

SUMMARY

Molecular-Population Research of Local Dogs in Bulgaria

The history of dog domestication is still under debate, but it is doubtless the process of an ancient partnership between dogs (*Canis familiaris*) and humans. Although data on ancient DNA for dog diversity are still incomplete, it is clear that several regional dog populations had formed in Eurasia up to the Holocene. During the Neolithic Revolution and the transition from hunter-gatherer to farmer societies, followed by civilization changes in the Antiquity period, the dog population structure also changed. This process was due to replacement with newly formed dog populations. In this study, we present for the first time mitochondrial data of ancient dog remains from the Early Neolithic (8000 years before present (BP)) to Late Antiquity (up to 3th century AD) and three native dog breeds from Bulgaria.

A total of 16 samples were analyzed, using the mitochondrial D-loop region (HVR1). The results show the presence of A (70%) and B (25%) clades throughout the Early and Late Neolithic Period. In order to clarify the position of our results within the ancient dog population in Eneolithic Eurasia, we performed phylogenetic analysis with the available genetic data sets. This data showed a similarity of the ancient Bulgarian dogs to Italian (A, B, and C clades) and Iberian (clades A and C) dogs' populations. A clear border can be seen between southern European genetic dog structure, on the one hand, and on the other hand, central-western (clade C), eastern (clade D) and northern Europe (clades A and C). This corresponds to genetic data for European humans during the same period, without admixture between dog populations. Also, our data have shown the presence of clade B in ancient Eurasia. This is not unexpected, as the B haplogroup is widely distributed in extant Balkan dogs and wolves. The spreading of this clade across Europe, together with the A clade, is related to the possible dissemination of newly formed dog breeds from Ancient Greece, Thrace, and the Roman Empire.

We also perform phylogenetic analysis of three native Bulgarian dog breeds. A total of 130 samples were analyzed at HVR1 (hypervariable region, D-loop region). The samples were taken from two hunting dog breeds (Barak, n=34; Gonche, (n=45) as well as from a Bulgarian Shepherd Dog (n=51). The results have shown the presence of almost all main clades A, B, C and D in the three dog breeds taken together, as expected. With regard to haplogroups distribution, there are clear differences among investigated breeds. While hunting breeds exhibit a prevalence of clade C, the mountainous Shepherd dog shows presence of the D2 haplogroup but absence of the C clade. The results in native hunting and shepherd dogs have revealed a clear difference of haplogroups dissemination, which suggests a dual independent phylogenetic origin. The Bulgarian native dog population is characterized by the highest frequency of clade A (55%), followed by clade B and C (about 18%) and the specific South-European clade D2 (about 10%).