

<p class="fixed">Bayesian Approach to Inferring Recent Selective Sweeps in Anopholes Gambiae Populations

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Abstract

Analyzing the distribution of microsatellite allele sizes in populations is of interest to understanding the genetic diversity of species and the evolutionary history of recent selective sweeps. We propose a Bayesian analysis of variance method for inferring loci involved in recent selective sweeps by analyzing the distribution of allele sizes at multiple loci in multiple populations. Our method is shown to be consistent with a recent multilocus test statistic, $\ln RV$, proposed by Schlotterer for identifying microsatellite loci involved in recent selective sweeps. Our method differs in that it accepts original allele size data rather than summary statistics. It also makes it possible to incorporate prior knowledge about allele frequencies using a hierarchical prior distribution consisting of lognormal and gamma probability distributions.

The utility of the method is illustrated by application to two sets of microsatellite allele size data for a group of West African Anopholes gambiae populations. Chromosomal regions that have likely been affected by recent selective sweeps are deduced for Anopholes populations in villages throughout West Africa that have been isolated from each other either by distance or differing chromosomal form. An interesting feature of the Bayesian procedure is its ability to simultaneously analyze allele size data for any number of populations and to cope with the presence of any number of selected loci.</p>