## Genetic drift does not outweigh natural selection at Toll-like receptor genes in the populations of Galápagos mockingbirds

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May 29, 2020

## Abstract

Population and conservation genetics seek to understand how adaptive diversity is shaped by the interweaving forces of molecular evolution in small and endangered populations. On the one hand, selection shapes variation, on the other hand, genetic drift impedes the selection by stochastic changes of allele frequencies. Drift is hypothesised to prevail if the population size is small. However, in practice empirical estimates of the population size are often challenging. Here we used island size as a proxy to population size to reveal the evolutionary constraints of molecular diversity in Toll-like receptors (TLRs) of mockingbirds (genus Mimus) inhabiting Galápagos islands. TLRs are crucial for pathogen recognition by host immunity and thus under various selection constraints. We focused on the interaction of drift and selection in TLR1B, TLR4, and TLR15 across 12 size-variable insular populations and compared them with the mainland population of the northern mockingbird (Mimus polyglottos), aiming to test if population size impacts selection efficiency. Nucleotide diversity positively correlated with the island size indicating an increasing effect of genetic drift in small populations. Despite this pattern, functional TLR properties were largely conserved, presumably due to purifying selection opposing drift independently on the island size. The degree of protein conservatism differed between the loci with TLR15 being the least conserved. Island colonisation did not lead to relaxed selection or to local adaptations. Together with the invariable physicochemical properties of the TLR variants, these observations imply that drift did not outweigh purifying selection despite restricted population size.

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