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FEEDBACK

Genetic divergence and ephemeral barriers: Reconciling genetic and geological timescales within geogenomics

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Understanding the timescales on which different geologic processes influence genetic divergence is crucial to defining and testing geogenomic hypotheses and characterizing Earth-life evolution. To see if we can recover a genetic signal produced by a hypothetical physical barrier to gene flow, we used a geographically explicit simulation approach. We used the CDMetaPop software to simulate heritable genetic, nonadaptive, data for 20 geographically distinct populations distributed throughout the Baja California peninsula of Mexico, a landscape where a transpeninsular seaway barrier has been proposed to have isolated the southern peninsula and caused the observed latitudinal genetic divergence in over 80 terrestrial species. We simulated 10,000 generations of isolation by a barrier under two dispersal scenarios (1 km and 100 km of max. dispersal from population of origin per generation) and three DNA substitution rates (10-7, 10-8 and 10-9 nucleotide substitutions per site per generation). Our simulations indicate that a physical barrier can produce strong genetic divergence within 10,000 generations, comparable to the continuum of values observed in nature for different taxonomic groups and geological settings. We found that the generation time of the organism was by far the most important factor dictating the rate of divergence. Evaluating different generation times (0.02, 0.2, 2 and 20 years), showed that species with longer generation times require longer periods of isolation to accumulate genetic divergence over 10k generations (~1 My). Simulating 10,000 generations of gene flow following removal of the barrier showed that the divergence signal eroded quickly, in less than 1,000 generations in every scenario, a pattern supported by theory from population genetics. These results are particularly relevant to geogenomic studies because they show that ephemeral gene flow barriers produce different magnitudes of genetic signals depending on attributes of the organism, particularly generation time, and that if reproductive isolation is not achieved during isolation, then the evolutionary signal of an ephemeral barrier may not develop. This work helps guide the limits of detectability when integrating genomic data with geological and climatic processes.

Feedback/Corrections?

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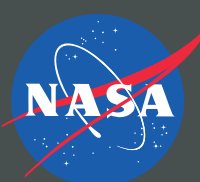
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