

Introduction

•There are 6 known native subspecies of aoudad: Ammotragus I. Iervia (Atlas Aoudad), A. I. ornatus (Egyptian Aoudad), A. I. blainei (Kordofan Aoudad), A. I. fassini (Libyan Aoudad), A. I. angusi (Aïr Aoudad), and A. I. sahariensis (Saharan Aoudad)

•Serological, chromosomal, morphological, anatomical, and other molecular datasets indicate aoudad share characters similar to both to goats and sheep.

•For example, aoudad have a similar chromosome number (54) to sheep (the chromosome number of goats is 58) whereas aoudad possess scent glands similar to goats (sheep lack these)

• Aoudad can interbreed with goats, but not with sheep, leading some to believe they are most similar to goats. However, Giest (1971) posits that aoudad are ancestors to goats and sheep, and that aoudad were not in close proximity with goats, so no reproductive barrier evolved between aoudad and goats, unlike aoudad and sheep.



Figure 1. Map depicting the distribution of aoudad in North Africa based on Cassinello et al. (2008) and Kingdon and Hoffman (2013).



Materials and Methods

• 232 aoudad samples were obtained from free-ranging individuals collected between 2018 - 2021 and 19 captive aoudad samples were collected from Fossil Rim.

 Genomic DNA was extracted from tissue samples using the Qiagen Dneasy blood and tissue kit.

• DNA was amplified, purified, and sequenced for four genetic markers: Cytochrome-b (Cytb), displacement loop (D-loop), Sex determining region Y (*Sry*), and prion protein (*PRNP*). • Gene sequences for all four markers were obtained from GenBank from Family Bovidae for comparison to A. lervia. • A Bayesian analysis was conducted to determine phylogenetic relationships to A. lervia.

AOUDAD: A GOAT IN SHEEP'S CLOTHING? ⁷ Zoe M. Bixler¹, Emily A. Wright¹, and Robert D. Bradley^{1,2} 1 – Department of Biological Sciences, 2 – Natural Science and Research Laboratory





Figures 3 (above) and 4 (left). Phylogeny of the *PRNP* and *Sry* genes, respectively. Bayesian posterior probability values are indicated by the * and represent ≥ 0.95 nodal support.





•Wright et al. (2022) demonstrated the presence of three mitochondrial lineages in the US, however, there does not appear to be any significant variation in Sry and PRNP genes.

•Although there is a lack of phylogenetic support across 2 of the 3 markers, the genetic distances, as indicated by the length of branches, indicate that acudad are more similar to goats than to sheep.

•In addition, mtDNA and Sry indicate that aoudad are placed in a unique clade that shares a common ancestor with goats.

It is important to determine their genetic similarity to other species in the Tribe Caprini in order to evaluate any potential environmental impacts. Similar evolutionary trajectories are a key risk factor for pathogen spillover and associated disease-induced population declines in wildlife, which is corroborated by the genetic similarity between strains of *M. ovipneumoniae* documented in both domestic and wild sheep and goats. Genetic distances, along with divergence events will provide more insight on phylogenetic relationships among taxa in Family Bovidae compared to aoudad.

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Ammotragus lervia, n = 30
Hemitragus javakari
     |H. jemlahicus, n = 7
       Capra sibirica, n = 5; C. cylindricornis, n = 1
        . hircus, n = 10; C. cylindricornis, n = 2; C. aegagrus, n = 4; C. caucasica, n = 3; C. falconeri, n = 2; C. ibex, n = 1
         Pseudois nayaur, n = 104
       Budorcas taxicolor, n =
 Hemitragus hylocrius
              Ovis aries, n = 9; O. ammon, n = 8; O. nivicola,
              n = 1; O. orientalis, n = 6; O. vignei, n = {
. !∛| O. nivicola, n = 3
🏌 0. dalli, n = 2
     ). canadensis. n = 10
    Oreamnos americanus. n = 10
                                                             Figure 5. Phylogeny of
   Capricornis crispus, n = 1; C. sumatrensis, n = 2
    Ovibos moschatus, n = 8
                                                             the Cytb gene.
      Vemorhaedus caudatus. n = 8
                                                              Bayesian posterior
       Rupicapra rupicapra, n = 58; R. pyrenaica, n = 19
                                                             probability values are
   Bison bison, n = 1; B. bonasus, n = 2
                                                              indicated by the * and
                             0.03
                                                              represent \geq 0.95 nodal
                                                              support.
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Discussion

Implications and Future Directions

Acknowledgments