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„Genetic diversity of the common shrew *Sorex araneus* and the pygmy shrew *Sorex minutus*  
in Poland and southern Sweden”

### ABSTRACT

Microsatellites (MS) as well as mitochondrial DNA (mtDNA) have developed into the most widely used markers in molecular ecology. They are very informative as they have a high mutation rate and, therefore, provide patterns of genetic diversity, phylogenetics and phylogeography of species. Based on listed molecular markers it is possible to draw conclusions about genetic relationships of examined populations as well as to look back on the history of species.

The common shrew (*Sorex araneus*) is considered as one of the most genetically variable species among mammals, due to its chromosomal differentiation. The cause of its karyotypic polymorphism comes from a mutation called Robertsonian translocations. More than 70 chromosomal races have been detected until now and they are classified into different karyotypic groups. It is thought that the chromosomal rearrangements may affect the gene flow between populations, hence this phenomenon is very interesting from genetic point of view.

The pygmy shrew (*Sorex minutus*) is considered as rather chromosomally monomorphic, but still there is a need to perform studies using different kinds of genetic markers to complete the information obtained on it so far.

The aim of this study was to investigate the genetic variability of the common shrew and the pygmy shrew in Poland and southern Sweden based on the analyses of different classes of genetic markers *i.e.* inherited from both parents (autosomal microsatellites), inherited from father (Y - linked microsatellite) and from mother (mtDNA). These genetic markers were selected to avoid false conclusions about genetic processes and the history of the species.

In this study microsatellite analyses were performed on 187 animals (110 individuals of *S. araneus* and 77 individuals of *S. minutus*), whereas mtDNA examinations included 21 individuals of *S. araneus* and 15 individuals of *S. minutus* (36 animals in total). The individuals representing the Polish and Swedish populations of the common shrew were collected from 10 sites for MS analyses and from 15 sites for mtDNA analyses. The pygmy

shrew analyses included animals obtained from 6 and 11 sites in Poland and Sweden for the MS and mtDNA examinations, respectively. The common shrews from Poland belonged to the Białowieża (Bi), Drnholec (Dn), Łęgucki Młyn (Łg) and Ulm (Ul) chromosomal races, whereas the Swedish animals were divided into two chromosomal races Hällefors (Hä) and Åkarp (Åk). These 6 races are classified into Eastern (Bi, Łg) and Western (Åk, Dn, Hä, Ul)

European Karyotypic Groups. In this study nine autosomal microsatellite loci (*L9*, *L14*, *L33*, *L45*, *L62*, *L68*, *L92*, *L97*, *L99*), Y - linked microsatellite (*L8Y*) and partial mitochondrial cytochrome b (*cyt b*) sequence were investigated.

The obtained results turned out to be similar for both species. The genetic diversity detected using microsatellite markers was high, both for the common shrew and the pygmy shrew. The level of population differentiation based on *FST* revealed weak genetic structuring for both species. *FST* estimated over all loci, both for *S. araneus* and *S. minutus*, revealed slightly higher values for females than males indicating a higher subdivision for females. However, based on AMOVA analysis, most of the genetic variation was found between localities, both for *S. araneus* and *S. minutus*. Chromosomal rearrangements did not significantly prevent gene exchange among different chromosomal races of *S. araneus*. Mantel's test indicated that there was no significant correlation between genetic differentiation and geographic distance, either for the common shrew or for the pygmy shrew. The number of genetic clusters (*K*) turned out to be lower than the number of localities for the common shrew (*K* = 3) likewise for the pygmy shrew (*K* = 2).

A high level of haplotype diversity for the *cyt b* sequence was detected. Genetic differentiation analysis revealed statistically significant genetic distinction between the Polish and Swedish populations. No significant differentiation in the *cyt b* gene between Western and Eastern Karyotypic Groups was found. No apparent phylogenetic subdivision was discovered for the common shrew. The exception was the lineage representing the Mediterranean region, which formed a separate group of haplotypes. The phylogenetic analysis of the pygmy shrew divided individuals into two clades. The first one consisted of individuals from North and Central Europe, while the second one included animals from North and South Europe (Balkan, Iberia, Italy).

**Key words:** common shrew, *Sorex araneus*, pygmy shrew, *Sorex minutus*, genetic differentiation, microsatellites, mtDNA

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