MENDB: a database of polymorphic loci from natural populations

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ABSTRACT

Summary: MENDB is an online database for genetic markers determined to be polymorphic in natural populations. The database contains primer sequences and conditions for PCR, taxonomic information, and links to GenBank records, as well as basic statistics on the level of polymorphism for the surveyed populations/individuals.

Availability: http://snook.bio.indiana.edu/
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Evolutionary biologists and ecologists are increasingly using molecular methods to study natural populations. Genetic markers with a high degree of variability can be used, for example, to estimate relationships among individuals within populations (see Van de Casteele et al., 2001 and references therein), the parentage of offspring (e.g. Morrison et al., 2002), and the amount of genetic differentiation between populations. These parameters may then be used to infer the genetic architecture of phenotypic variation (Ritland, 2000), the mating system of the population (e.g. Haydock et al., 2001; Ji et al., 2001) or the action of demographic and evolutionary processes affecting the subjects under study (e.g. Goldstein et al., 1999; Estoup et al., 2001; Schlötterer, 2002).

The raw sequence data used to develop markers are usually submitted to a public sequence database as a requirement of publication. These database records, however, do not provide primer sequences, assay conditions, or measures of variability needed to use the markers in a research program. More importantly, these records reflect only the original cloning record, whereas many researchers are interested in whether the assay has been attempted in closely related species. Consequently, the Molecular Ecology Notes database (MENDB) was established to provide a searchable resource of molecular markers with demonstrated high variability from a broad range of taxa.

Publication of the database coincided with the launching of Molecular Ecology Notes (http://www.blackwell-science.com/men), a journal that publishes Primer Notes detailing the development of markers for ecological and evolutionary applications. The initial database records came from the Primer Notes published in Molecular Ecology between 1993 and 2000. New database submissions come from articles published in Molecular Ecology Notes, from direct submissions via a web interface, and from other published articles. Currently, the database includes 12,525 primer × taxon entries from 1232 species from 322 families.

To provide complementarity to public sequence databases, MENDB focuses on the primers, assay conditions, and additional information necessary for genotyping. Each database entry (Fig. 1) contains the taxon (family and species); locus name, with a link to all database records from other taxa where genotyping has been attempted; sources of the marker, links to GenBank records and to the MENDB record if the assay was originally developed in another species; publication reference and contact information; type of marker, including repeat motif for microsatellites; primer sequences; primer annealing/denaturing temperature for PCR and product size; expected and observed measures of variability; and any notes the author wishes to include.

Users access the database through a simplified www interface. As the database has more breadth across taxa than depth within a taxon, and researchers are predominantly interested in finding markers for a particular taxon, searches are made on family, genus, or species. Alternatively, specific records may be retrieved by their unique database identifier. Searches return a list of all records for the taxon, and users may then retrieve details for any particular locus.

The database receives a substantial amount of use (ca. 500 hits/week). In addition to searches, new submissions arrive with a frequency of approximately seventy new records per week, predominantly from authors of Molecular Ecology Notes articles. We stress, however, that all relevant data are welcome and invite researchers to submit their marker data to this centralized resource.

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Fig. 1. A typical record from MENDB.

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REFERENCES


