

## **The role of hybridisation in the evolutionary response to environmental changes: Establishing the genus *Canis* as an ideal model**

The dichotomy between the domestic dog and the grey wolf – “man’s best friend” *versus* the fairy tale villain – reflects the human perception of detachment of the human-modified world from the natural world. Yet the space between the dog and the wolf is not and has never been empty. A recent study by the applicant demonstrated that more than 60% of wolves in Eurasia carry in their genomes small DNA fragments originating from hybridisation with dogs in earlier generations of wolves. Wolf-dog hybrids are fertile and can interbreed with individuals from populations of their both parents, resulting in the retention of hybridisation-derived genetic variants in gene pools of wolves and dogs – a process called introgression. Recent studies based on the analyses of complete genomes showed that introgression has played a profound and complex role in evolution, affecting a broad range of animal and plant species. Introgression can lead to a decreased fitness of admixed individuals or even the extinction of a species via “genetic swamping” – a gradual increase in the frequency of genetic variants originating from a different species until native variants disappear from the gene pool. However, in some circumstances exchange of genetic variants between species or subspecies can help them adapt to rapid environmental change. Therefore, ability to predict the consequences of introgression is crucial for effective mitigation of impacts of the ongoing climate change on wild animals. Yet factors determining the costs and benefits of hybridisation are largely unknown, and difficult to study in cases where interbreeding species are similar phenotypically and ecologically.

The aim of the planned study is to develop the genus *Canis* (consisting of grey wolves, dogs, coyotes, golden jackals and other related species) as a model system for studies on the role of hybridisation in the evolutionary response to environmental changes. The advantage of genus *Canis* is that all its representatives – from apex predators heavily affected by anthropogenic changes to domestic dogs that are well adapted to living in human-dominated ecosystems – can naturally interbreed despite their great morphological and behavioural diversification. This exceptional diversification is a cause of a perceived dichotomy between dogs and their wild relatives, as a result of which they have been rarely studied together except the studies on dog domestication. The planned project will jointly analyse genomic variation in wild and domesticated canids considered as a single model system, using their exceptional phenotypic variability as a key characteristic that facilitates our understanding of the hybridisation process. In particular, we plan to address the understudied topic of the effect of hybridisation on heritable behavioural traits. The genus *Canis* is ideal for this purpose, thanks to the large differentiation of behaviour between dogs and their wild relatives, and the extensive knowledge on the subject.

The proposed study will address important questions regarding the introgressive hybridisation process: What factors affect the introgression rate of hybridisation-derived variants? In which circumstances the benefits of hybridisation are higher than its costs? Does it depend on the evolutionary distance between the cross-breeding taxa? What are the functions of genes where hybridization-derived variants are under positive selection? Are they associated with local environmental adaptations or with global fitness benefits for all admixing taxa? Do populations of wild representatives of the genus *Canis* living in human-dominated habitats display higher proportions of dog-derived genetic variants compared with populations from less transformed habitats? How does hybridisation with dogs affect behavioural traits of wild canids?

The planned project will address these and related questions using a combination of cutting-edge genomic approaches, environmental analyses using the Geographic Information Systems and the modelling of the effect of landscape characteristics on the introgression process. The study will be based on over thousand samples of wolves, golden jackals and free-ranging dogs originating from across three continents, which will be analysed using high-throughput genome sequencing approaches and novel analytical methods for the detection of introgression based on genome-wide variability and the identification of environmental factors affecting introgression. The combination of these cutting-edge methods with the excellent empirical model will enable a significant advance in knowledge of the role of hybridisation in evolution, allowing us to define the circumstances when hybridisation can constitute an adaptive evolutionary process or when it should be prevented as a threat to the species. This will guide the management strategies and legal regulations for increasingly common admixed populations.

This project will enable the creation of a new research team by an experienced researcher, who has recently returned to Poland after 12-years of working in the UK. The project will allow her to consolidate her position as an internationally recognised expert in canid genetics, train early career researchers in cutting-edge methods in evolutionary genomics, bioinformatics and landscape genetics, and develop bioinformatic resources at the host institution (Museum and Institute of Zoology of the Polish Academy of Sciences) that will enable the full utilisation of the existing state-of-the art equipment for next-generation sequencing.