

Speciation Reversal: The Case of the Common Raven



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BACKGROUND

Speciation reversal results when two or more distinct species interbreed to form one species. This phenomenon is most widely known in human history; our evolutionary background consisting up to four separate lineages, now reduced to a single species. Speciation reversal is also noted in other organisms, such as fish and birds. However, unlike fish, the documented cases of speciation reversal in birds are not influenced by humans, and reflect a natural occurrence. We focus on the case of Common Ravens, which suggests a likely case of speciation reversal.

Speciation:

-The splitting of one lineage into two. Results in net gain of species.

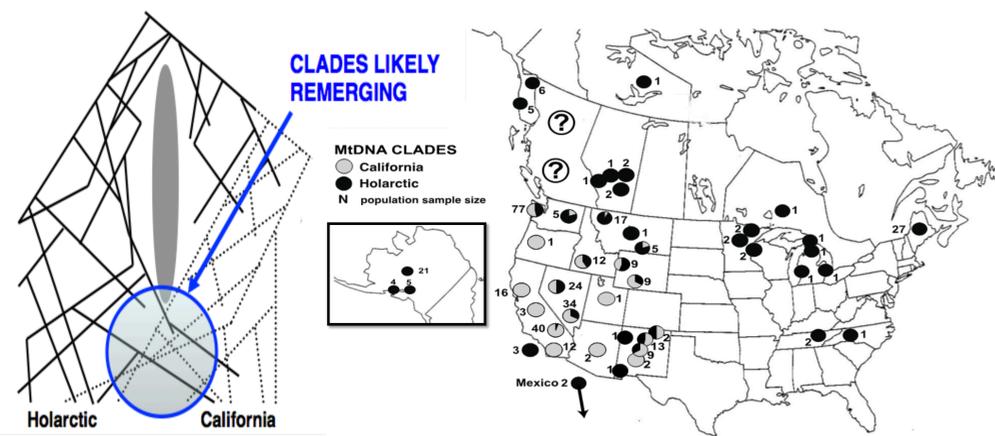
Speciation Reversal:

- Separate species intermixing to form one species. Results in net loss of species.



COMMON RAVEN (*Corvus corax*)

The Common Raven (*Corvus corax*) has a very wide range, spanning throughout North America, Europe, and Asia. Within this species, there exist two deep mitochondrial lineages, the California clade (found exclusively in south-western U.S.) and the Holarctic clade (found throughout the entire range). The estimated time of divergence is calculated to be 2 million years between these two lineages. These two genetically distinct clades now have overlapping ranges and Holarctic and California alleles are intermixing, which is likely causing the merging of these two lineages.



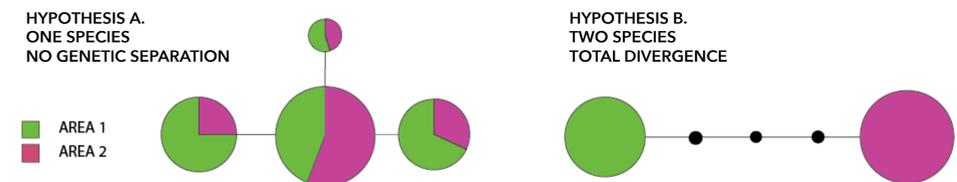
SEQUENCING AND ALLELE NETWORKS: ACO1 Nuclear Intron

We sequenced the ACO1 nuclear intron located on the Z chromosome, a sex chromosome in birds (males are ZZ and females are ZW). We looked for single nucleotide polymorphisms (SNPs) to determine the number of haplotypes found in our data sample.

Allele Networks:

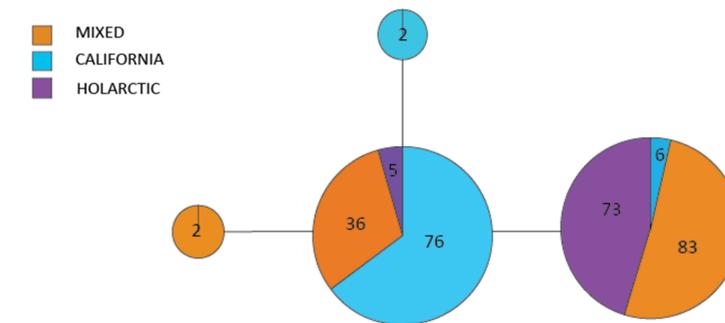
Visual representations of clusters of alleles.

Alternative Predictions:

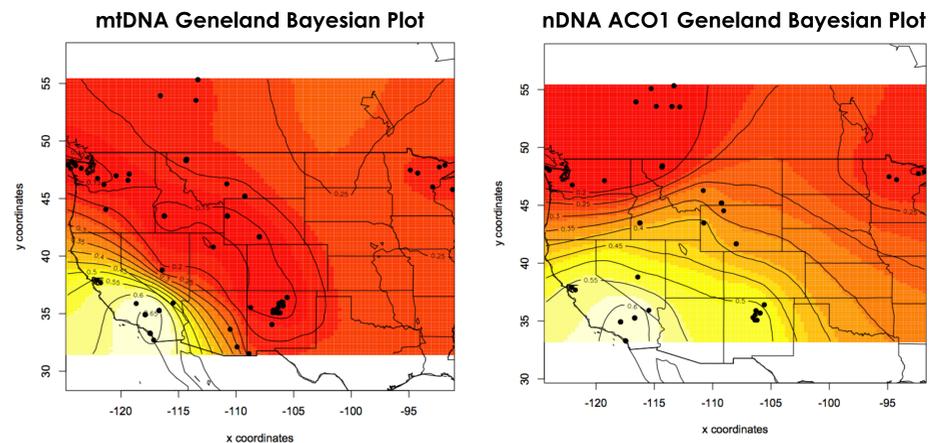


NUCLEAR DNA RESULTS

Our allele network shows that the majority of Holarctic and California ravens are in separate groups, demonstrating the divergence between the two groups. However, the fact that alleles from different regions are present in both groups indicates interbreeding, which supports our hypothesis of speciation reversal in Common Ravens.



GENELAND Results: R Program for Spatial Analysis of Alleles



Conclusions and Future Steps

These maps clearly support our hypothesis of speciation reversal. Nuclear ACO1 and mitochondrial DNA data suggest a large area of genetic mixing in the western U.S. In the future, we plan to:

- Compare autosomal nuclear data to ACO1 and mitochondrial data
- Use the UMBC High Performance Computing Facility to determine amount of gene flow between North American and Eurasian Common Ravens.

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Two undergraduates needed for continuation of this UBM project: Mathematics/Statistics Major and Biology/Bioinformatics Major.