



## CAT DOMESTICATION THROUGH THE LENS OF PALEOGENOMICS

*PhD Student:* Marco De Martino/ *Academic Tutor:* Prof. Claudio Ottoni

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The aim of this project is to shed light on the domestication process of one of the most popular pets in the world, the domestic cat. State-of-the-art studies based on mtDNA evidence demonstrated that the Near Eastern and North African wild cat (*Felis silvestris lybica*) is the ancestor of the domestic cat. To date, only one paleogenetic study has brought new insight in the dispersal of the domestic cat in the ancient world but many questions still remain to be addressed mainly because ancient nuclear genomic data are lacking.

Plant and animal domestication represent a major transition in human subsistence strategies, leading to the development of sedentary communities that ultimately resulted in complex societies. The domestication of animal is a highly relevant topic for scientific research, attracting scholars from many different fields. Recent evidence, from archaeozoology to paleogenomics, demonstrated that domestication it is not a discrete process where human intentionally and unilaterally modify the biology of other animals. Rather, domestication is a complex and multistage process by which both humans and the targeted species gain mutual benefit. Moreover, domestication in animals seems to lead to the development of a common suite of behavioural and morphological traits, also known as “domestication syndrome”. Paleogenomic data have also shown that studying the process of domestication exclusively through modern genetic data could be problematic as these represent just a contemporary snapshot of a long-term process with complex demographic histories: population bottlenecks, human mediated translocations and population turn-overs can be hardly detectable with modern genetic data. Nonetheless, the analysis of ancient mitochondrial data alone cannot account for admixture patterns as well as for selection signatures that shaped the genomes of species under investigation.

By applying cutting-edge methodologies in the ancient DNA field, I aim at generating complete mitogenomes and nuclear genomic data of hundreds of ancient cats sampled across Europe, South West Asia and North Africa spanning several millennia, from 15000 years ago to the 18<sup>th</sup> century. These data will allow to assess patterns of admixture between (and within) wild and domestic cat populations, as well as to scan nuclear genomes for selection signatures thus unravelling the times and modes of cat domestication.