

Genetic variation and differentiation among nordic raccoon dogs

AIM

The genetic variation among raccoon dogs sampled in Sweden, Finland and Denmark was evaluated using nine microsatellite loci. The aim was to estimate the connectivity between the locations and evaluate the possibility to detect first generation migrants among individuals sampled in Sweden.

Table 1. Genetic variation (allelic richness and heterozygosity \pm SD) and differentiation (F_{ST}) among raccoon dogs sampled in Sweden (S), northern Finland (Fn), southern Finland (Fs), Björkö (B), Åland (Å) and Denmark (D).

	S (n=173)	Fn (n=10)	Fs (n=14)	B (n=10)	Å (n=10)	D (n=20)
S						
Fn	0.006					
Fs	0.037***	0.013				
B	0.059***	0.055**	0.059***			
Å	0.087***	0.032*	0.046**	0.131***		
D	0.147***	0.128***	0.129***	0.18***	0.159***	
Allelic richness	3.7 \pm 0.6	4.2 \pm 0.9	4.4 \pm 1.1	3.3 \pm 0.9	3.2 \pm 0.9	3.6 \pm 1.1
Heterozygosity	0.68 \pm 0.08	0.72 \pm 0.07	0.72 \pm 0.09	0.54 \pm 0.18	0.57 \pm 0.19	0.61 \pm 0.21

RESULTS

The connectivity between the Swedish and Finnish mainland populations was high, indicated by low levels of differentiation ($0.006 < F_{ST} < 0.05$) and only slightly lower genetic variation among Swedish raccoon dogs (Table 1). Without prior knowledge about the location, the Danish raccoon dogs clustered as a genetically distinct population (Figure 1A and 2C) while Swedish and Finnish individuals form weak clusters (Figure 1B and 2B), mainly accounted for by the two Finnish island populations.

The possibility to detect first generation migrants (from Finland to Sweden) was limited and will require many more markers or better knowledge about the relatedness among Swedish raccoon dogs. The average relatedness among Swedish raccoon dogs was low ($r = 0.076$), even though a few individuals were potentially highly related (Figure 3).

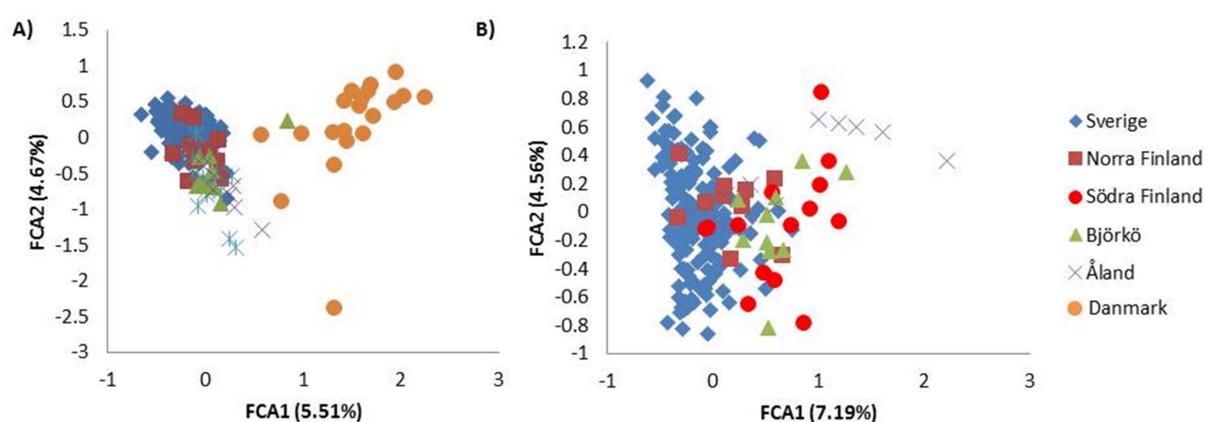


Figure 1. Factorial correspondence analysis (FCA) of the genetic variation among Nordic raccoon dogs, including (A) and not including (B) Danish animals. This is a way of reducing the genetic variation into trajectories where the explained variation in the sample is maximized. The clustering of individual genotypes indicate large genetic similarity.

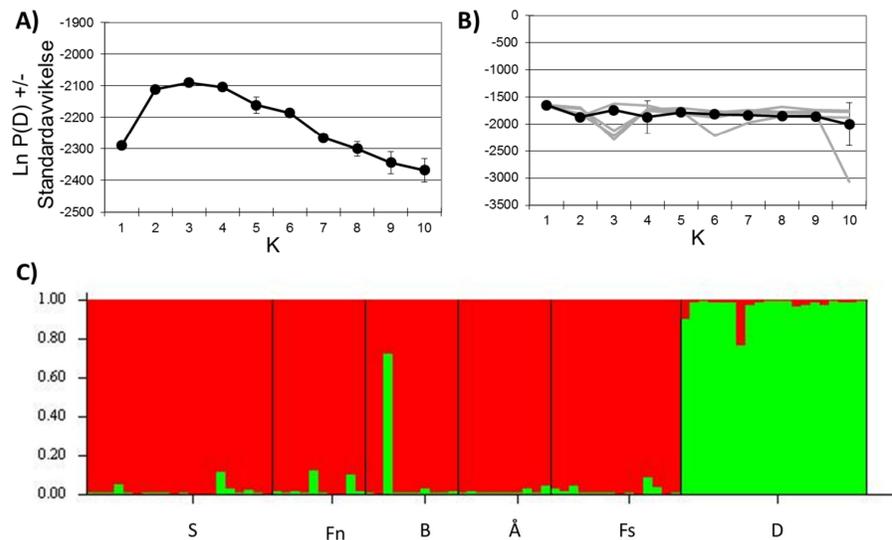


Figure 2. Bayesian cluster analysis. The probability $\ln(P(D))$ of K differentiated populations is illustrated when including (A) and not including (B) Danish raccoon dogs. Moreover, the individual assignment when assuming two populations ($K = 2$) is illustrated in graph C. Graph A and C show indications of $K = 2$ as the most parsimonious number of subpopulations, where one population is comprised mainly of Danish individuals. Among Swedish and Finnish individuals there appear to be no subpopulation clustering indicated by the relatively high $\ln(P(D))$ when $K = 1$ in graph B.

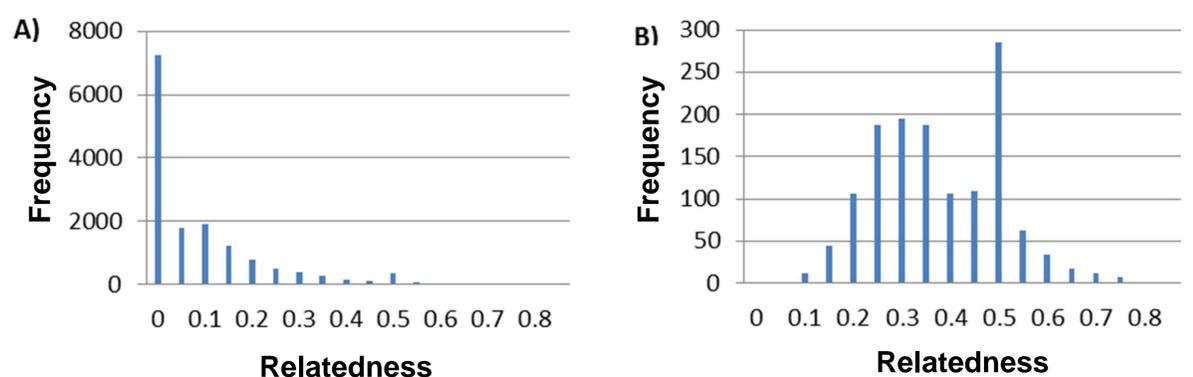


Figure 3. The pairwise relatedness (using triadic likelihood estimation in Coancestry v1.0) among 173 Swedish raccoon dogs. The graphs illustrate the frequency of all relatedness scores (A) and scores where relatedness were significant (B).