

Revisiting museum collections in the genomic era: potential of MIG-seq for retrieving phylogenetic information from aged minute dry specimens of ants (Hymenoptera: Formicidae) and other small organisms

ABSTRACT

Multiplexed inter-simple sequence repeat genotyping by sequencing – MIG-seq – is an effective PCR-based method for genome-wide SNP detection using the Next-Generation Sequencing platform, and it provides a potential solution to a central problem in museomics – the difficulties of obtaining useful sequence data from aged specimens with often degraded and / or low yields of DNA. We demonstrate and validate the cost effectiveness and utility of the MIG-seq workflow in obtaining useful and robust sequence data from aged museum specimens. We applied the MIG-seq approach to 55 aged (10 - 23 years old) millimeter-sized dry-mounted specimens of the hyper-diverse ant genus *Pheidole*. A total of 50,782,736 reads were generated from the 55 samples (259,902 - 3,693,375 reads per sample). The reads corresponded to 36,862 SNPs from 4,849 polymorphic loci; the SNP dataset was then used to construct a Bayesian phylogenetic tree. The topology of the phylogenetic tree was highly compatible with existing knowledge of phylogenetic relationships among species of *Pheidole*. Therefore, we recommend the MIG-seq method as a cost-effective and highly applicable pipeline for conducting phylogenetic and population genetic studies on aged museum specimens, potentially enhancing the relevance of specimen repositories in general towards modern biodiversity science and conservation biology.