

Testing of low-density SNP panel in wild and domestic reindeer populations (*Rangifer tarandus*)

Deniskova T.E¹., Dotsev A.V¹., Solovieva A.D¹., Layshev K.A²., Yuzhakov A.A²., Romanenko T.M³., Fedorov V.I⁴., Reyer H⁵., Wimmers K⁵., Brem G^{1,6}., Zinovieva N.A¹.

¹L.K. Ernst Federal Science Center for Animal Husbandry; ²FGBNU North-West center of interdisciplinary researches of problems of food maintenance; ³FCIARctic Nenets Division — Agro-Experimental Station; ⁴FGBNU YANIISH; ⁵Institute of Genome Biology, Leibniz Institute for Farm Animal Biology; ⁶Institute of Animal Breeding and Genetics, VMU.

INTRODUCTION: A territory of the northern Russia is the world largest dwelling of wild and domestic reindeer (**Fig.1**).



Fig 1. Evenk domestic reindeer

Development of species-specific SNP arrays is still in progress. However, evaluation of state of gene pool of reindeer populations cannot be paused to prevent dramatic losses in genetic diversity.

Our **AIM** was to select SNPs to create low-density panel to perform genetic assessments without losing biological content.

MATERIALS: SNP genotypes of wild (WLD, n = 83), and domestic reindeer from the Nenets District (NEN, Nenets breed, n = 100), Murmansk Region (MUR, Nenets breed, n = 19), Yakutia (YAK, Evenk breed, n = 19) obtained using Illumina BovineHD BeadChip.

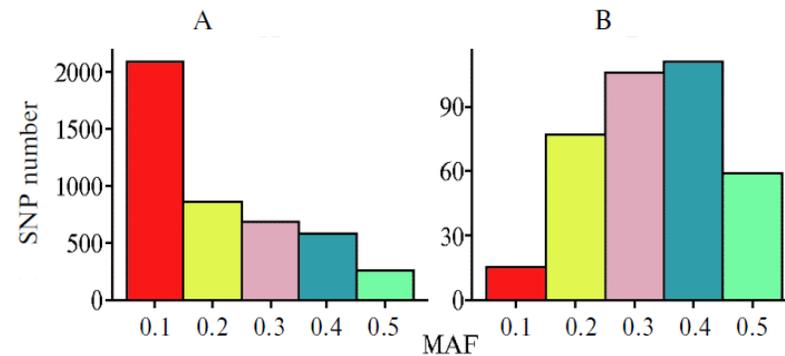


Fig 2. Distribution of the SNPs depending on MAF by comparison of two marker panels: A — final data set comprised 4456 SNPs for the domestic and the wild reindeer; B — 368 SNPs selected to create a custom DNA microarray.

METHODS: The data processing performed in PLINK 1.9 revealed 4456 polymorphic SNPs. Using Delta method implemented in the TRES software, 368 informative SNPs were selected. To compare the resolution power of low-density SNP panel with a whole set of polymorphic SNPs, we estimated minor allele frequencies (MAF) and performed PCA analysis.

RESULTS: In case of low-density panel, we observed obvious bias to higher MAF (≥ 0.30), and 4% of SNPs had MAF around 0,1. Among whole set of polymorphic SNPs 70% SNPs had $MAF \leq 0.2$ (**Fig.2**)

PCA (**Fig.3**) obtained with low-density panel and whole SNP set provided similar pattern of genetic differentiation between studied groups. Wild animals were clearly separated by PC1 from their domestic relatives. Besides Evenk reindeer was distant from two Nenets groups.

CONCLUSION: Thus, the minimum required number of SNPs was selected, allowing for genetic studies in the reindeer populations without the loss of bioinformatics content. Next step of our study will be developing custom DNA array based on 368 selected informative SNPs.

ACKNOWLEDGMENTS: The reported research was funded by RSF № 16-16-10068.

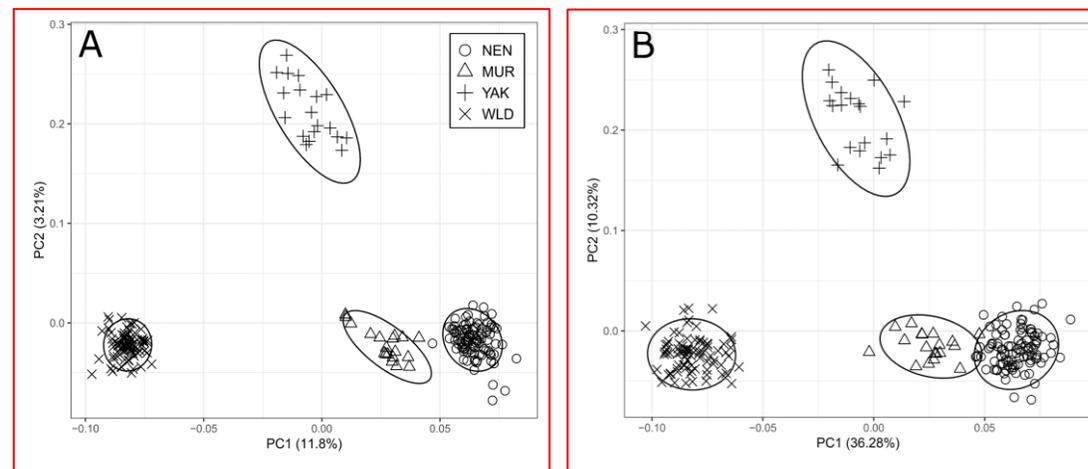


Fig.3. Results of PCA, based on data from two SNP panels: A — final data set comprised of 4456 SNPs detected with the BovineHD BeadChip; B — 368 SNPs selected to create a custom DNA microarray

CORRESPONDING AUTHOR:
Tatiana Deniskova
horarka@yandex.ru