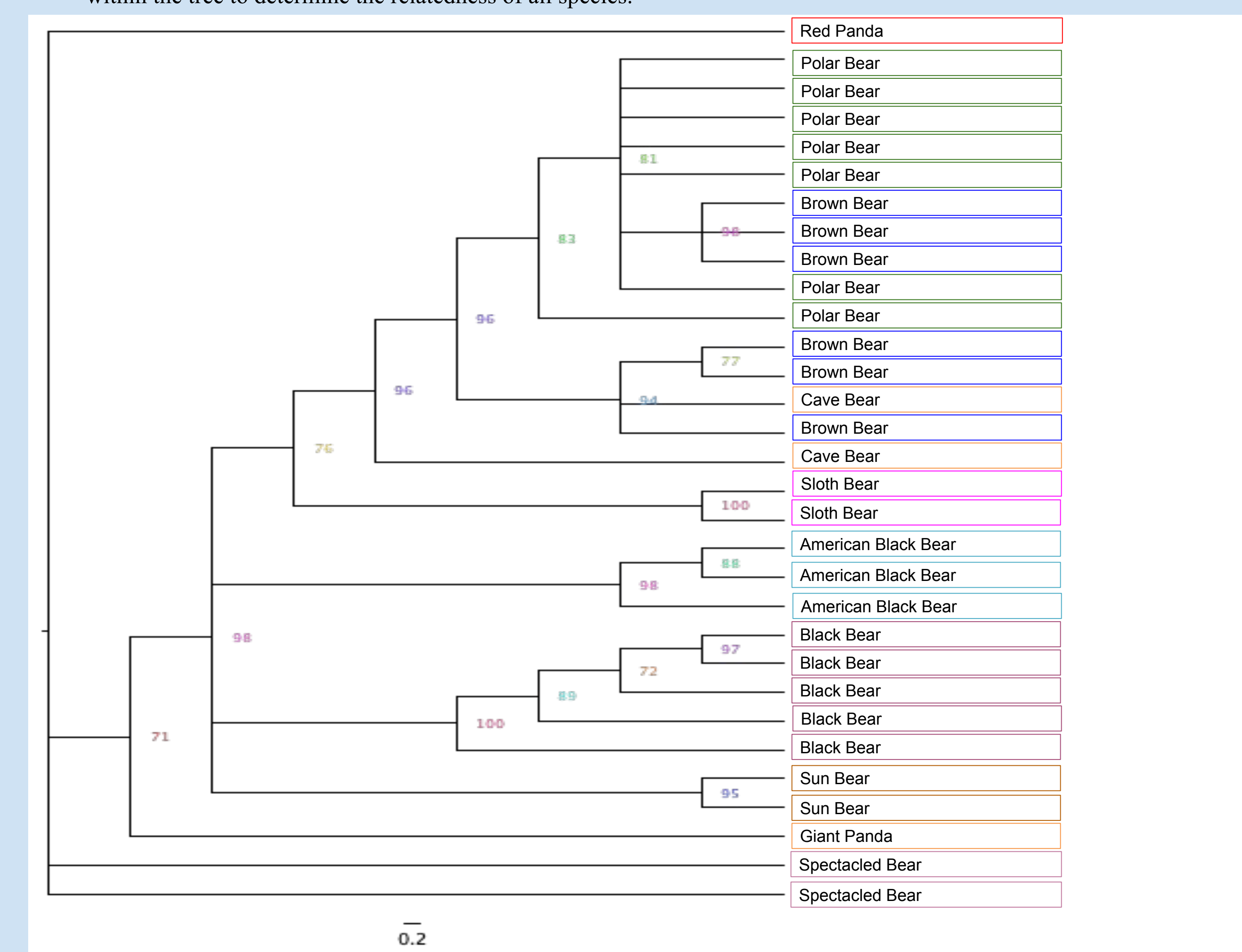


Fig. 4. Phylogeny of the ND1 gene within family Ursidae.