European bison is a species of unique demographic history. It has been through an extremely severe bottleneck in the 1920s. The whole contemporary population originates from a meager group of founders. Just two of them turned out to be predominant, and their share in the contemporary gene pool is above 80%. The effects are extremely low genetic variation and highly increased inbreeding level, reaching 75%. That means, that 75% of DNA of each Eurpean bison show no genetic variance due to the fact, that his/her parents were related. The potential inbreeding depression symptoms are related with skeleton conformation. It has been believed that rapid growth of autozygosity (homozygosity by descent) in the European bison had to influence the morphometrics of the skulls, like it does in other animals.

The development of genomic techniques enables precise calculation of inbreeding level with application of high density genomic markers (SNPs). Such set of over 700.000 markers will be applied in the project, allowing for accurate inbreeding estimations.

The project will be performed on hundreds of modern and historical European bison skulls. We will use hundreds of 3D skull scans from European collections and museums and juxtaposition them with their inbreeding level information based on SNP markers.

This project enables the actual effect of extreme inbreeding on skull conformation in a historical context to be estimated, by association of genomic and morphometric data in one of the most inbred mammals known – the European bison. The skulls and tissues will come from the collections of the Mammal Research Institute of the Polish Academy of Sciences in Białowieża and other, Polish and foreign collections, with numerous bison skulls from before the decrease in the size of the species.

The project will be realized on 2 levels:

Morphometry - 3D scanning of approx. 600 skulls – historic and contemporary from Mammal Research Instute PAS in Białowieża and other foreign collections.

Genome analyses - based on bovine, high density SNP tool: approx. 350 genoms of the studies skulls, either modern or historic will be analyzed.

As a result, the landmark data set will be determined, actual inbreeding will be calculated and genotype – phenotype associations will be described.

The obtained data will allow to specify whether and in what extent inbreeding level shaped the skull conformation of European bison individuals. Our preliminary results indicate promising variation of skull morphometry in its contemporary population.

European bison is a unique species, with dramatic demographic history and extremely low genetic parameters. ***Combining morphometric analysis of the skulls with detailed genomic information of the same individuals offers a rare opportunity to trace the ways in which the increasing inbreeding is affecting the skull conformation of the species.*** Since we will use skulls of different age, the acquired information will not only trace the inbreeding shaped changes but also developmental conformation of the European bison skulls.

The access to hundreds of the European bison skulls measurements and effective genomic analyses will allow to answer theese 3 questions:
1. Has the skull of the European bison changed over time?
2. Has the growing inbreeding of the European bison affected its skull conformation?
3. If yes, then which skull features have been affected by growing inbreeding?