Response to “Cross-Species Application of SNP Chips is Not Suitable for Identifying Runs of Homozygosity” by Shafer, Miller, and Kardos

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The application of commercially available single nucleotide polymorphism (SNP) chips to non-model animals has been described by several authors in previous publications (Boixley et al. 2009; Pertoldi et al. 2010; Miller et al. 2011; Ogden et al. 2012; Haynes and Latch 2012; vonHoldt et al. 2012; Hoffman et al. 2013). In our recent Brief Communication (Kharzinova et al. 2015), we primarily aimed to verify the applicability of these chips to whole-genome analysis of reindeer Rangifer tarandus. All 4 reindeer samples in our study were representative of 1 group inhabiting the south of Eastern Siberia (Todzha district of Tuva Republic) and were randomly selected from 30 collected samples.

The results obtained after genotyping 4 animals using the Bovine SNP50 v2 BeadChip (23 481 out of 54 609 SNPs) and Ovine SNP50 BeadChip (25 512 out of 54 241 SNPs) indicate on one hand the specific design of those chips (mainly based on data from the commercial breeds of livestock), on the other hand they indicate the possibility of using detected SNPs to characterize the relationship between animals or to control the level of inbreeding in reindeer populations.

Following our research we consider Bovine SNP 50 BeadChip v2 preferable to Ovine SNP50 BeadChip for whole-genome analysis in reindeer due to the detection of a greater number of polymorphic SNPs (1257 against 519 SNPs). We used the runs of homozygosity (ROH) analysis to estimate the homozygosity of the studied animals. We would like to clarify that we used a sliding 100-kb window with a size of 100 SNPs to research ROH. In general, the window size was 10 000 kb, not 100K SNPs as described in Shafer et al. By default PLINK has a minimum density of 1 SNP/50 kb (Purcell et al. 2007).

In fact, we had first attempted to carry out our experiment exclusively using polymorphic loci and had obtained no ROH results. This was due to the small size of the effective population and the low number of representative samples.

Since our main goal was to evaluate the possible employment of 2 commercially available SNP chips developed for domestic animal species to whole-genome analysis in reindeer, we decided to proceed with our study using all areas of SNP loci. The value of ROH obtained in this way among the animals was more than 16 Mb. This indicates the consanguinity and level of kinship, and may also suggest the effect of population bottlenecks, selection pressure and breeding management (Purfield et al. 2012).

The conclusion of Shafer et al. (this issue) regarding inbreeding is based on results obtained through a genome simulation carried out with a large number of polymorphic SNPs, and not on a real population with specific geographic and phylogenetic conditions. In fact, the probability of inbreeding in reindeer should be considered according to the area that they inhabit. The study of Holand et al. 2007 (mentioned by Shafer et al. (this issue)) was conducted at the Field Reindeer Research Station in Finland (a 15 km² fenced area), whereas the area in our study is more than 44 000 km².

We take into account the scholastic reasoning of our opponents. Nevertheless, we used genetic material from endemic reindeer groups, which are of great interest in Russia, to conduct model studies to analyze the accumulation of inbreeding inheritance and breeding problems, to look at conservation in situ in a unique species, and to find genes under selection (which relates to the impact of ethnography).

We invite researchers to collaborate and further exchange genetic data in scientific co-operation, in order to further the discussion of the controversial issues that have been raised by Shafer et al.

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