

Characterization of the Prion Protein Gene in Eight Breeds of Ethiopian Camels



Madison B. Reddock¹, Emily A. Wright¹, Gad Perry², Yoseph W. Legesse^{3,4}, and Robert D. Bradley^{1,5}

Department of Biological Sciences¹, Division of International Research and Development, Office of International Affairs, Texas Tech University², Department of Animal and Range Sciences, College of Dryland Agriculture, Jijiga University, Ethiopia³, Department of Animal Production, College of Agriculture and Environmental Sciences, Haramaya University, Ethiopia⁴, Natural Science Research Laboratory⁵

Introduction

- Spongiform encephalopathies are prion diseases known to result in neurodegeneration caused by cellular prion proteins folding into alternate conformations, or PrP^{Sc}.
- Prion diseases occur in three different mechanisms: familial, sporadic, and transmissible.
- Many forms of transmissible prion diseases have been discovered: scrapie in sheep and goats, bovine spongiform encephalopathy (BSE or Mad Cow Disease), Creutzfeldt-Jakob disease and Kuru in humans, Chronic wasting disease in cervids, and more recently Camel prion disease in dromedaries.

PRNP Nucleotide Position	Nucleotide change	Amino Acid
231*	T to a C	G77G
243*	A to a T	G81G
246*	C to a A	G82G
264	T to a C	H88H
765	A to a T	G255G

Table 1. Nucleotide and amino acid substitutions between *Camelus dromedarius* and *C. bactrianus*. The asterisk indicates phylogenetically informative characters.

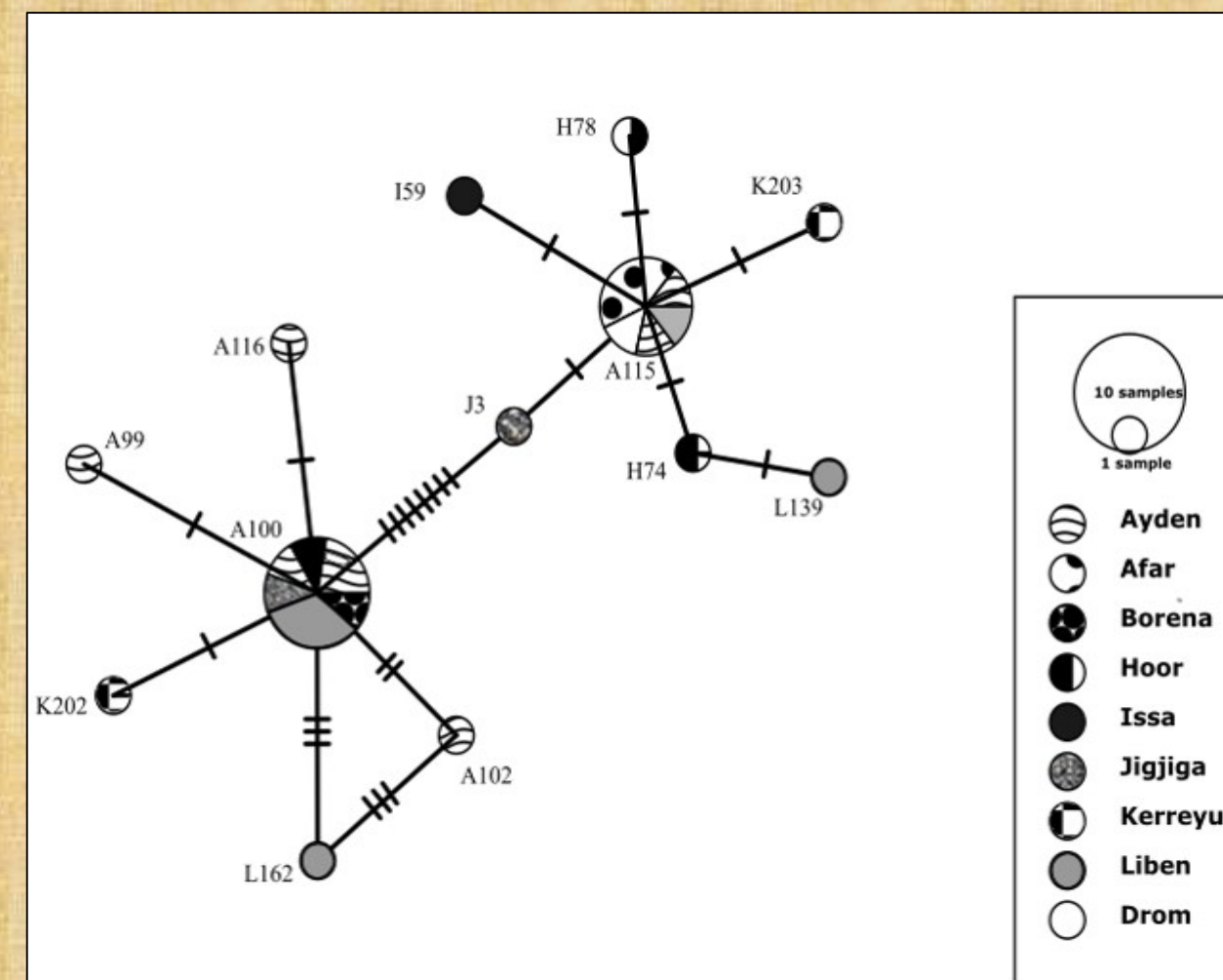


Figure 1: Haplotype network depicting genetic relationships between the 8 breeds of dromedaries used in this study.

Methods

- Obtain tissue samples of Ethiopian camels, which were placed in the Natural Science Research Laboratory, through international collaborations
- Supplement *PRNP* samples with both dromedary and Bactrian camel *PRNP* sequences from NCBI GenBank
- Perform DNA extraction procedures on samples, amplify, and sequence.
- Examine entire *PRNP* genome and note any nucleotide substitutions between Ethiopian, Algerian, and Bactrian camels.
- Perform a phylogenetic analysis on all selected samples (including those from GenBank and selected outgroups).

Results

- PRNP* sequences for *C. dromedarius* and *C. bactrianus* were obtained from GenBank for comparison purposes.
- No nucleotide changes were found within the *PRNP* gene of *C. dromedarius* from both Ethiopia and Algeria.
- Potentially significant single nucleotide substitutions were found at positions 231, 243, and 246 between *C. dromedarius* and *C. bactrianus*.
- These substitutions did not have any effect on the amino acid sequences after visual analysis on MEGA.

Hypothesis

- This study examines the *PRNP* gene of *C. dromedarius* from Ethiopia to determine if there is a link between the *PRNP* gene sequence and susceptibility to the development of CPD.
- Genetic diversity between individuals would indicate varying levels of susceptibility to the contraction or development of prion diseases within *Camelus*.



Objectives

- To examine the *PRNP* gene of Ethiopian camels
- Compare *PRNP* sequence identities to Algerian camels shown to be symptomatic with CPD
- Explore the implications of camel susceptibility to CPD by examining the *PRNP* sequence

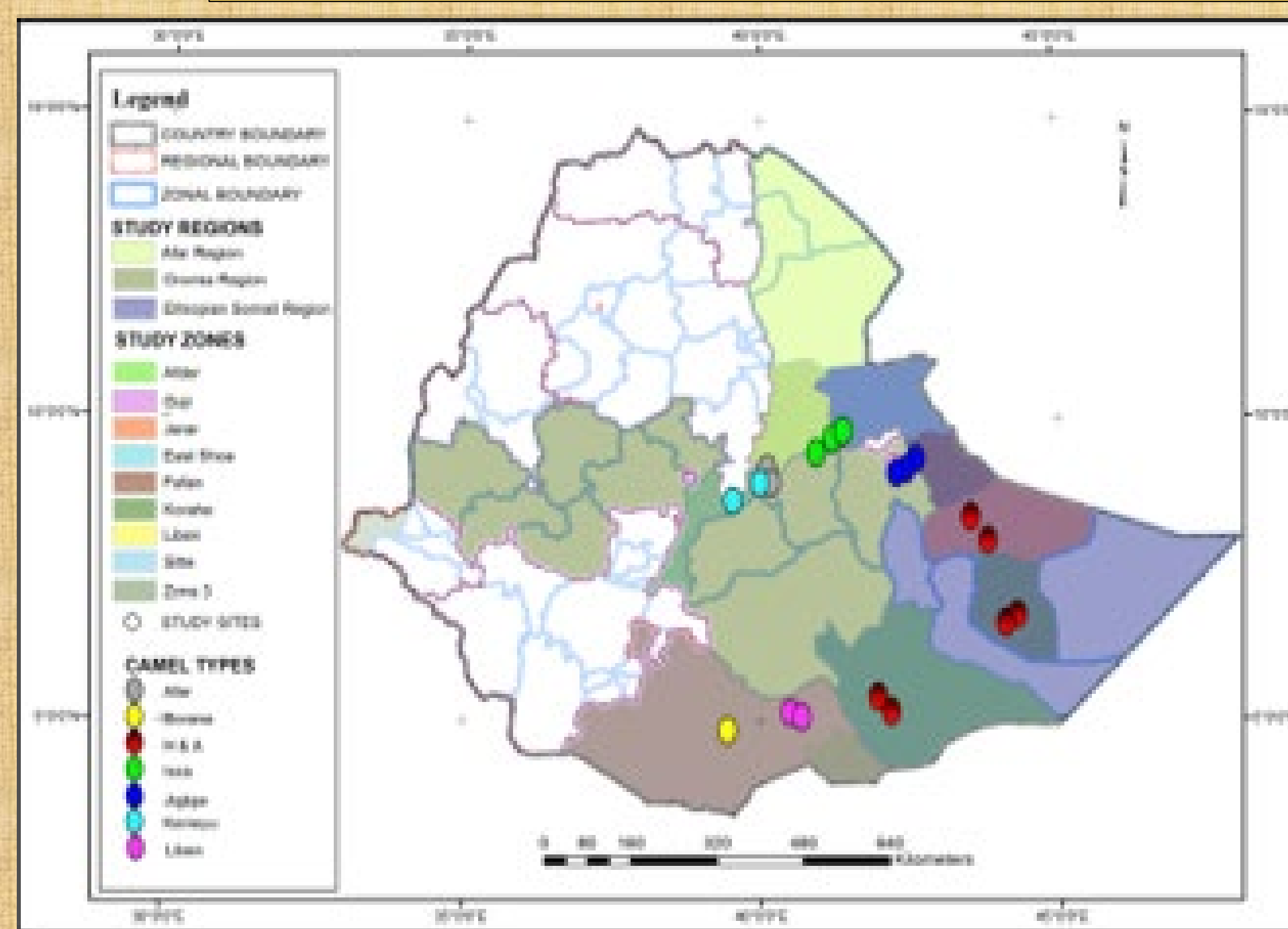


Figure 2: Map depicting the collection locations of *C. dromedarius* in Ethiopia.

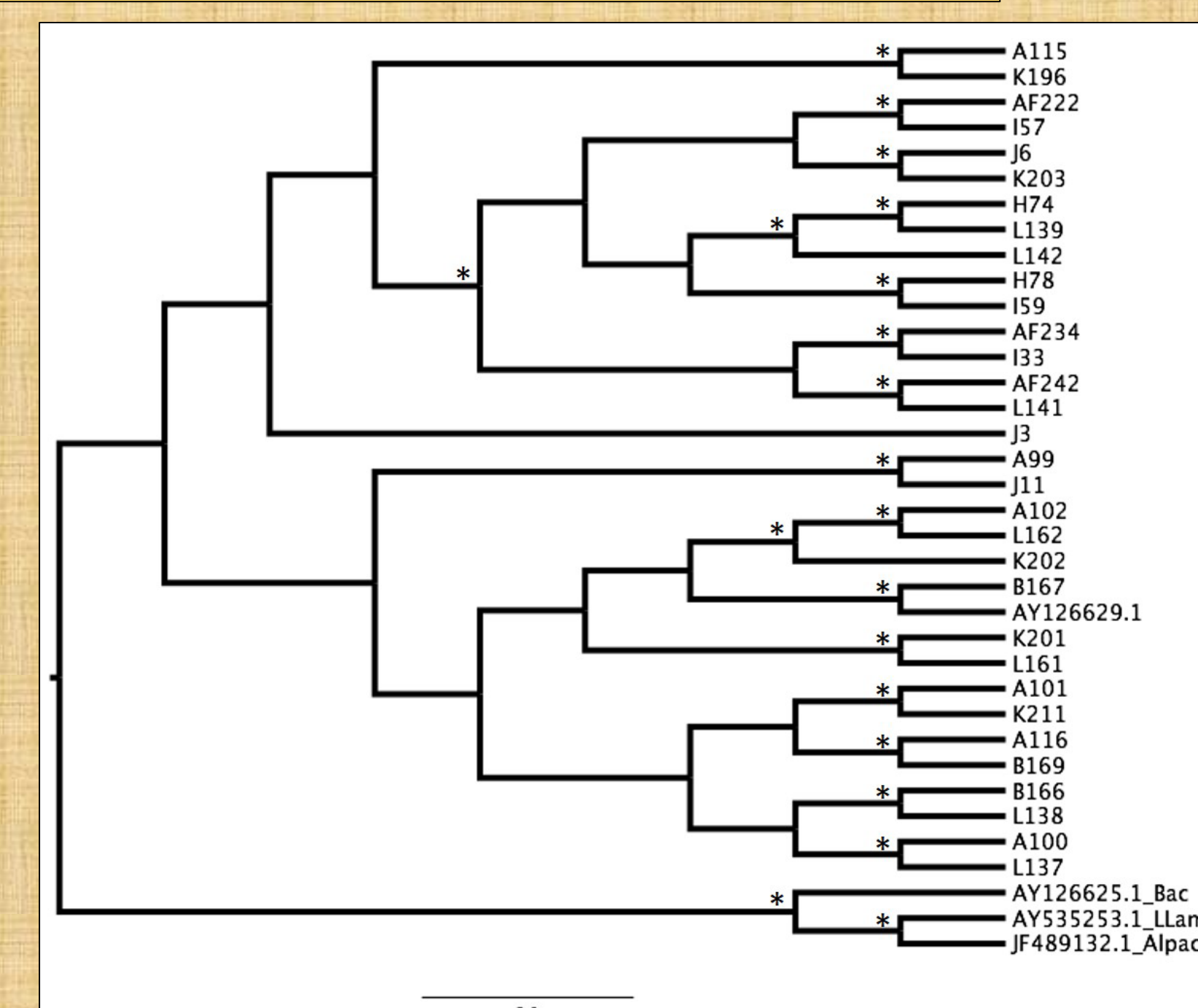


Figure 3: Bayesian tree displaying differences in Cytochrome-b sequences between *C. dromedarius* individuals with probability values of .95 or higher.

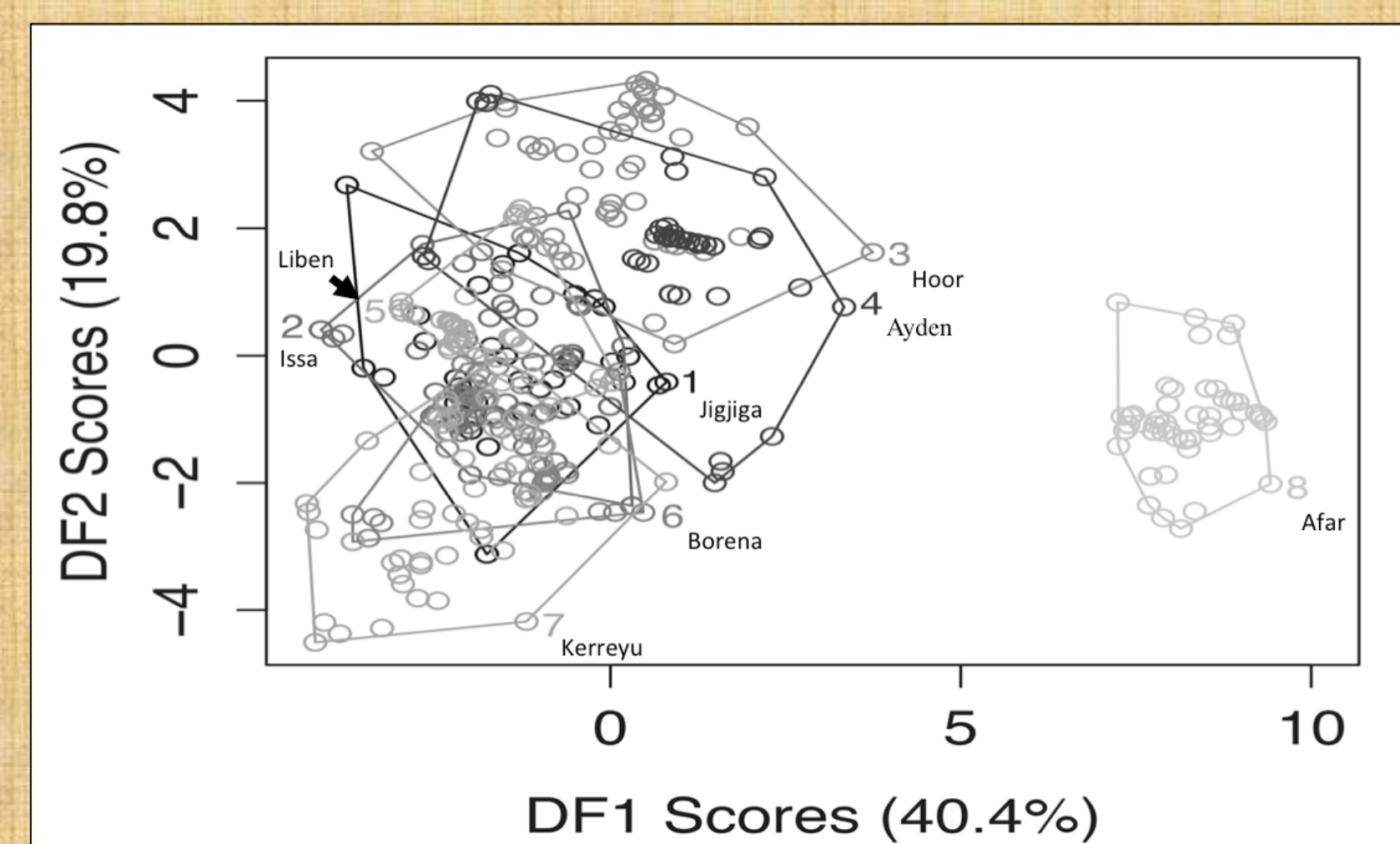


Figure 4: DFA results from physical measurement of Ethiopian camels demonstrating size differences between the Afar breed and others.

Implications

- As a novel prion disease, CPD's capabilities surrounding interspecies transmissibility is currently unknown.
- Examining the *PRNP* gene could give clues as to how susceptible *Camelus* individuals are to contracting CPD.
- With the rise in chronic wasting disease (CWD) cases in the United States, researching how to prevent more camels from developing CPD is paramount. Since camel meat is widely consumed in Africa, the Middle and Near East, as well as in parts of the Western world, controlling the spread and discovering more about CPD could help keep a new prion disease from entering the human population as well as keep dromedaries in these localities healthy.

Conclusions

- Initial study of the *PRNP* gene in Ethiopian camels demonstrate similarities to the Algerian camels, which were documented to naturally possess CPD.
- Further study is required to determine if nucleotide (but not amino acid) changes at sites 231, 243, and 246 in the *Camelus PRNP* gene are relevant in terms of susceptibility to CPD.



Table 2: MEGA PRNP gene sequences with arrows displaying nucleotide differences between *C. dromedarius* and *C. bactrianus*.



Acknowledgments

Thanks to the curators and staff of the NSRL for providing tissues used in this project. Thanks to Yoseph W. Legesse, Christopher D. Dunn, Gad Perry, and Robert D. Bradley for collecting tissues and providing cytochrome-*b* data. Thanks to Jijiga University for their assistance in collecting tissues for the project.

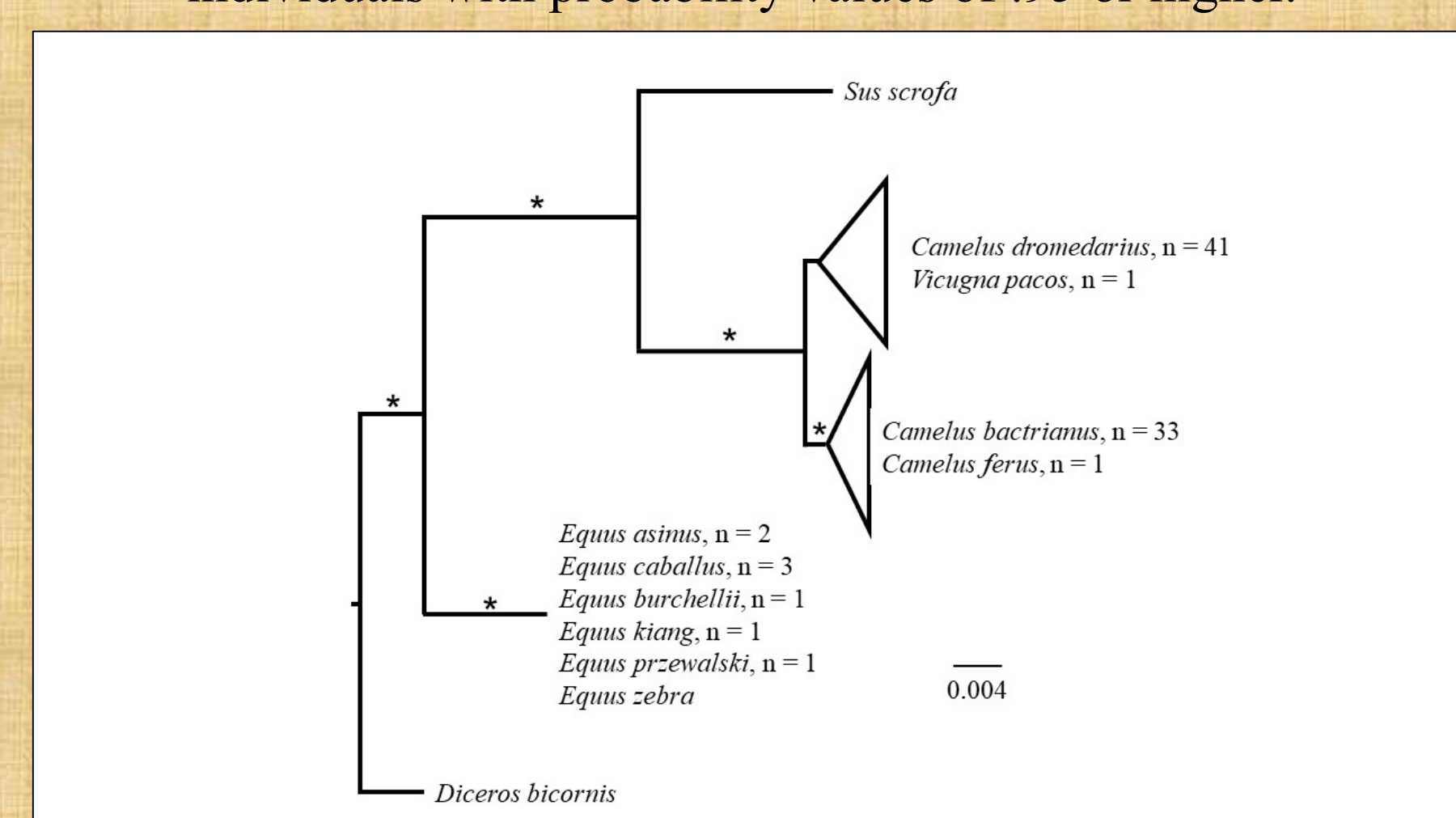


Figure 5: Phylogenetic tree generated from *PRNP* sequences.