

Carmichael, L. E., J. Krizan, J. A. Nagy, E. Fuglei, M. Dumond, D. Johnson, A. Veitch, D. Berteaux, and C. Strobeck. 2007. Historical and ecological determinants of genetic structure in arctic canids. *Molecular Ecology* 16:3466-3483.

Wolves (*Canis lupus*) and arctic foxes (*Alopex lagopus*) are the only canid species found throughout the mainland tundra and arctic islands of North America. Contrasting evolutionary histories, and the contemporary ecology of each species, have combined to produce their divergent population genetic characteristics. Arctic foxes are more variable than wolves, and both island and mainland fox populations possess similarly high microsatellite variation. These differences result from larger effective population sizes in arctic foxes, and the fact that, unlike wolves, foxes were not isolated in discrete refugia during the Pleistocene. Despite the large physical distances and distinct ecotypes represented, a single, panmictic population of arctic foxes was found which spans the Svalbard Archipelago and the North American range of the species. This pattern likely reflects both the absence of historical population bottlenecks and current, high levels of gene flow following frequent long-distance foraging movements. In contrast, genetic structure in wolves correlates strongly to transitions in habitat type, and is probably determined by natal habitat-biased dispersal. Nonrandom dispersal may be cued by relative levels of vegetation cover between tundra and forest habitats, but especially by wolf prey specialization on ungulate species of familiar type and behaviour (sedentary or migratory). Results presented here suggest that, through its influence on sea ice, vegetation, prey dynamics and distribution, continued arctic climate change may have effects as dramatic as those of the Pleistocene on the genetic structure of arctic canid species.

Key words: *Alopex lagopus*, arctic fox, *Canis lupus*, dispersal, genetic structure, grey wolf, microsatellite, prey specialization.

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