

Inference of assortative mating and selection on heterozygotes from multi-locus gene families.

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Abstract

1. The fixation index, FIS has been a staple measure to detect selection or departures from random mating in populations. However, current Next Generation Sequencing (NGS) cannot easily estimate Fis, in multi-locus gene families, which contain multiple loci having similar or identical arrays of variant sequences of [?]1 kilobase, which differ at multiple positions. In these families, high-quality short-read NGS data typically identify variants, but not the genomic location, which is required to calculate Fis (based on locus-specific observed and expected heterozygosity). Thus, to assess assortative mating, or selection on heterozygotes, from NGS of multi-locus gene families, we need a method that does not require knowledge of which variants are allelic at which locus in the genome. 2. We developed such a method. Like Fis, our novel measure, 1His, is based on the principle that positive assortative mating, or selection against heterozygotes, reduces within-individual variability relative to the population. 3. We demonstrate high accuracy of 1His on a wide-range of simulated scenarios, and two datasets from natural populations of penguins and dolphins. 4. 1His is important because multi-locus gene families are often involved in assortative mating, or selection on heterozygotes. 1His is particularly useful for multi-locus gene families such as toll-like receptors, the major-histocompatibility-complex in animals, homeobox genes in fungi and self-incompatibility genes in plants.

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