Abstract

This thesis is focused to population genetics of selected species of genus Stylops in Europe. Within this genus, five species was analysed by usage of two approaches – microsatellite analysis in Stylops ater and analysis of mitochondrial DNA in all five species. Mitochondrial gene for cytochome c oxidase (1st subunit) was used. For microsatellite analysis was performed bayesian clustering analysis and ABC approach (Aproximate Bayesian Computation). Mitochondrial markers were processed by making haplotype networks and demography analysis by computing Bayesian skyline plots.

For *Stylops ater*, surprisingly low lewel of population subdivision was detected, yet with clearly differentiated population clusters from Scandinavia and baltic coast of Europe, which may imply period of isolation of these populations or relativelly recent population expansion and genetic differentiation due to lower population sizes.

Next, hypotesis of possible temporal segregation of subpopulations of *Stylops nevinsoni* based on different aktivity period of their host species groups, was supported. In other three species, population subdivision was observed to be related either due to host specialisation (*Stylops mellitae)* or geographic consequences *(S.nassonowi, S.spreta*).

Interesting finding is also detection of population size reduction in all five studied species, which took place in relatively recent time (about 8 to 2 kya)