
The population genetic origins of domestic dogs

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Résumé

Despite numerous investigations leveraging both genetic and archaeological evidence, the geographic origins of dogs remain unknown. On the basis of an ancient Irish dog genome and an assessment of the spatiotemporal appearance of dogs in the archaeological record, a recent paper suggested that dogs may have been domesticated independently in Eastern and Western Eurasia from distinct wolf populations. Following those independent origins, a mitochondrial assessment suggested that the Mesolithic dog population in Western Europe may have been replaced by a population from the East. To test this hypothesis, we are generating nuclear genomes of ~10 Mesolithic dogs sampled from sites in Europe and Western and Eastern Russia, and mitochondrial genomes from ~400 dogs spanning the last 15,000 years across Eurasia. The results of this analysis will reveal the phylogenetic affinities of dogs that were present across the Old World prior to the introduction of dogs associated with farming communities. This study will also allow us to pinpoint the timing of the European mitochondrial turnover and to assess whether there was a commensurate turnover at the nuclear level, thus directly addressing whether dogs were domesticated from more than one population.

Mots-Clés: dogs, domestication, ancient DNA

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