Identification of 10 microsatellite loci in the earwig Labidura riparia (Dermaptera, Labiduridae)

MAREIKE GUETH* and WALTER DURKA†

*Brandenburg Technical University, Chair General Ecology, Siemens-Halske-Ring 8, D-03046 Cottbus, Germany, †UFZ Centre for Environmental Research Leipzig-Halle GmbH, Department of Community Ecology (BZF), Theodor-Lieser-Strasse 4, D-06110 Halle, Germany

Abstract

Ten microsatellite loci were isolated from the earwig Labidura riparia (Pallas, 1773). The polymorphism of the loci was assessed in 24 individuals from one population. The number of alleles ranged from four to 11 alleles and observed and expected heterozygosities from 0.250 to 0.833 and from 0.551 to 0.861, respectively.

Keywords: Dermaptera, earwig, Labidura riparia, microsatellites

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The earwig Labidura riparia (Pallas, 1773) inhabits sandy but damp sites free of vegetation or with sparse vegetation (Beier 1953, 1959; Klausnitzer 2001). It has an almost cosmopolitan distribution (Albouy & Caussanel 1990; Steinmann 1993). In Western, Central and Eastern Europe, the species occurs naturally along the sea coasts and near rivers or waters. First observations of L. riparia in Lusatia (Germany) were made in the middle of last century in secondary habitats like open cast mines or sand and gravel pits (Jordan 1957; Höregott 1959; Donath 1988).

Labidura riparia is used as a model organism for physiological studies (Vancassel et al. 1984; Sayah et al. 1998). Wing-dimorphism has been detected, but flying individuals were rarely observed (Kleinow 1971; Matzke & Klaus 1995). However, colonization of new habitats seems to take place rather rapidly (Gross & Spink 1971; Matzke & Klaus 1996). Rivers with their open sandy banks were postulated to have served as colonization routes of Central Europe (Harz 1957; Müller-Motzfeld et al. 1990; Adis & Junk 2002).

For further analysis of the genetic population structure of L. riparia, and patterns of colonization of new habitats, we developed microsatellite markers.

For library construction, we used a composite sample of DNA from 30 individuals from one population live trapped in Lower Lusatia (51°46’56.7’’N, 13°46’13.0’’E) and stored in liquid nitrogen. To avoid contamination of DNA of the zoophagous insects, only heads and legs were used for DNA extraction. The tissue was mashed with a plastic pestle, and the DNA was extracted using DNeasy Tissue Kit (QIAGEN) following the manufacturer’s instructions for insects applying 50 µL H2O at the final step. A microsatellite-enriched genomic library was made, from which recombinant colonies were sequenced by ecogenics GmbH (Zurich, Switzerland). Size-selected DNA was ligated into SAULA/SAULAB-linker (5’-GGCTACCCGGGAAGCTTGG/5’-GATCAGCTTCCCCTACCGGC, Armour et al. 1994), and enriched by magnetic bead selection with biotin-labelled (CA)13 and (GA)13 oligonucleotide repeats (Gautschi et al. 2000a, b). From 384 recombinant colonies screened, 106 gave a positive signal after hybridization. Plasmids from 50 positive clones were sequenced using the M13/pUC sequencing primer. Primers were designed for 20 microsatellite inserts using PRIMER 3 (Rozen & Skaletsky 2000) and tested for polymorphism.

For analysis of genetic variability, we analysed 24 individuals (9 males, 15 females) from the same population used for library construction. This site is a secondary, sandy habitat with sparse vegetation, which developed spontaneously after dumping of the open cast mine Schlabendorf-Süd. DNA was extracted from one leg per individual using the Chelex resin extraction protocol described by Estoup et al. (1996). Microsatellite DNA amplification reactions were performed in a 20 µL volume containing approximately 20 ng DNA, 0.8 U Taq polymerase (MBI Fermentas), 200 µM dNTPs, 1.5 mM MgCl2, 5 pmol of fluorescent-labelled forward primer and unlabelled reverse primer and 2 µL 10x polymerase chain reaction...
to perform exact tests for deviations from Hardy–Weinberg or inbreeding. These deviations might be results of null alleles, nonrandom sampling, mating systems, or inbreeding coefficients are shown in Table 1. The number of alleles at each polymorphic locus, their size range, and observed and expected heterozygosities together with inbreeding coefficients are shown in Table 1. The number of alleles for the 10 loci ranged from four to 11 (mean over loci was 6.9) and the mean expected heterozygosity was 0.728. Significant deviations from Hardy–Weinberg equilibrium were found for three loci (see Table 1). Four of the 45 pairs of loci compared exhibited significant genotypic disequilibria, mostly including loci (Lari18, Lari17, Lari05, Lari10, Lari37) that also showed deviations from Hardy–Weinberg equilibrium. These deviations might be results of null alleles, nonrandom sampling, mating systems or inbreeding.

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References


