

# Using genetics to understand population structure of inshore and offshore bottlenose dolphins (*Tursiops truncatus*)

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## Hypoxia and Health

Deep-diving whales often hold their breath for hours while foraging, so marine mammals may hold the answer to developing new ways to protect hypoxia-sensitive species and creating new clinical interventions for hypoxia as it relates to human health. Preliminary results have pinpointed a series of gene expression pathways associated with hypoxia tolerance in marine mammals and also highlighted genetic variation in two ecotypes (inshore and offshore) of bottlenose dolphins that occupy distinct habitats and engage in different diving behavior.

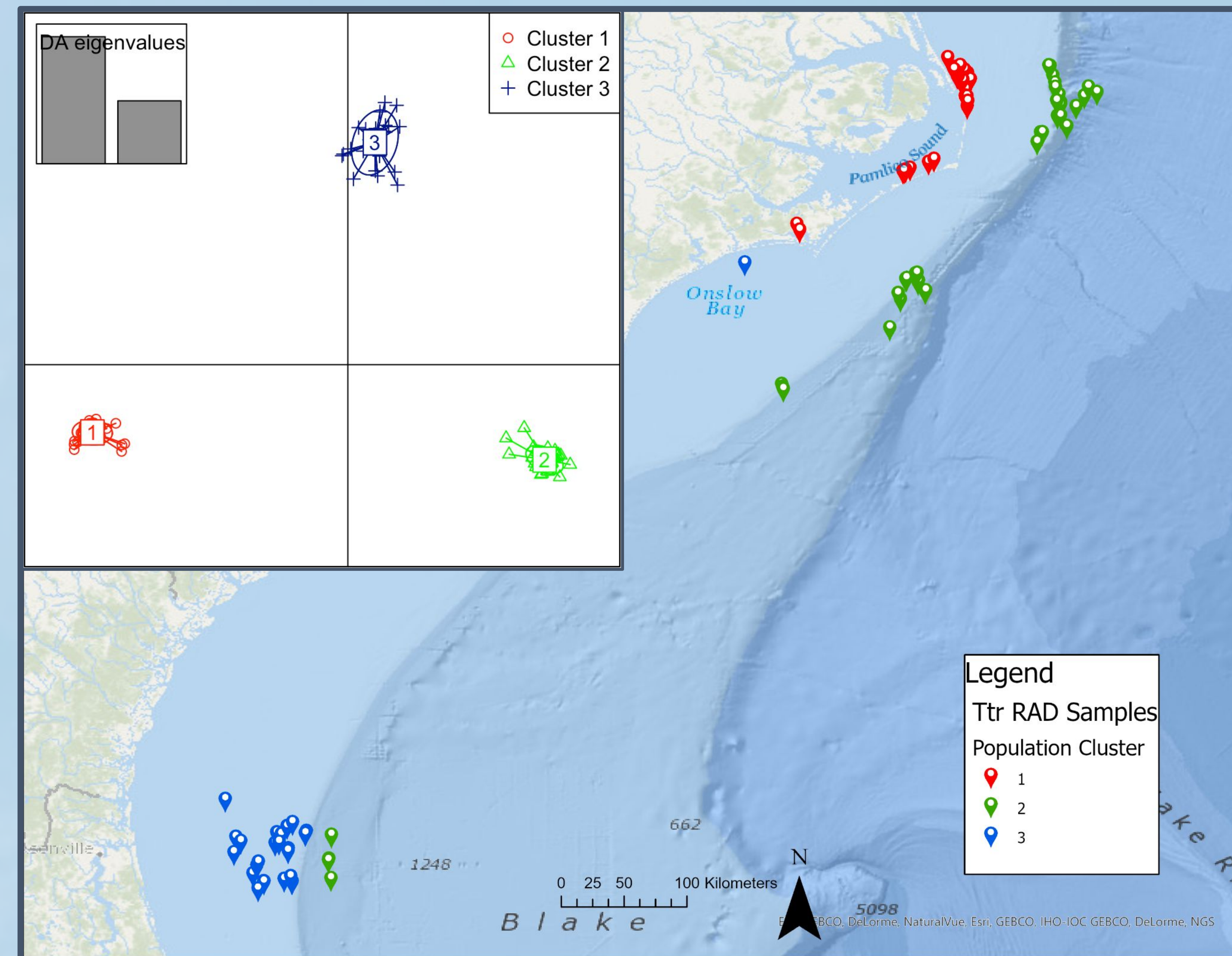


Figure 1: Results give 3 populations. Individuals are mapped and color-coded by cluster assignment. There is an inshore (red), offshore (green), and shelf population (blue). The upper left is the Discriminant Analysis of Principal Components that also resulted in 3 populations.

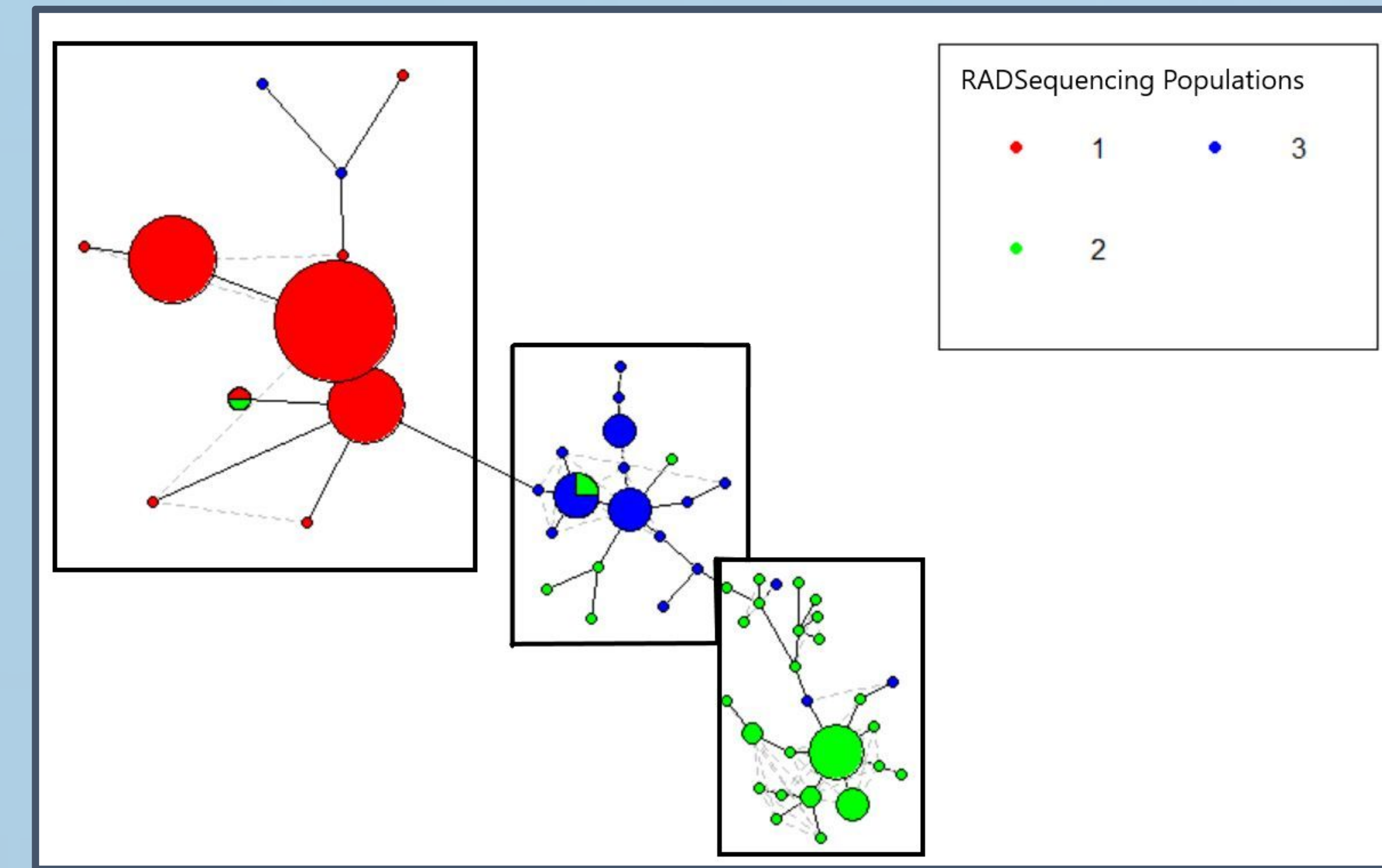


Figure 3: Haplotype network revealed 3 distinct clusters (boxes). The colors represent the populations determined with RADseq.

Population	Number of individuals	Number of haplotypes	Haplotype diversity	Nucleotide diversity	Tajima's D		
					Value	p-value (normal)	p-value (beta)
1	32	9	0.7903	0.0047	-1.6221	0.1048	0.0889
2	38	30	0.9787	0.0134	-0.5815	0.5609	0.6001
3	26	19	0.9631	0.0119	-0.2576	0.7967	0.8359

Figure 4: Statistics based on the haplotype network. Results indicate that there is a high degree of haplotypes unique to the populations and a low degree of polymorphisms

## Key Takeaways

- Fine-scale genetic resolution of population structure
- Genomic wide data allows us to look at ancestry and evolutionary history to reconstruct phylogeny

## Future Work

- Use Nanopore sequencing to further explore different marine mammals' evolution of hypoxia tolerance

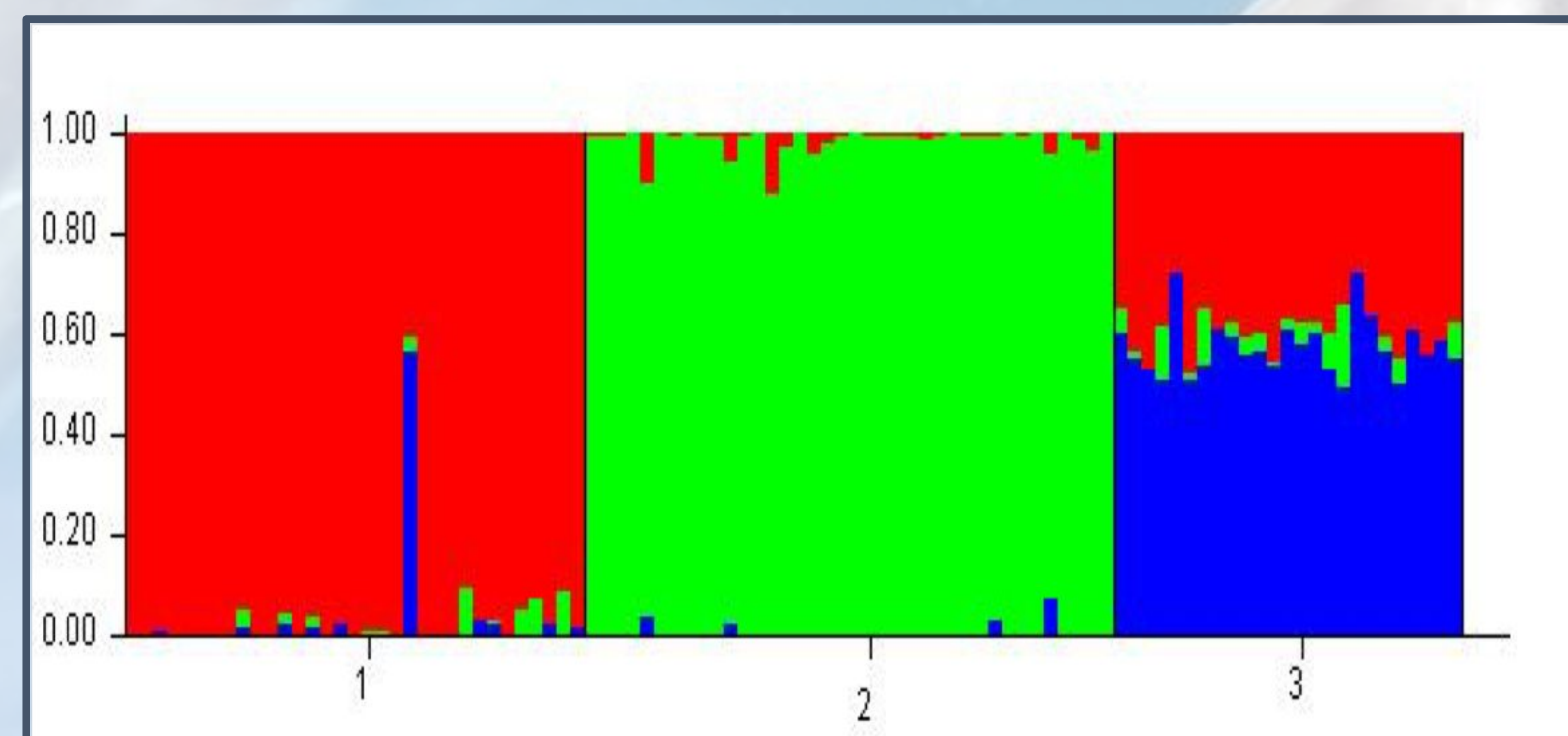
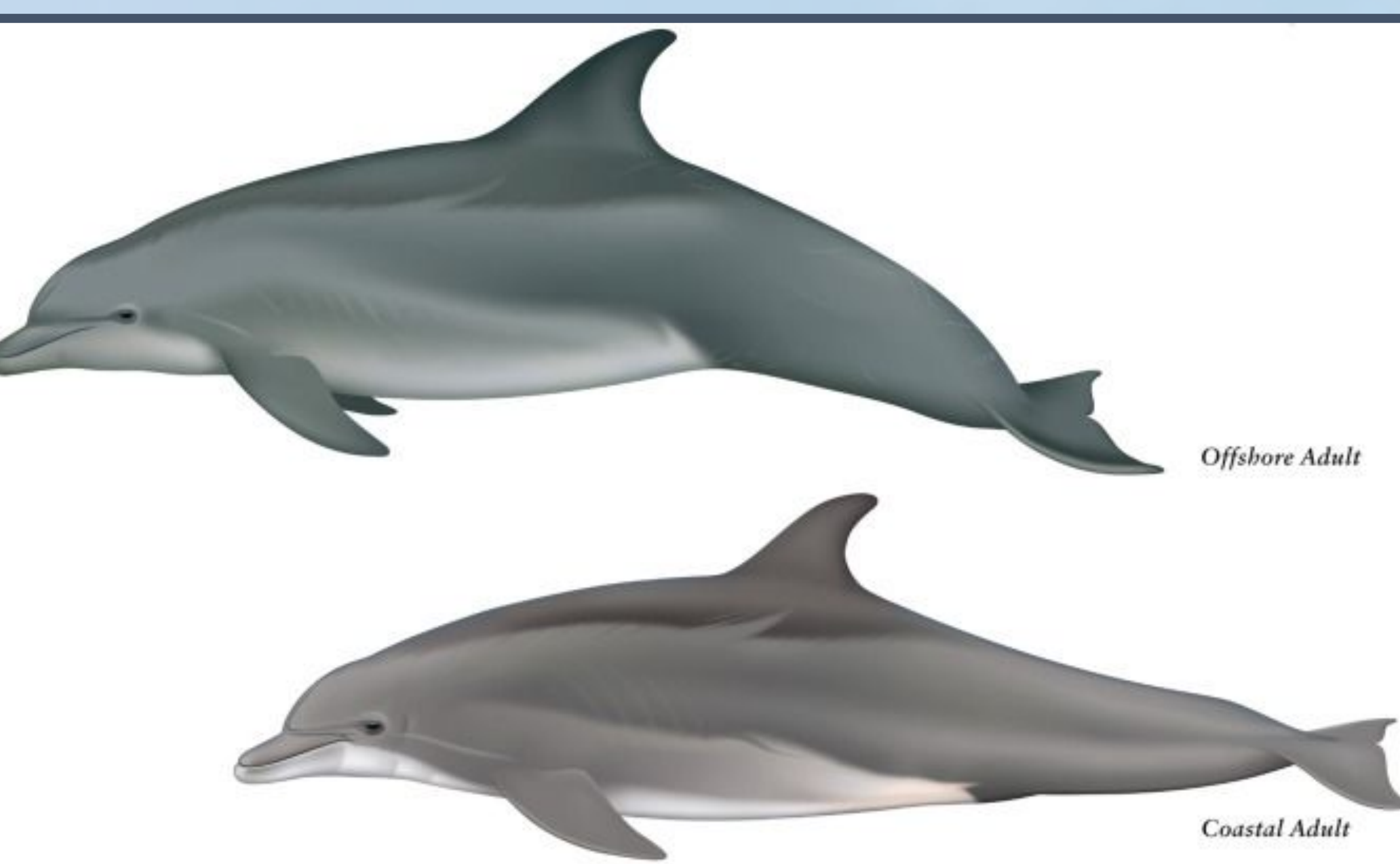


Figure 2: Bayesian clustering shows admixture between the North Carolina and Jacksonville populations, providing potential evidence of historical or current gene flow.



## Genetic Approaches

- Restriction Site Associated DNA sequencing (RAD seq) (Figures 1-2)
- Mitochondrial DNA (control region) (Figures 3-4)