



KTH Biotechnology

Molecular Profiling of the Population Dynamics: Foundation and Expansion of an Archaic Domesticated

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Doctoral Thesis

Which with the approval of the Royal Institute of Technology (KTH) in Stockholm, Sweden, will be presented for public review in fulfillment of the requirements for a Doctor of Philosophy in Science, on Friday **June 8, 2012** at **13:00** in **Hillarp Hörsal**, Retzius väg 8, Karolinska Institute, Solna, Sweden.

Faculty opponent:

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Abstract. An ‘exponential growth of science’ throughout modern history has been frequently boasted by numerous narcissistic accounts of ‘modern human.’ Nonetheless, ‘modern science’ seems to have overwhelmingly cut back on its promises, fitting into an ‘industrial scheme.’ With this concern, ‘molecular phylogeographics with conservational ambitions’ would look an intact ground for research efforts in a ‘school of biotechnology.’ The dog (*Canis familiaris*) as an earliest domestic animal has a history of conflicts over its origins and dispersal. Having those disputes addressed, valuable knowledge could be acquired on the nature and dynamics of domestication, and of human societies particularly of pre-agricultural ages. We employed two most widely-used genealogical markers, the mitochondrial DNA (mtDNA) and the non-recombining portion of the Y-chromosome (NRY), to address dog demography. Through 582 bps of mtDNA Control Region, complemented with whole mitochondrial genomes, it was established that almost all maternal lineages of the domestic dog worldwide coalesce to a population of at least 51 and perhaps many more female wolves in Asia South of Yangtze River (ASY) approximately 16,000 years before present (BP). This was based on the presence of a maximal diversity in this area, a descending gradient of diversity outward it, and a ubiquitous population structure everywhere in the world. A closer examination of this portrait in Southwest Asia (SwAsia) and the Fertile Crescent (FC), a region which has supplied persuasive evidence on early presence of the domestic dog, retrieved the same information, with implications for backbreeding with the local wolf population. Analyses of mtDNA dispersal showed that dogs took the long way via land to Madagascar Island, and not together with humans via sea. By the other approach, the NRY data in 14,437 bps length supplemented the mtDNA in reporting the height of diversity from ASY with a founding population of at least 13 male wolves, but expectably produced lower inter-regional differentiations by diversity. NRY screening of NRY by a SNP assay in the dingoes of Australia Island as a population of feral dogs revealed restricted and similar dispersal patterns for sires and dams. Prospects of ancient, multilocus and whole genome assays with the emerging high-throughput technologies has still more to promise on finer elaborations of these issues.

Keywords: Dog, wolf, dingo, mtDNA, NRY, SNP, Madagascar, Australia, domestication

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