The number of alleles, product size and heterozygosity at each of the eight microsatellite loci are shown in Table 1. All of the examined loci showed a distinct allelic variation ranging from 2–8 alleles in the bear examined. Alleles at each locus differed by multiples of two in size. All the polymorphic loci conformed to Hardy–Weinberg expectations except for MSUT-3, which may have null alleles (Table 1). The eight loci showed relatively low allelic variations and low heterozygosities. This may be caused by a small sampling area for this species or by the population being isolated. To elucidate the cause, the genetic diversity of the present population has to be compared with that of other larger populations.

To the best of our knowledge, no original microsatellite DNA loci for this species have yet been described, although several sets of microsatellite primers have been developed for other bear species (Paetkau & Strobeck 1994; Paetkau et al. 1995; Tuberlet et al. 1997), some of which may be applicable to this species. The present microsatellite loci will become a potent DNA marker to investigate genetic variations in the Asiatic black bear.

Acknowledgements

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References


Microsatellites in the hermaphroditic snail, Lymnaea truncatula, intermediate host of the liver fluke, Fasciola hepatica

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Keywords: DNA markers, genetic variability, heterozygosity, Lymnaeidae, mating system, mollusc

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Host-parasite interactions are strongly affected by differential gene flow in host and parasite populations. In this context, genetic markers are particularly useful to estimate population structure and heterozygosity level associated with infection. The freshwater snail, Lymnaea truncatula (Gastropod, Mollusc), is the main species acting as intermediate host in the life cycle of the liver fluke, Fasciola hepatica (Trematoda, Platyhelminth), which is responsible for important human health and veterinary problems worldwide. The mollusc is hermaphroditic and usually inhabits small temporary ponds and streams. While isoenzymatic markers have already been developed in L. truncatula, a total monomorphism was encountered at 18 enzymatic loci in each of 19 populations originating from France, Portugal, Morocco and Bolivia (Jabbour-Zahab et al 1997). Extinction colonization events due to the temporality of the habitat as well as a reproduction through self-fertilization could explain the low level of variability observed.

To investigate the role of mating systems and population dynamics in the genetic variability of L. truncatula as well as to analyse population genetic of host–parasite interactions, we developed polymorphic microsatellite markers.

A genomic library of 2174 clones was constructed and screened for (CA)10 and (GA)19 repeats using standard hybridization techniques (Estoup et al. 1993). A total of 18 positive clones were sequenced. We selected clones for which appropriate flanking sequence could be defined (i.e. nine loci: Table 1). For amplification of microsatellite loci, primers were designed using Primer 0.5 program (Lincoln & Daly 1991).

Each polymerase chain reaction (PCR) consisted of a 10.5-μL mixture containing 0.076 mM each of dCTP, dTTP,
Table 1. Microsatellite core sequences, primer sequences, size of cloned allele and genetic variability of microsatellite loci of the freshwater snail, *Lymnaea truncatula*. $H_0$ and $H_E$ are observed and expected heterozygosity, respectively.

<table>
<thead>
<tr>
<th>Locus</th>
<th>Repeat motif</th>
<th>Primer sequence (5’–3’)</th>
<th>Size (bp)</th>
<th>Individuals scored</th>
<th>No of alleles</th>
<th>$H_0$</th>
<th>$H_E$</th>
</tr>
</thead>
<tbody>
<tr>
<td>16</td>
<td>(A)ₙ</td>
<td>GGGCT...CGGAGCTGGG</td>
<td>224</td>
<td>26</td>
<td>7</td>
<td>0.072</td>
<td>0.517</td>
</tr>
<tr>
<td>20</td>
<td>(CA)₉(A)₉(CA)₉</td>
<td>GAGGAG...GAGGAGGAGG</td>
<td>121</td>
<td>7</td>
<td>4</td>
<td>0</td>
<td>0.667</td>
</tr>
<tr>
<td>21</td>
<td>(TA)₉(TA)₉(TA)₉(TA)₉(TA)₉</td>
<td>CTGCTG...CTGCTGCTG</td>
<td>112</td>
<td>22</td>
<td>5</td>
<td>0.035</td>
<td>0.443</td>
</tr>
<tr>
<td>24</td>
<td>(C)₉(C)₉(C)₉(C)₉(C)₉(C)₉</td>
<td>ATGGAT...ATGGATATG</td>
<td>223</td>
<td>24</td>
<td>6</td>
<td>0.1</td>
<td>0.541</td>
</tr>
<tr>
<td>29</td>
<td>(CT)₉(CT)₉(CT)₉(CT)₉(CT)₉(CT)₉</td>
<td>GGGGAG...GGGGAGGG</td>
<td>152</td>
<td>24</td>
<td>3</td>
<td>0.052</td>
<td>0.346</td>
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<tr>
<td>32</td>
<td>(CA)₉(TAC)₉(TAC)₉(TAC)₉(TAC)₉(TAC)₉(TAC)₉</td>
<td>GGGGAG...GGGGAGGG</td>
<td>149</td>
<td>7</td>
<td>2</td>
<td>0</td>
<td>0.333</td>
</tr>
<tr>
<td>36</td>
<td>(GT)₉(GT)₉(GT)₉(GT)₉(GT)₉(GT)₉(GT)₉</td>
<td>GGGGAG...GGGGAGGG</td>
<td>190</td>
<td>8</td>
<td>3</td>
<td>0</td>
<td>0.242</td>
</tr>
<tr>
<td>37</td>
<td>(TC)₉(TC)₉(TC)₉(TC)₉(TC)₉(TC)₉(TC)₉</td>
<td>GGGGAG...GGGGAGGG</td>
<td>120</td>
<td>7</td>
<td>4</td>
<td>0</td>
<td>0.667</td>
</tr>
<tr>
<td>43</td>
<td>(AC)₉</td>
<td>GGGGAG...GGGGAGGG</td>
<td>105</td>
<td>7</td>
<td>2</td>
<td>0</td>
<td>0.667</td>
</tr>
</tbody>
</table>

*GenBank Accession nos AF269798 to AF269896.

dGTP: 0.008 mM dATP; 0.3 μM [γ-32P]-ATP; 1.2 mM MgCl₂; 1× PCR buffer (200 mM Tris-HCl pH 8.4; 500 mM KCl); 0.2 mg/mL BSA; 5 pmol of each primer; 0.5 U 7 Uq polymerase (GIBCO BRL); = 5 ng of genomic DNA. Amplifications were performed in a PTC-100 thermocycler (MJ Research) using: an initial 3 min denaturation step at 95 °C, followed by 30 cycles of 1 min at 94 °C, 30 s at the annealing temperature of 52 °C, and 45 s at 72 °C, and then a final elongation step for 10 min at 72 °C. PCR products were denatured and separated on 6% polyacrylamide and 8 M urea sequencing gels. Clones served as size controls.

To characterize each locus we genotyped *L. truncatula* snails originating from seven populations in Switzerland. The number of individuals studied varied from 7–26 because of snail availability. The samples were studied at nine loci (Table 1). For locus 20, which presents a short microsatellite in the primer sequence, we particularly checked for repeatability following several PCR processes performed with different thermocyclers. The pattern obtained was always unambiguous and the size of the alleles was repeatable.

All the loci studied are polymorphic and the number of alleles ranges from 2–7 across the sampling area. Although this indicates a low to moderate polymorphism, this result appears interesting as the level of polymorphism obtained with microsatellite markers is much higher than the one observed with allozymes.

The mean observed heterozygosity is low ($H_0 = 0.029$) compared to the mean expected heterozygosity ($H_E = 0.492$). This indicates a clear deficit of heterozygotes within populations. Although the population dynamic (bottlenecks) due to the temporality of the habitat might explain the low level of genetic variability (estimated by the number of alleles and heterozygosity) found in *L. truncatula*, compared with other temperate freshwater snails (Jarne & Städler 1995 for review; Monsutti & Perrin 1999), a reproduction predominantly through selfing certainly constitute the main cause.

Cross-species amplification was tested on another *Lymnaea* from Switzerland, *L. vaughani*. Among the seven primer pairs used (16, 20, 21, 24, 29, 36, 37), only two (20 and 21) successfully amplified the PCR products. Although only six individuals were screened, two alleles appeared for locus 21.

The diversity of these loci make them valuable tools for population genetic differentiation, mating system investigations as well as for host genetic analyses in relation to parasitism.

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This work is dedicated to the memory of José Oviedo. Special thanks to J.C. Casanova, G. Dreyfuss, S. MasComa, J.P. Pointier and D. Rousselet for having kindly provided different *Lymnaea* samples. This work received the financial support from the CNRS and from the French Embassy in Switzerland. ST has benefited from a fellowship from the 'Fondation Singer-Polignac'.

References


Characterization and isolation of DNA microsatellite primers in wood mice (Apodemus sylvaticus, Rodentia)

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The wood mouse (Apodemus sylvaticus) is widely distributed in European forests and bush land and is an interesting model animal to study the evolution of social behaviour and mate choice. In this context we were interested in the dynamics of genetic structure over several generations that might indicate clustering of kin groups and recruitment of individuals. Animals were caught at different places in the wild and therefore were assumed to be unrelated. These animals were livetrapped at different localities near Konstanz, South Germany. Before releasing the animals, pieces of tissue were collected from the ear, fixed with 100% ethanol and preserved until DNA extraction.

Allelic variability and heterozygosity of the loci was determined with DNA extracted from tissue samples of wood mice according to standard protocols (Sambrook et al. 1989) with proteinase K treatment. Polymerase chain reaction (PCR) amplification (Saiki et al. 1988) was carried out in a DNA thermal cycler (Biozym) in 10 μL of reaction mixture containing about 1–100 ng of template DNA, 0.2 mM dNTP, 0.5 μM of each primer, ddH2O, 1× PCR buffer (Amersham Pharmacia Biotech, 50 mM KCl, 1.1 mM MgCl2, 10 mM Tris-HCl), and 0.25 units of Red-taq polymerase (Amersham Pharmacia Biotech). Twenty-five PCR cycles were performed: denaturation at 94°C for 30 s, annealing temperature). The sequences were submitted to GenBank (acc accession nos)

Table 1 Microsatellite loci in wood mice, Apodemus sylvaticus. Size range refers to the observed PCR product sizes. Number of alleles were determined from 30 individuals. Animals were caught at different places in the wild and therefore were assumed to be unrelated. (n, number of alleles; Ho, observed heterozygosity; He, unbiased expected heterozygosity; T_a, annealing temperature). The sequences were submitted to GenBank (acc accession nos)

<table>
<thead>
<tr>
<th>Locus acc</th>
<th>Size</th>
<th>Repeat in clone</th>
<th>n</th>
<th>Ho</th>
<th>He</th>
<th>T_a (°C)</th>
<th>Primer sequence (S’–3’)</th>
</tr>
</thead>
<tbody>
<tr>
<td>As-7</td>
<td>114</td>
<td>(GT)_{19}</td>
<td>10</td>
<td>0.74</td>
<td>0.61</td>
<td>47.8</td>
<td>F: CAGATCATTTATCTGCCGTTA</td>
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<tr>
<td>AF246520</td>
<td>248</td>
<td>(GT)_{33}</td>
<td>15</td>
<td>0.97</td>
<td>0.90</td>
<td>50.5</td>
<td>R: ACATGCTTAAACTGGACC</td>
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<tr>
<td>As-11</td>
<td>246</td>
<td>(GT)_{19}</td>
<td>14</td>
<td>0.73</td>
<td>0.88</td>
<td>53.6</td>
<td>F: CGAATTTTGCTGCCGTTG</td>
</tr>
<tr>
<td>AF246521</td>
<td>249</td>
<td>(GA)_{22}</td>
<td>14</td>
<td>0.73</td>
<td>0.88</td>
<td>53.6</td>
<td>R: GCTGCGCTTCTCAGAGAG</td>
</tr>
<tr>
<td>As-12</td>
<td>144</td>
<td>(GT)_{25}</td>
<td>11</td>
<td>0.84</td>
<td>0.86</td>
<td>55.0</td>
<td>F: CTCTGCGGACAGCTCACAGG</td>
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<td>AF246522</td>
<td>138</td>
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<td>55.0</td>
<td>R: AGCCGCAAGCGGATAGACAG</td>
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<tr>
<td>As-20</td>
<td>150</td>
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<td>12</td>
<td>0.84</td>
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<td>47.1</td>
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<tr>
<td>AF246523</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td>R: TTAGGATAAGCTTAGATCG</td>
</tr>
</tbody>
</table>

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