POPULATION STRUCTURE OF THE BROWN BEAR IN NORTH EASTERN EUROPE

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Fennoscandia and North Western Russia possess one of the largest brown bear (*Ursus arctos*) populations in Europe. North Western Russia is assumed to be a reservoir for large carnivores immigrating towards the west. Finland and Norway share a border with Russia and border crossings of brown bears are observed regularly. Studies on the dispersal of bears equipped with GPS devices have shown movement in both directions. In the presented studies we have used population genetic methods to investigate the status of brown bears in Finland, Norway and North Western Russia and the connectivity and continuity of the populations. All Samples consisted of scats and hairs collected non-invasively as well as tissue samples from legal harvest. Molecular genetic analyses were performed using 13 different microsatellite markers. The analysis is still ongoing, but so far the genetic variation showed an overall heterozygosity for the different areas of an average of H_O = 0.75. We found that the number of alleles (9.3 - 8.2) decreases from east towards west whereas the F_{IS} numbers (0.04 - 0.07) increase. The AMOVA-analysis revealed that

most variation can be found within the populations and little differentiation between the populations. Nevertheless, different analyses of population differentiation including Bayesian approaches, suggested the subdivision of the brown bears into several subpopulations. A significant negative relationship between geographic distance and genetic relatedness was found and pointed to isolation by distance. Analyses of migration between the sampled areas resulted in low numbers for migration. These findings were supported by an assignment analysis, which detected only a few migrants per generation. More data is currently under analysis and results will be presented at the symposium. This research and its results represent the start of the long-term genetic monitoring and research of the brown bears in Finland, Norway and North Western Russia.

Key-words: Brown bear, *Ursus arctos*, population structure, non-invasive sampling, Finland, Russia, Norway

INTRASPECIFIC VARIABILITY OF RACCOON DOG ON MACRO- AND MICRO GEOGRAPHICAL SCALES.

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Craniometrical variability of raccoon dog *Nyctereutes procyonoides* (a total of 381 skulls in 6 samples) from native populations of Amur and Khabarovsk Regions as well as from the populations introduced in Tver and Vologda Regions was investigated at different stages of its dispersal using multivariate analysis. The measurement design included 21 variables taken with an accuracy of 0.01 mm. In spite of evident sexual dimorphism in general skull sizes, variability was, in principle, similar in both sexes, but the extent of morphological divergence differed. On the micro geographical scale (within Tver Region and on the border of Vologda Region), the skull morphological habit in