

Inferring the timing and strength of natural selection and gene migration in the evolution of chicken from ancient DNA data

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Abstract

With the rapid growth of the number of sequenced ancient genomes, there has been increasing interest in using this new information to study past and present adaptation. Such an additional temporal component has the promise of providing improved power for the estimation of natural selection. Over the last decade, statistical approaches for detection and quantification of natural selection from ancient DNA (aDNA) data have been developed. However, most of the existing methods do not allow us to estimate the timing of natural selection along with its strength, which is key to understanding the evolution and persistence of organismal diversity. Additionally, most methods ignore the fact that natural populations are almost always structured, which can result in overestimation of the effect of natural selection. To address these issues, we propose a novel Bayesian framework for the inference of natural selection and gene migration from aDNA data with Markov chain Monte Carlo techniques, co-estimating both timing and strength of natural selection and gene migration. Such an advance enables us to infer drivers of natural selection and gene migration by correlating genetic evolution with potential causes such as the changes in the ecological context in which an organism has evolved. The performance of our procedure is evaluated through extensive simulations, with its utility shown with an application to ancient chicken samples.

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