



# **Selected Research Findings from the Institutes of the Polish Academy of Sciences**

Warsaw 2008





## SELECTED RESEARCH FINDINGS FROM THE INSTITUTES OF THE POLISH ACADEMY OF SCIENCES

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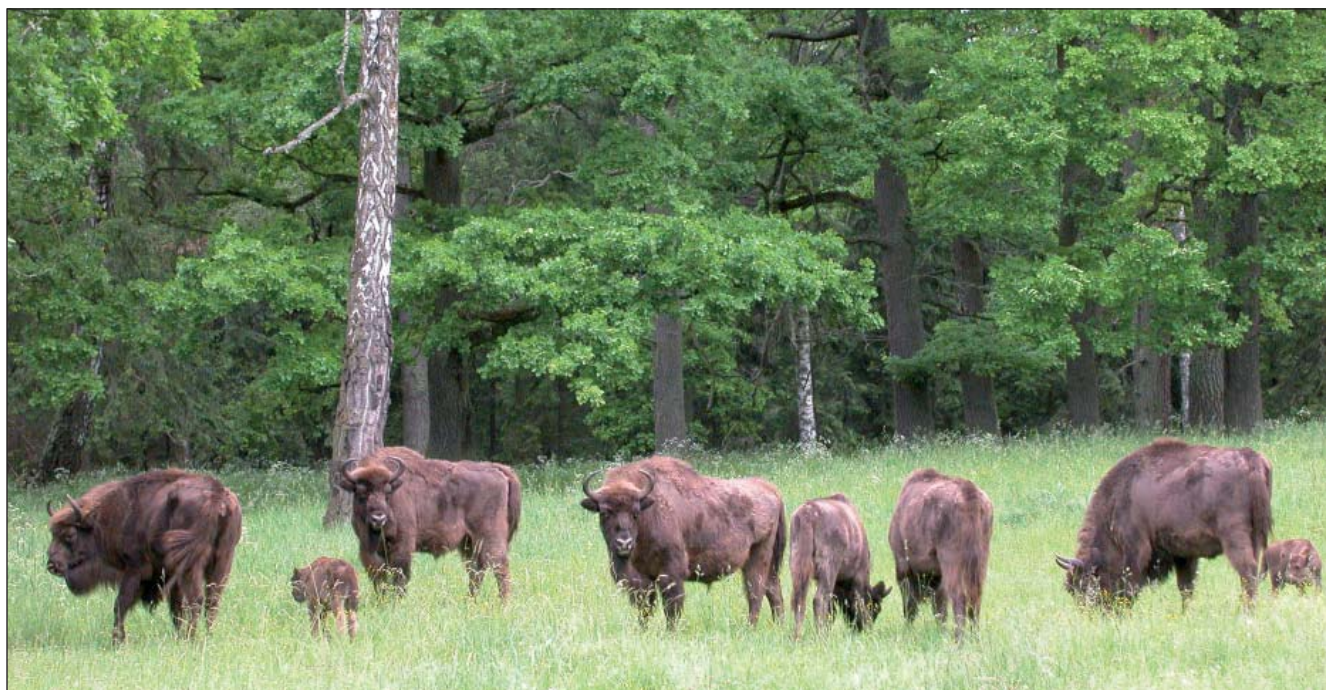
## ESTIMATION OF GENETIC VARIABILITY OF THE EUROPEAN BISON USING BOVINESNP50 GENOTYPING BEADCHIP (ILLUMINA®)

The Białowieża European bison (*Bison bonasus*, L.), Europe's largest mammal species, went through a severe bottleneck at the beginning of the 20th century. Only seven individuals founded the Lowland line of European bison and nearly 90% of the genes in the contemporary population derive from only two founders. The genetic diversity of the species is very low, threatening its survival. The European bison's viability, however, does not seem to be directly related to its level of heterozygosity and has more to do with complex intra- and inter-gene interaction which can only be investigated with quantitative genetic approaches. Given the fact that evolutionary response in quantitative traits cannot be predicted using molecular measures, an approach which investigates both neutral (non-coding) and non-neutral (coding) markers is necessary in which

quantitative genetic analysis will play a central role in the assessment of extinction risk in conservation biology.



European bison bull (R. Kowalczyk)

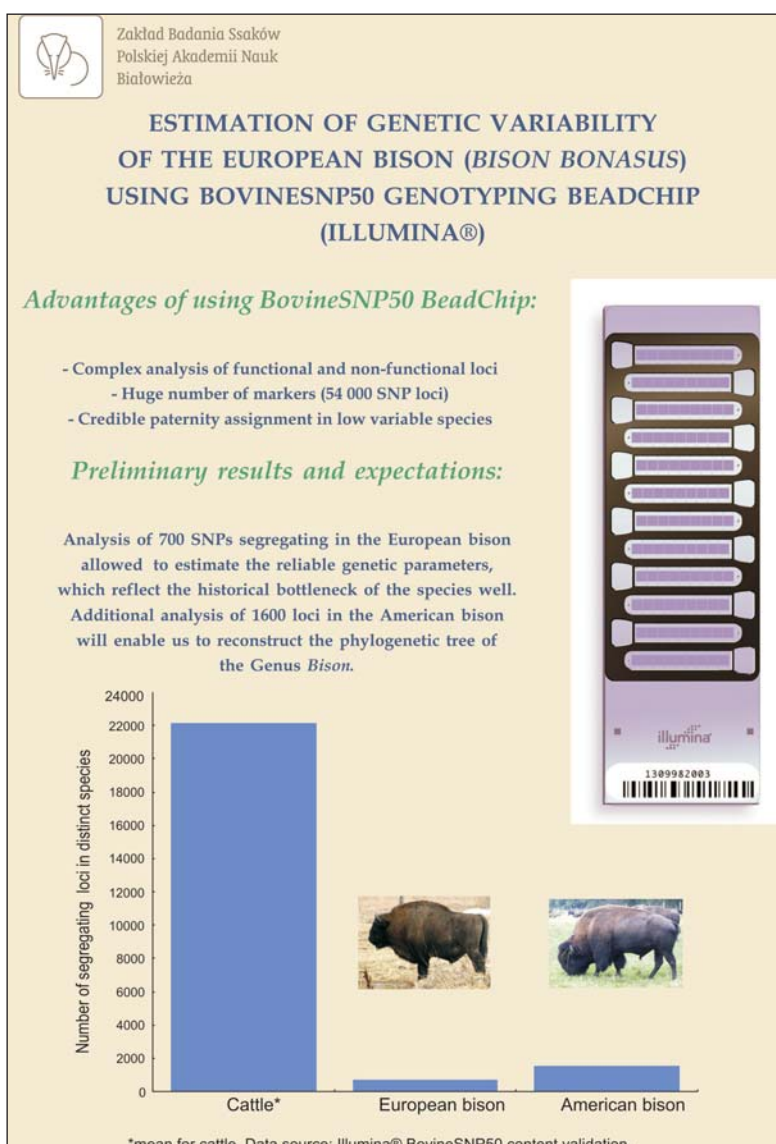


European bison herd (R. Kowalczyk)

Attempting to correlate neutral and non-neutral variability is now possible by using a new and very promising tool in conservation genetics: single nucleotide polymorphisms (SNPs), which are the most abundant polymorphic genetic marker in most genomes. SNPs hold the potential to significantly expand our ability to survey both neutral (non-coding region) variation as well as genes under selection (coding region) in natural populations, providing broader genome coverage compared to mitochondrial DNA or microsatellites. The

BovineSNP50 BeadChip (ILLUMINA®) offers 54 000 SNP loci uniformly covered with an average probe spacing of 51.5 kb, providing satisfying SNP density for robust genome-association studies in cattle.

The studies performed so far on 11 European bison samples have enabled reliable estimation of genetic parameters while subsequent association of additional samples of the American bison will provide a detailed genetic comparison between the two species and create a credible phylogenetic tree with other Bovids.



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