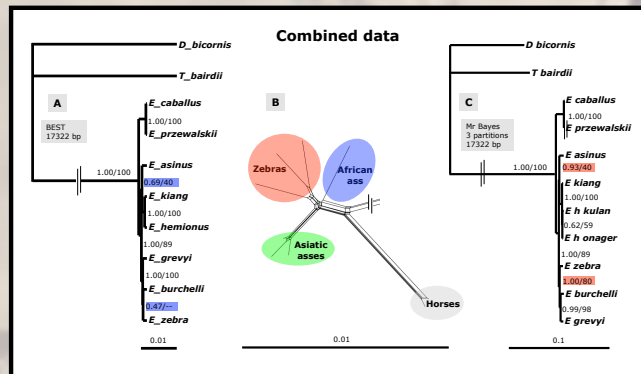
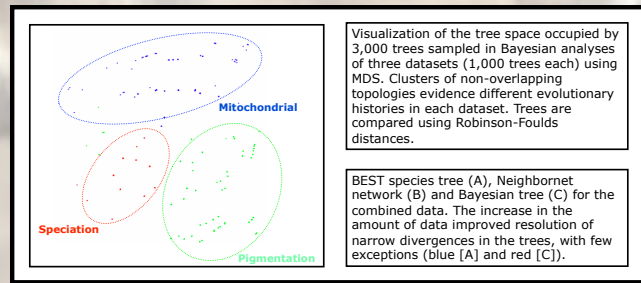
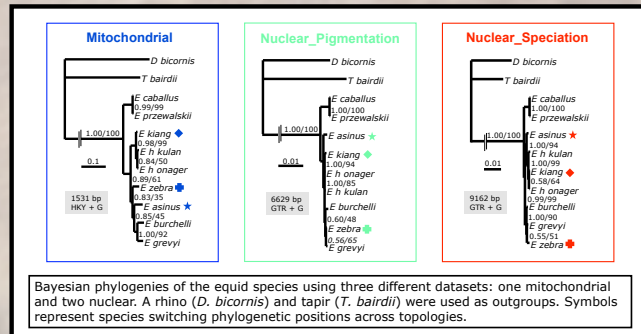


Phylogeny and conservation of equids

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INTRODUCTION

In conservation, the main goal of phylogenetics is to establish an evolutionary framework for understanding species boundaries and patterns of intraspecific genetic variation, necessary to identify evolutionary significant units (ESUs)^(1,2). However, processes such as hybridization and lineage sorting might confound phylogenetic inferences, jeopardizing species' designation^(3,4). This is particularly relevant in the case of endangered species, where no conservation policies have been established for hybrids⁽⁵⁾. Here, we examine the phylogenetic relationships of eight species of equids by analyzing mitochondrial and nuclear datasets, and evaluate the role of speciation processes in determining patterns of intraspecific genetic variation.

METHODS

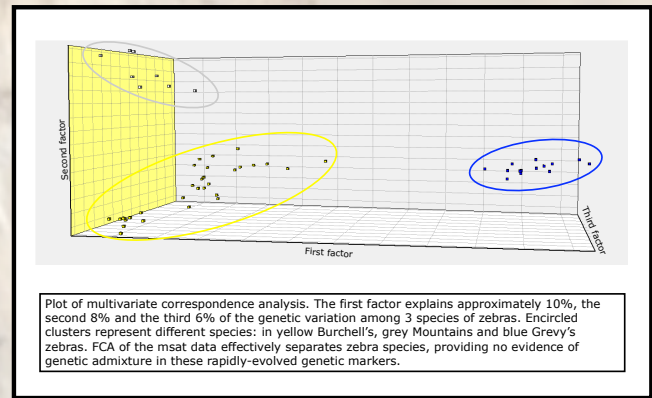
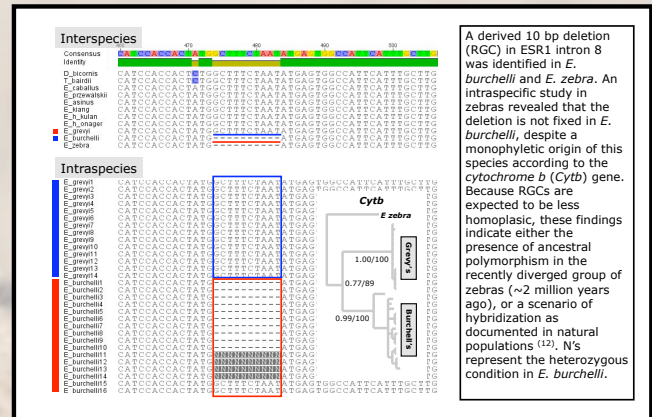
Three datasets that include a total of 22 genes (2 mitochondrial, 9 [pigmentation] and 11 [speciation] nuclear) were sequenced and analyzed in 8 equid species (plus 2 outgroups). MrBayes 3.7⁽⁶⁾, PHYML⁽⁷⁾, and BEST⁽⁸⁾ were used in phylogenetic analyses, and Splitstree⁽⁹⁾ in network reconstructions. Multidimensional Scaling⁽¹⁰⁾ (MDS) was employed for visualizing and comparing the tree space of different datasets. For intraspecific analyses, the Estrogen Receptor 1 gene (ESR1) was sequenced and 12 microsatellites (msats) screened in 55 zebras (14 Grevy's, 32 Burchell's, and 9 Mountains), and then analyzed through Factorial Correspondence Analyses (FCA) using Genetix 4.04⁽¹¹⁾.

RESULTS

In equids, discrepancies among gene trees were detected among the independent and combined datasets, likely due to lineage sorting or genetic introgression. The combined data supported the position of the African ass as sister taxon of Asiatic asses, and the Mountains zebra basally located relative to Burchell's and Grevy's zebras. Intraspecifically, the ESR1 gene showed signature of genetic admixture between the common species, Burchell's zebra, and the endangered Grevy's zebra for a Rare Genomic Change (RGC). Genetic admixture was not confirmed at a large genomic scale, as evidenced by the msat data.

CONCLUSIONS

Our results emphasize the importance of understanding lineage sorting and genetic introgression as evolutionary processes potentially limiting the resolution of phylogenetic trees, despite the amount of genomic data analyzed. This is relevant in a conservation context, validating the incorporation of ecological and demographic/population data in addition to phylogenies for consistently identifying ESUs among equids.



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