

Project title: Genetic background of a lethal *posthitis* disease in the European bison males

Necrotic inflammation of the prepuce (*posthitis*) is a serious disease affecting approx. 6% of European bison males in Białowieża Forest a year. The first symptoms are swelling of male genital and purulent exudate. Then necrotic changes lead to autoamputation of the penis and death due to general infections of the organism. The disease affects either adult males and few months old calves. *Posthitis* occurs also in other animals (goats, sheep, cattle) as a seasonal disease but in none of the species it has such troublesome, lethal character as in the European bison.

During over 30 years of its presence in the Polish part of Białowieża Forest, a series of studies were performed to define the source of infection and indicate the primary pathogen. The analyses covered different aspects of European bison biology: bacteriological, biochemical, immunochemical or genealogy. So far, neither source of infection nor the primary pathogen have been indicated. There is also no significant correlation between inbreeding and *posthitis* occurrence and thus in spite of many years of research, the etiology of the disease remained unknown.

The recently published results shows an association between certain regions on European bison chromosomes and the *posthitis* occurrence. The results were obtained using cattle specific tool, which was enable to identify the regions of the bison genome associated with the occurrence of bison *posthitis*, but not specific enough to indicate SNP markers, genes and their mutations related with *posthitis* in European bison. Application of cross-specific tools (bovine) may results in obtaining non-specific data, containing the common polymorphism resulted from phylogeny but hardly the species specific data ('ascertainment bias').

Thus, to explain etiology of the disease and model of its inheritance to design molecular diagnostic test for verification of individual susceptibility to the disease, it is necessary to design a bison specific attempt.

The aim of the project is to identify genes and their variants associated with the development of *posthitis* in the European bison, explain the inheritance model of the disease and to design a simple diagnostic test for genotyping the susceptibility to *posthitis* of males as well as the carriers of the unfavorable genetic variants.

The project will be performed using cutting-edge technique SBG (Sequence-Based Genotyping), the use of which allows for obtaining a huge amount of species-specific data from the whole genome, while eliminating the possibility of so-called 'ascertainment bias', resulting from cross-specific analytic tools.

The study material will consist of *posthitis* diagnosed males, the reference group of healthy males and family groups with *posthitis* history for developing the inheritance model analyses.

Explanation of *posthitis* etiology is one of the most important tasks for the conservation of the European bison. The discovery of genetic basis of the disease and the mechanisms of inheritance will make it realistic to reduce or even eliminate its occurrence, at least in the fenced populations. Additionally, the results of the project will help to understand the genetic background of analogue, urogenital diseases in other mammal species, including human.