Abstract

Microsatellites have served as popular markers in molecular ecology since 1990s. However, traditional electrophoretic genotyping of microsatellites suffers from many errors of technical nature. Such errors can be avoided with the use of genotyping-by-sequencing (GBS) methods that allow direct access to microsatellite sequence variation. Microsatellite GBS has been usually done utilising up to tens of markers. The process described here allows microsatellite isolation from shotgun sequencing data, followed by multiplexing and filtering of multiplexed markers based on *in silico* PCR simulation. The process, applied to *Nomada* cuckoo bees and their primary host genus *Andrena*, yields up to hundreds of candidate primer pairs for subsequent laboratory optimisation. In addition, this thesis describes the application of a similar selection process focused specifically on microsatellites present in ultraconserved elements (UCE) in *Nomada*. The UCE-derived microsatellites were selected to be present and variable in various subgenera of *Nomada* in order to produce a conserved set that could potentially amplify polymorphic loci in the majority of *Nomada* species. The sets developed herein can be eventually utilised for the first ever semi-genomic population analyses of cuckoo bees and their hosts, paving the way for testing the usefulness of cuckoo bees as indicator taxa of bee community health.

Keywords

Nomada, Andrena, microsatellites, marker development, SSR-GBS, population genetics, brood parasites