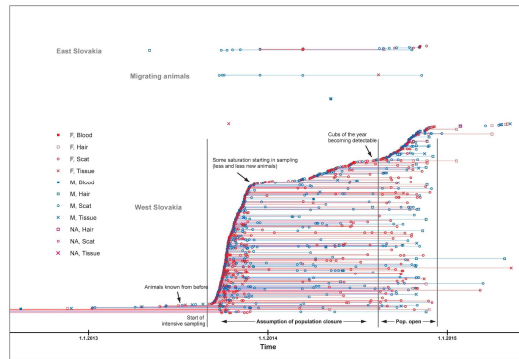
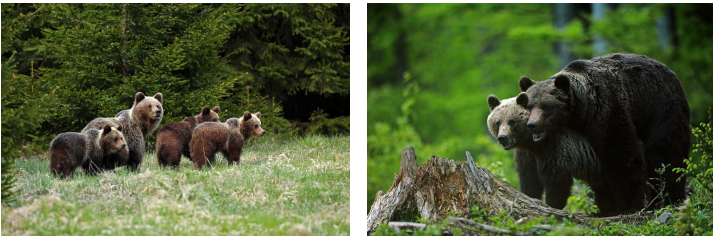


# GENETIC INVENTORY OF BROWN BEAR POPULATION FROM WESTERN CARPATHIANS USING NON-INVASIVE SAMPLES

## Introduction

In 1932 the protection of brown bear in Slovakia was introduced and since then the population size has started to increase. Estimates of the population size differ significantly from about 500 to 2000 individuals depending on the source (NGOs vs. hunting statistics). In 2013–2015 a project of genetic inventory of the brown bear population in Slovakia using non-invasive samples was carried out.



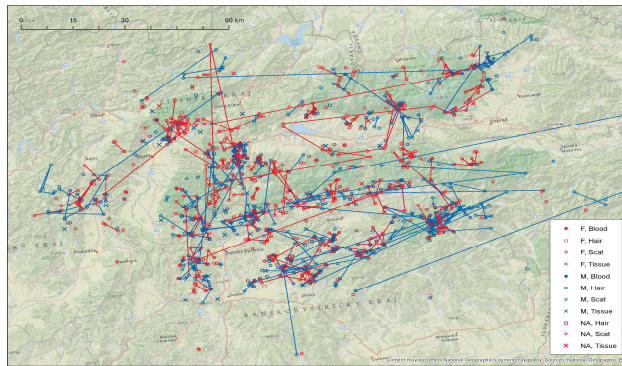
**Figure 1:** Graph of mark-recapture process. Each marker symbol is a sample, lines connect multiple samples of the same animal.

The samples included in the closed population models were collected between 4 September 2013 and 25 August 2014 when the probability of detecting cubs of the year becomes high, as also visible from the mark-recapture graph.

## Methods

The genetic inventory was based on collecting the non-invasive samples (feces and hair traps) in two autumn periods (2013 and 2014). In total 2977 scat, hair, blood and tissue samples were sampled. Altogether 12 microsatellite loci (G10C, G10H, G10L, G10P, G10X, G1D, Mu10, Mu15, Mu23, Mu50, Mu59, and Mu9) and a sex determination locus (SRY) were analysed. Due to data quality problems loci G10H, G10X, Mu23 and Mu9 were exclude from analyses.

All genotypes in the database from the Slovak bear population were matched on pairwise basis with the intent of identifying individual animals. A single “allelic dropout” (Miquel *et al.* 2006b) mismatch was allowed for a reliable match pending that the entire amplified locus panel in both matched samples reached PIsib value of maximum 0.01 and PI value of maximum 0.00001 (Waits *et al.* 2001). Incompatible genotypes with different alleles were not allowed. All nearly-matched genotypes with up to two allelic dropout or incompatibility differences were manually checked against raw data and sample metadata.



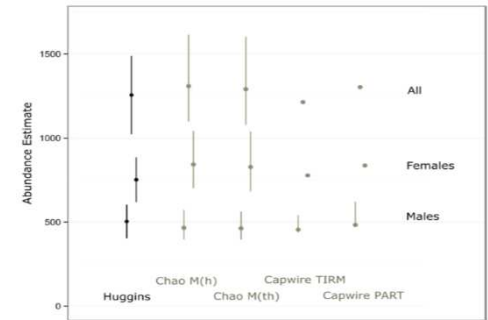
**Figure 2:** Spatial distribution of samples collected in the study

## Results

For the closed-population models 1100 successfully genotyped samples were used. Detected in the dataset were 625 animals, 260 males in 415 captures (recapture rate 1.60) and 356 females in 478 captures (recapture rate 1.34). Recapture rates were relatively low, and lower for females than for males. The sex ratio of directly observed animals is 41.6% males and 58.4% females, however this may not reflect the actual sex ratio in the population since capture probability of different sexes may not be the same.

Model selection for CMR

- capture heterogeneity
- variation in capture success by time and sex of the individual.



Huggins’ heterogeneity model was statistically the strongest of the models used for this analysis, has a reasonably good fit and its estimate is used as the final result of this analysis. **During the sampling period of 2013-2014 there were around 1256 bears in Slovakia (1023–1489 95% CI).** This includes also all bears that were detected as dead for various reason during this period, and excludes all cubs born in 2014. Estimated sex ratio is skewed towards females (59.9% females vs. 40.1% males), very close to what was observed in directly detected individual genotypes.

The results of this genetic inventory of brown bear population should be considered as the basic estimate for Western Carpathians based on non-invasive sampling and will be used as population size estimate for further modelling of population growth and for the purposes of the brown bear management plan.



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