Fragmentation of landscapes and deer habitats results in disintegration of natural populations into several subpopulations having a more or less pronounced genetic exchange. The presence of a genetic pattern is an important wildlife management issue, because the reduced gene flow between different populations may lead to genetic depletion [1]. Gene flow, maintained by the dispersal of animals, enhances genetic diversity, thus knowledge of the genetic diversity and the genetic exchange between neighboring populations is a precondition to discovering and evaluating potential problems and to determining the appropriate countermeasures [2]. Our objectives were to quantify genetic diversity and assess genetic structure of red deer (Cervus elaphus) populations in the Carpathian Basin. Samples were obtained from 267 free-ranging red deer legally harvested in six regions of the Carpathian Basin, 81 from Gemenc, 56 from Baranya, 58 from Somogy, 27 from Bakony, 9 from Csorna and 36 from Zemplén Mountains (Fig. 1). Samples were genotyped using 10 autosomal microsatellites [3]. Allele frequencies as well as allelic richness and diversity indices were calculated based on individual genotypes with the help of the Cervus and GenAlEx softwares; individual genotypes were also processed with the Structure software. Autosomal microsatellites showed a high genetic diversity in red deer: the number of alleles per locus varied between 6 and 25, with an average number of 16.4 alleles per locus. Heterozygosity values were also high; mean expected and observed heterozygosities were 0.832 and 0.773, respectively. Heterozygosity and allelic richness values per population were in the same range as for the whole sample set. Other diversity indices also showed high values for all populations; PIC was between 0.722 and 0.837 with an average value of 0.832, Shannan-Weaver Index values were between 1.668 and 2.046 with an average value of 1.940. Genetic structure was detected by the software Structure, the second order rate of change in log Pr indicate the presence of three clusters (K=3). Although the weak differentiation found in our samples (Fig. 2) could indicate some structuring, the numerous mixed genotypes suggest an extensive admixture between populations of different sites. Various demographic and historical factors may contribute to the lack of a clear genetic structure. A more extensive sampling would be desired in the Carpathian Basin, associated with genotyping and evaluation of results.
Figure 1. Sampling sites for genetic study of red deer in the Carpathian Basin. Dots – Gemenc, Diamonds – Baranya, Squares – Somogy, Stars – Bakony, Circle – Csorna, Triangles – Zemplén.

Figure 2. The cluster assignment of the red deer in different sites of the Carpathian Basin based on autosomal microsatellites in the case of three clusters (K=3). 1 – Gemenc, 2 – Baranya, 3 – Somogy, 4 – Bakony, 5 – Csorna, 6 – Zemplén.

References