

**7th  
Baltic**



# **Theriological Conference**

**October 1. - 5. 2008 Lepanina, Estonia**

**ABSTRACTS**



<i>Syphacia petrusewiczii</i>	+	-	-	-	-	2
<i>Syphacia stroma</i>	-	+	-	+	-	1
<i>Syphacia</i> sp.	-	+	-	-	-	1
<i>Syphacia vandenbrueri</i>	-	-	-	-	+	1
<i>Trichocephalus muris</i>	+	-	-	-	-	1
Total number of helminth species in a host	6	5	-	1	1	-

Analyzing all seasons and all species together, the difference in helminthes infection prevalence of small mammals on beaver lodges and in the control habitats was not significant ( $E(\%)=56.2$  on beaver lodges and  $E(\%)=39.4$  in the control habitats;  $\chi^2=0.021$   $df=1$ ;  $p=0.885$ ). In different seasons, the highest infection prevalence was observed in small mammals on beaver lodges in spring, in summer and in autumn, but in the control habitats it was higher in winter (Table 2). However, this difference was not statistically significant, probably due to small samples.

**Table 2. Infection prevalence (E(%)) and mean abundance (̄) of helminthes of small mammals on beaver lodges and in the control habitats in different seasons**

Small mammal species	All helminthes											
	Spring			Summer			Autumn			Winter		
	N*	̄	E(%)	N	̄	E(%)	N	̄	E(%)	N	̄	E(%)
Beaver lodges												
<i>Myodes glareolus</i>	1	113.5	100.0	4	2.6	25.0	11	1.4	36.3	4	1.6	17.0
<i>Apodemus flavicollis</i>	3	4.1	44.4	3	0.9	50.0	1	1.0	100.0	-	-	-
<i>Microtus agrestis</i>	-	-	-	1	7.0	100.0	-	-	-	-	-	-
<i>Apodemus agrarius</i>	-	-	-	1	-	-	3	0.7	33.3	-	-	-
Total	4	58.8	72.2	9	3.5	58.3	15	1.0	56.5	4	1.6	17.0
Control habitats												
<i>Myodes glareolus</i>	6	1.5	40.0	13	0.8	34.6	39	1.6	23.7	10	0.7	25.0
<i>Apodemus flavicollis</i>	7	0.8	23.8	10	1.6	10.0	28	2.3	14.3	6	4.3	22.2
<i>Microtus agrestis</i>	-	-	-	1	-	-	-	-	-	-	-	-
<i>Apodemus agrarius</i>	-	-	-	-	-	-	1	2.0	100.0	-	-	-
<i>Micromys minutus</i>	-	-	-	-	-	-	-	-	-	1	2.0	100.0
Total	13	1.2	31.9	24	1.2	22.3	68	2.0	46.0	17	2.3	49.1

N\* – number of dissected individuals

The diversity of helminthes community infecting small mammals was found to be higher in the control habitats than on the beaver lodges (Shannon-Wiener index for all seasons:  $H'=0.39$  on beaver lodges and  $H'=0.56$  in the control habitats). Similar tendency was found for particular species, e.g., for *Myodes glareolus* and *Apodemus flavicollis*.

In most cases helminthes were distributed not evenly among infected individuals (coefficient of dispersion, CD varied between 1 to 68,3). The aggregation of helminthes was higher in control habitats (CD=10.92) than on beaver lodges (CD=6.16). Infection of small rodents did not depend on the host sex, except two cases in autumn: females of *Myodes glareolus* were more infected by *Heligmosomum mixtum* helminthes on beaver lodges and males – in forest.

Our very preliminary data did not show distinct differences in parasitological state of small mammals dwelling on beaver lodges and the control habitat a forest. One of possible reasons could be small samples of dissected mammals, especially caught on beaver lodges, thus more intensive investigations in this field are needed.

## MOLECULAR ANALYSIS FOR HYBRID DETECTION BETWEEN EUROPEAN MINK (*MUSTELA LUTREOLA*) AND POLECAT (*MUSTELA PUTORIUS*)

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Natural hybridization is a common event widely documented in Mustelids, especially among *Mustela lutreola* and *Mustela putorius*. Morphological traits have been frequently used for species identification due to putative hybrids seems to show a mixture of characters. Although, morphological and phenotype characters are more likely to lead to ambiguous hybrid detection. Thus, multilocus genotypes were assessed using 13 microsatellites loci and analysed with two different Bayesian approaches in order to identify the admixture proportions, the different classes of hybrids ( $F_1$ ,  $F_2$  and backcrosses) and the assignment of individual to population. Moreover, mitochondrial DNA (maternally inherited) and Y chromosome (paternally inherited) sequencing was used to infer the direction of the interspecific mating. A total of 446 samples were analysed comprising 110 polecats, 318 European minks and 18 putative hybrids. A high level of genetic differentiation with low level of hybridization, mainly based on  $F_1$  genotypes, was observed between these two mustelids. Slight genetic introgression was detected only in polecat populations as revealed by the backcrosses genotypes. Furthermore, the preferential mating occurred between males of polecat and females of European mink.

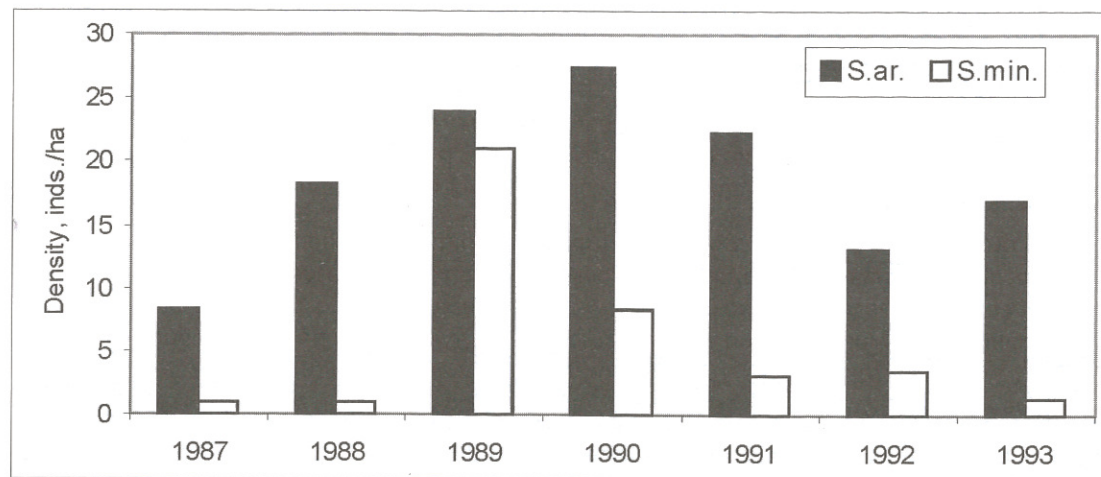


Figure 1. The dynamics (inds./ha) of the population of the common shrew and the pygmy shrew in the growing up clear-cuttings in Lithuania in 1987-1993.

**Key words:** common shrew, pygmy shrew, population dynamics, clear-cutting, Lithuania.

## PHYLOGEOGRAPHIC HISTORY OF NORTH EUROPEAN MAMMALS: IMPLICATION ON THEIR GENETIC DIVERSITY AND THEIR CONSERVATION

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Quaternary climatic oscillations have played a major role in shaping the present geographical distribution of both species and their genetic diversity. This resulted in extinctions of the northern populations during ice ages followed by subsequent northward expansions from refugia during interglacials. Recent phylogeographic studies evidenced that the refuges for European small mammals were mainly located in the Mediterranean, the Urals and the Caucasus/Carpathian region. However, some other studies also proposed that much more Nordic regions such as Western Scandinavia or the Baltic area would have also played the role of additional refuges for mammals and their parasites. The first aim of our presentation will be to present and discuss these different hypotheses, to clarify the existence or not of Nordic refuges.

Moreover, different authors hypothesized that rapid expansion from refuge populations involved serial bottlenecking with progressive loss of allelic diversity, resulting in less genetic diversity among populations present in the more recently colonized places. In contrast, it is expected that populations living in the refuge regions were less affected by climatic changes and will be more genetically diversified. These hypotheses are of particular interest for conservation purposes, as generally, populations and species being genetically well diversified will have more chances to survive to changes of their environment. The research of refuge regions is therefore of prime importance for the conservation of many European species. Using different examples, the second aim of our presentation will be to discuss the importance of refuge regions (notably in Northern Europe) as "hotspots" of intraspecific biodiversity and their interest for reintroduction programs.

Finally, we will discuss about the role of the Baltic region as well as Western Russia as post glacial recolonisation routes for the Fennoscandian mammal populations.