

## Dog genome evolution: A strategy to segregate biogeographic effects from human selection

The article of Boyko et al. (1) supports the general biological rules underlying evolution: barriers to gene flow will result in genetic drift. In contrast to wild animals, in dog populations this is modified by human selection. The weighted center of the principle component analysis explaining 38% of the variance (figure 4 in ref. 1) indicates that dogs of northern Namibia and Egypt (>5,000 km apart) show little genetic difference consistent with a continuous gene flow across the African continent. In contrast, the Middle Eastern Salukis and the Afghan hounds (from Afghanistan) differ more substantially from Western indigenous African dogs of Egypt (only 2,500 km apart, or half the distance between Namibia and Egypt). This difference underscores that biogeographic distance is distorted by other factors such as barriers to gene flow and human selection. The case of the Basenji highlights this discrepancy even better: Basenjis come from the Congo basin and one would expect them to be genetically somewhere between Ugandan and northern Namibian village dogs—the Congo basin being situated slightly off but somewhat between Uganda and Namibia. The great genetic differences of the Basenji from these village dogs suggest that other factors such as breeding preferences in the countries of origin or a small Western breeding

stock from which the samples were taken has perhaps distorted biogeographic differences. Controlling for this aspect would require a direct comparison between local village dogs and breeds originating from the same areas. Existing data suggest that both segregation [Sloughis and North African village dogs (2)] as well as some intermixing [Salukis with Akbash (3)] will be found between Western dog breeds and other local dogs in the country of origin. More such comparisons of internationally recognized\* indigenous African breeds such as Aidi, Azawakh, Basenji, and Sloughi with biogeographically overlapping village dogs would complement this study and would reveal the influence of biogeographic differences and human selection better than comparing with breeds originating outside of Africa (e.g., Afghan Hound, Pharaoh Hound, Saluki).

**Dominique Crapon de Caprona and Bernd Frittsch<sup>1</sup>** Department of Biology, College of Liberal Arts and Sciences, University of Iowa, Iowa City, IA 52242

1. Boyko AR, et al. (2009) Complex population structure in African village dogs and its implications for inferring dog domestication history. *Proc Natl Acad Sci USA* 106: 13903–13908.
2. Pires AE, et al. (2006) Mitochondrial DNA sequence variation in Portuguese native dog breeds: diversity and phylogenetic affinities. *J Hered* 97:318–330.
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<sup>1</sup>To whom correspondence should be addressed. E-mail: bernd-frittsch@uiowa.edu.

\*Fédération Cynologique Internationale (FCI) recognizes and registers some 350 breeds in Europe, Asia, South America, Africa, and Australia outside of the American Kennel Club (United States) and the Kennel Club (United Kingdom).