Biodiversity in deer population observed by microsatellite markers

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Abstract

Deer (Cervidae) are, today as well as in ancient times, among the most important species. Thus, not unexpectedly, people have been translocating deer all over the world. Deer is used as a farm animal as well as hunting wild animal. Population genetic analysis has been performed on deer population originated from New Zealand and Hungary. The allele frequencies of 9 microsatellite loci were analyzed in 88 deer from two sources. A total of 74 alleles combined in 149 genotypes were observed in New Zealand population and 92 alleles combined in 181 genotypes in Hungarian deer population. The mean FST value of 0.119 from all the loci indicated that 89.1% of the genetic variation was caused by differences among individuals and 11.9% only due to differentiation among the origin of animals. All individuals from observed deer were assigned to their population of origin by using a direct as well as by leave one out approach. Graphical view of both analysed populations has been designed by PCA method.

Introduction

A thorough understanding of population genetic structure is important for species management, as genetically isolated populations with limited diversity are often associated with inbreeding and reduced reproductive fitness. Population bottlenecks can have a pronounced effect on genetic diversity and can result in reduced mean number of alleles and heterozygosity (Webley et al., 2007). The consequences of a bottleneck have been widely documented, with historical records often congruent with molecular data, as shown by (Broders et al., 1999; Lenny Williams et al., 2002; Webley et al., 2004).

Deer (Cervidae) are, today as well as in ancient times, among the most important species. Thus, not unexpectedly, people have been translocating deer all over the world. Deer is used as a farm animal as well as hunting wild animal. Nowadays two main methods are preferred for analyzing of genetic structure of population. Nine polymorphic microsatellite loci and mitochondrial DNA control region has been analysed in northern Germany population (Zachos et al., 2007). Both methods have been also verified by Hmwe et al. (2006) on samples from 69 British red deer (Cervus Elaphus scoticus). Similar work based on microsatellite markers focused on admixture in deer population and disequilibrium a selected group have been described by Slate and Pemberton (2007). Another view on genetic biodiversity is provided by Péroz-Espona et al. (2008), authors have analysed gene flow in deer population originated from Scottish Highlands by 21 microsatellite markers. Biodiversity in French deer population has been described by Frantz, Haemman and Klein (2008).

Aim of this study is population genetic structure evaluation of farm deer originated from New Zealand and Hungary, analysis of population biodiversity and genetic similarity within and between animals.

Material and methods

DNA was isolated from peripheral blood from a total 88 deer originated from New Zealand region (49 animals) and Hungarian region (39 animals). DNA extraction followed the protocol of Promega (Wizard Genomic DNA Purification Kit). PCR products have been tested by ABI 310 Genetic Analyzer and their fragment size by Genescan software. Basic population genetic analyses have been calculated in POWERMARKER 3.23 (Liu and Muse, 2003). To represent geometric relationships among the pig breeds, a principal component analysis (PCA) was applied using gene frequencies of all variable loci by GENETIX software package (Belkhir et al., 1996). Population structure was evaluated by the hierarchical F statistics—Fis, Ft, Fst (Weir and Hill, 2002). Several studies have shown that microsatellites can be used to identify the population origin of an individual (Rannala and
According to Maudet et al. (2002), two approaches using observed population allele frequencies to assign individuals to a breed were compared. A "direct" method similar to the one commonly used in livestock studies (Buchanan et al., 1994) and a simulation-based method that provides a level of certainty (P-value) for each animal assigned (Cornuet et al., 1999). The assignment tests were carried out by the GENECLASS 2 software (Piry, 2004). The exclusion method was carried out using the Bayesian approach, which has showed better accuracy than the frequency- and distance-based methods (Cornuet et al., 1999). Assignment of each individual was tested by the "leave one out" procedure what means that each individual was excluded from the data set when performing its assignment.

Results and discussion
The allele frequencies of 9 microsatellite loci were analyzed in 88 deer from two sources. A total of 74 alleles combined in 149 genotypes were observed in New Zealand population and 92 alleles combined in 181 genotypes in Hungarian deer population. The average number of alleles per New Zealand population was 8.2, ranging from 6 (RM188) to 10 (BM888, T193) and 10.2 ranging from 6 (RT1) to 14 (T501) per Hungarian population as could be seen in the Table 1. Selected microsatellite markers are more polymorph as a marker used in Frantz, Hamman and Klein (2008), number of alleles in this ranged from 2 to 14.

<table>
<thead>
<tr>
<th>Microsatellite</th>
<th>FIS</th>
<th>FIT</th>
<th>FST</th>
<th>New Zealand</th>
<th>Hungarian</th>
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<td>FIT</td>
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<td></td>
<td></td>
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<tr>
<td>OarFCB5</td>
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<td>0.191</td>
<td>0.110</td>
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<td>0.209</td>
<td>0.131</td>
<td>13</td>
<td>6</td>
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<tr>
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<td>0.195</td>
<td>0.124</td>
<td>13</td>
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<tr>
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<td>0.184</td>
<td>0.110</td>
<td>9</td>
<td>7</td>
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<tr>
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<td>0.156</td>
<td>0.116</td>
<td>20</td>
<td>9</td>
</tr>
<tr>
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<td>0.190</td>
<td>0.110</td>
<td>17</td>
<td>10</td>
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<tr>
<td>Average</td>
<td>0.076</td>
<td>0.186</td>
<td>0.119</td>
<td>16.555</td>
<td>8.222</td>
</tr>
</tbody>
</table>

Table 1: Genetic structure of New Zealand and Hungarian deer population

The overall FIS values per locus ranged from 0.044 (RT13) to 0.090 (OarFCB5), showing an overall FIS of 0.076 (Table 1). The FST values ranged from 0.156 (RT13) to 0.209 (EM188). The mean FST value of 0.119 from all the loci indicated that 89.1% of the genetic variation was caused by differences among individuals and 11.9% only due to differentiation among the origin of animals. Different results were observed in isolated French deer population (female FIT 0.045 and male FIT 0.003) by Frantz, Hamman and Klein (2008). Between populations variability observed in present work (FST 0.119) is also higher as computed in Péroz-Espona et al. (2008) for Scottish Highlands deer (FST 0.019).

Table 2 shows the percentage of individuals correctly assigned to their population of origin. All individuals from observed deer were assigned to their population of origin by using a direct approach, whereas the accuracy of assignment of individuals from New Zealand and Hungarian origin were 97.95% and 100%, respectively. By exclusion simulation (10 000 simulated individuals) on confidence level P<0.01 and P<0.001 results were slightly different. In New Zealand population 87.75% of animals was correctly assigned to their origin on P<0.01 and P<0.001 level, and 89.74% of Hungarian deer.

Graphical view of both analysed populations has been designed by PCA method (Figure 1). Arrow inside the Figure 1 highlight one animal, which in spite of New Zealand origin were assign the Hungarian deer population. According to computed FST 0.119, graphical view presents only 11.9% of differences in analysed deer population.

Figure 1: Scatter diagram showing relative position of 88 individuals defined by principal component factor scores based on correlation matrix from allele frequency of the 9 microsatellites.
Conclusion
Population genetic analysis has been performed on deer population originated from New Zealand and Hungary. We can affirm, selected microsatellite markers are polymorph and suitable for this kind of evaluation. All population of observed deer is homogenous and according to computed FIS value (0.076) probably affected by inbreeding. Present detection method was able to observed 11.9% (FST 0.119) genetic differences between analysed groups of deer. Breed assignment test results, shows high percentage of individuals correctly assigned using the "direct" approach or the "exclusion–simulation" approach, which indicate genetic stability in observed deer groups. Graphical view was able to detect one animal showing genetic relation to Hungarian population in spite the import from New Zealand.

Literature