The effect of environmental factors on adaptive genetic variation in grey wolves (*Canis lupus*) and free-ranging dogs (*Canis lupus familiaris*)

Thesis summary Gdańsk/ 12/November/2025

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Adaptive evolution is the process by which organisms change from generation to generation through genomic modifications to improve survival and reproductive rates under environmental selective pressures. Investigating this process allows for us to learn how organisms evolve to adapt to their enviroments. This thesis encompasses an investigation into the adaptive evolution of two representatives of the genus *Canis*, grey wolves and domestic dogs. Domestic dogs are the descendants of grey wolves and owe their ecological success in great part to their relationship with humans. Most of the dogs in the world (i.e., ~ 1 billion), are free-ranging dogs (FRD) that live unconfined with minimal human assistance. Grey wolves and FRDs are closely related taxa with overlapping geographic ranges that are adapted to different habitats throughout their wide ranges. These canids also exploit different ecological niches, with grey wolves being apex predators and FRDs human commensals. Thus, these canids are good models for investigating molecular adaptations under selective pressures from varied habitats as well as adaptive potential under environmental shifts.

This thesis aimed to investigate whether grey wolves and FRDs show similar molecular adaptations under selective pressures within similar habitats, and whether they retain adaptive potential under climate change. To answer these questions I investigated genetic differentiation, genes under diversifying selection, genes associated with environmental variables and adaptive potential with SNP genotypes of 370 FRDs and 232 grey wolves from 10 different biomes across Eurasia.

Four different approaches employed to investigate population genetic structure consistently showed that FRDs have weaker genetic differentiation than grey wolves, implying a stronger connectivity among FRDs subpopulations. The stronger connectivity in FRDs has been likely facilitated by their relationship with humans. I also investigated genes under diversifying selection i.e., genes with variants associated with different phenotypes being favoured by natural selection in different subpopulations. The approaches applied for this purpose were based on detection of outliers using the measures of genetic differentiation among populations; hence the approaches are influenced by population structure. There was a strong overlap among the genes with signatures of diversifying selection in FRDs and wolves. Thus, FRDs and wolves have evolved under selective pressures that favour many of the same phenotypic traits (e.g., olfaction, morphological traits).

To investigate the genes with signatures of local adaptation I used a dual approach to detect SNPs associated with environmental variables. The approaches detect high correlations between SNPs and environmental variables, while accounting for population structure. There was little overlap among the genes with signatures of local adaptation in

grey wolves and FRDs. However, the phenotypic traits associated with these genes were similar in both taxa. Furthermore, the genes under diversifying selection and local adaptive evolution showed overlap in FRDs, but not in grey wolves. The difference among the genes with signatures of diversifying selection and with signatures of local adaptive variation, could be due the presence of genes that are under other types of selection (e.g., balancing), population genetic factors (e.g., genetic drift, historic bottlenecks) and environmental gradients. These results may indicate that both taxa have unique genetic mechanisms enabling adaptation to their local enviroments.

Dogs are human commensals and therefore it may be predicted that they are not well adapted to natural environments. However, dogs may retain an adaptive potential for the natural landscapes in which their ancestral wild population lived. To that end, I investigated the adaptive potential of domestic dogs and attempted to identify environments where they are best suited to survive with minimal human assistance. The combined analysis of dogs' adaptive potential and suitable ecological niche modelling contributed evidence into the location of geographical centre of dog domestication.

Based on genomic offset and risk of maladaptation analyses, FRDs are predicted to retain lower adaptive potential than grey wolves under climate change. Populations of FRDs in Southern Eurasia are predicted to retain the highest adaptive potential under climate change. If dogs have retained the adaptive potential from the ancestral population that underwent domestication, our results suggest that dogs may have been domesticated in Southern Eurasia. The modelling of the most suitable habitats based on modern dogs' distribution showed Southern Eurasia as the geographical region with the most suitable habitats for dogs. The combined findings of adaptive potential and the most suitable habitat for dogs suggest that dogs were domesticated in Southern Eurasia, although it is not possible to point to a precise location of the domestication centre for the species.

This work shows the complex dynamics of selective pressures in two widespread canid species with different ecological niches. Our findings may be useful in informing conservation efforts for grey wolves and population control of FRDs. Our results also suggest that local adaptation of closely related taxa may involve similar phenotypic traits but not necessarily the same genes. Furthermore, this work contributes knowledge to reduce the uncertainty surrounding the dog domestication place.

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