



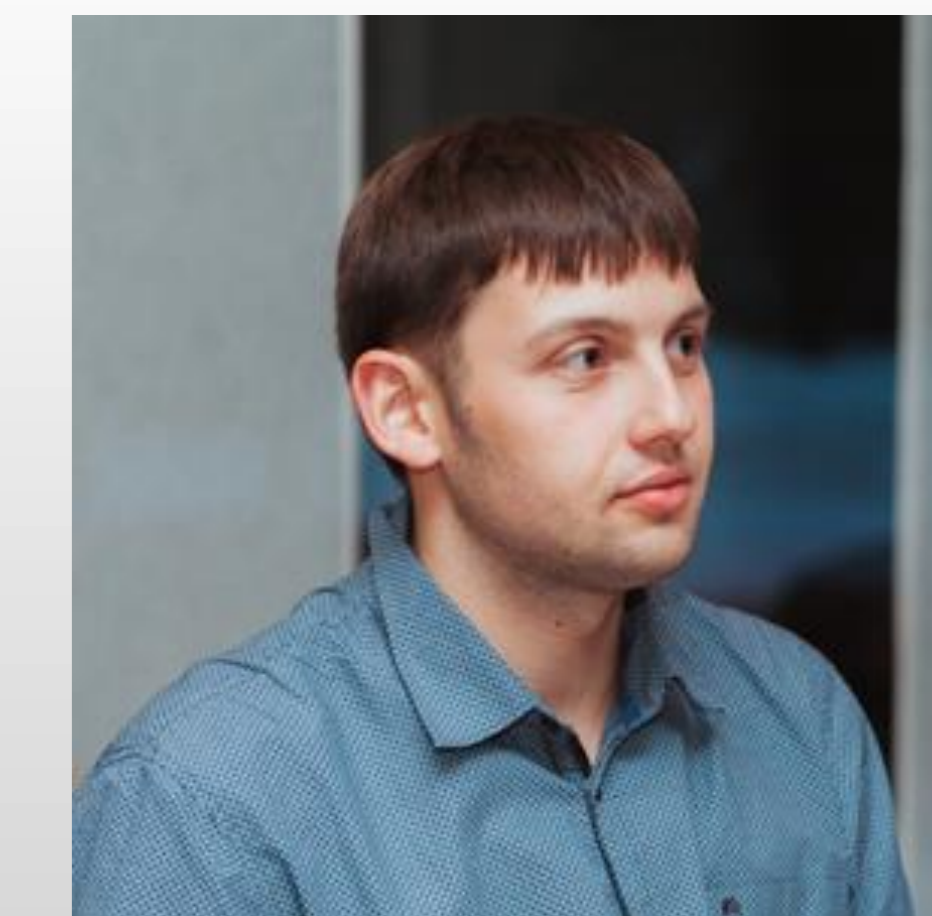
Population structure and Holstein ancestry analysis of modern Russian Black and White cattle for accurate genetic evaluation in Leningrad region.

Andrei A. Kudinov^{1,2}, Arina I. Michina¹, Michael G. Smaragdov¹

¹Russian research institute of farm animals genetics and breeding, Pushkin, Saint-Peterburg, Russia

²University of Helsinki, Finland

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Main Author

Abstract

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Worldwide popularity of Holstein (HOL) breed is based on high milk abilities and perfect genetic response. During early 1900th Soviet government registered new Russian Black and White (RBW) dairy breed made by crossing of local cows with imported Dutch, German and Latvian Frisian bulls. After 1950th semen and animals importation strategy was changed to pure breeding. Starting from 1990 in an attempt to gain milk production farmers start actively use US and Canadian Holstein bulls for mating purpose. Leningrad region (LR), as highest average milk producing region in Russia, intensively using North American semen and Europe young bulls for AI purpose. Process of moving forward from old official Contemporary Comparison to modern Single-Step SNP-BLUP evaluation model cause question: should be effect of heterosis accounted in the mixed model equation? Due to pedigree data pitfalls, accurate estimation of ancestry proportion between RBW and HOL breed sometimes was difficult. Aim of our research was to check population structure of modern RBW breed in LR using modern genomic tools. The study included 1100 cows and 400 bulls genotyped using illumina 50Kv2 SNP BeadChip and IBDv3 BeadChip. Cows were randomly selected from 13 large (>700 milking cows) breeding herds placed in different parts of region. Population structure was estimated using Multi-dimensional scaling (MDS) analysis and Fst statistics in Plink 1.9, maximum likelihood estimation of individual ancestries from multilocus SNP genotype in Admixture software. According to MDS plot on vector C1, 6 and 42 animals were respectively extremely (-0.4) and slightly (-0.3 to -0.1) outlying from main cluster. Admixture plot shown no critical difference between animals for all tested K. Calculated Fst was 0.008. Using those evidences, we conclude there is no need to use multi-breed statement in genetic and genomic evaluation model. Supported by FASO state assignment AAAA-A18-118021590138-1.



Old times RBW cow



Photo by Anastasia Baranova

Modern RBW cow



Old days RBW bull



Photo by Nevskoe AI-station

Modern RBW bull



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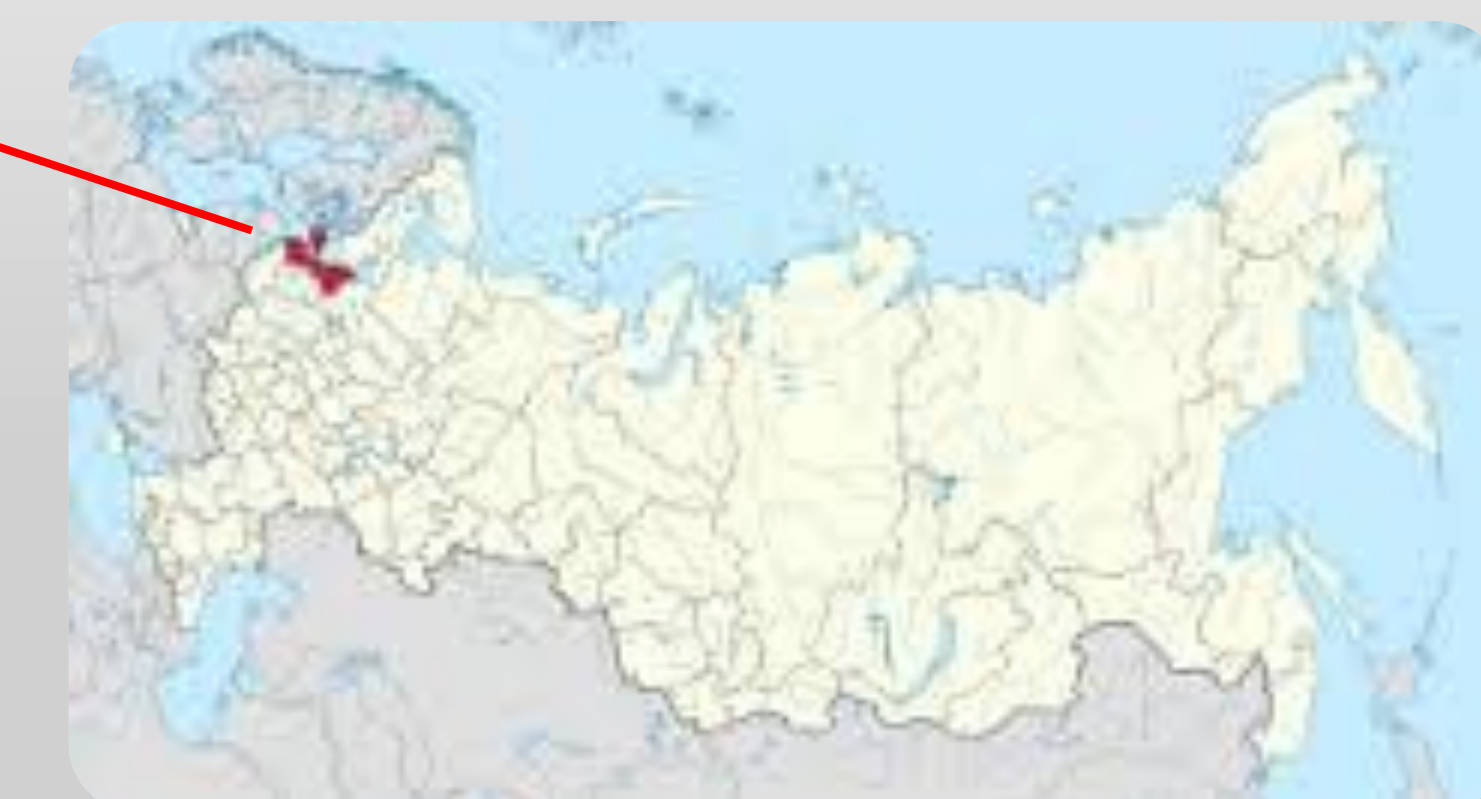
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Intro

- Leningrad region is pleased in North Western part of Russia.
- Region have highest average milk production level per cow (8432 kg).
- Milking breeds in region:
 - **Russian Black and White or Russian Black Pied (RBW)**
 - **Holstein (HOL)**
 - **Ayrshire**
- RBW cattle was formed by crossing of local cows with Ost-Frisian bulls during 1920-1958.
- Holstein bulls are used by farmers to improve type and dairy traits of RBW cows.
- Different proportion of Holstein ancestry presented in different herds.
- Some herds change breed status from RBW to HOL.
- Genomic selection (prediction) not part of industrial breeding program yet.
- Genetic evaluation for RBW and HOL could be done using one of the following strategy:



Three strategies.

Objective

Image

Strategy I

Define join population of RBW and HOL bulls as common and make genomic prediction using single model.

Strategy II

Use same strategy as S-1, but include heterosis effect in to the model.

Strategy III

Use separate models – one per breed.

- Collect evidence of using developed single genomic evaluation model for both breeds, without including any additional effects.
- To see how genetically close RBW and HOL cattle in population of Leningrad region.

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Animals

Animals included in to the analysis were presented by modern cows, modern and historical bulls. Cows were selected from 13 herds using strategy of low relationship.

Subset of animals were presented by:

- 183 USA and Canadian Holstein sires.
- 95 Europe (Germany, Netherlands) Holstein sires.
- 90 Russian sires born in RBW and HOL herds within Leningrad region.
- 607 Russian cows born in HOL herds.
- 516 Russian cows born in RBW herds.

Total: 1491.

Genotyping

- DNA was extracted from blood samples (cows) and semen (bulls) using phenol/chloroform method.
- Genotyping were performed using illumina 50Kv2 and IDBv3 Bead Chip.
- Quality control were performed using Plink 1.9 software.

Following criteria were used:

Minor allele frequency (MAF) - 0.05;

Hardy-Weinberg equilibrium (HWE) - 0.01;

Messing rate per SNP - 0.1 .

- Total number of SNP's left was 31,645.

Population structure

Population structure was studied using **Principle Component Analysis** (PCA) in Eigensoft 6.1.4 and **Maximum likelihood estimation** of individual ancestries from multilocus SNP genotype (Structural analysis) in Admixture software.

Genetic evaluation

Repeatability Animal Model BLUP was used for pedigree based breeding value evaluation of productive traits.

Single-step SNP-BLUP was used for genomic evaluation.



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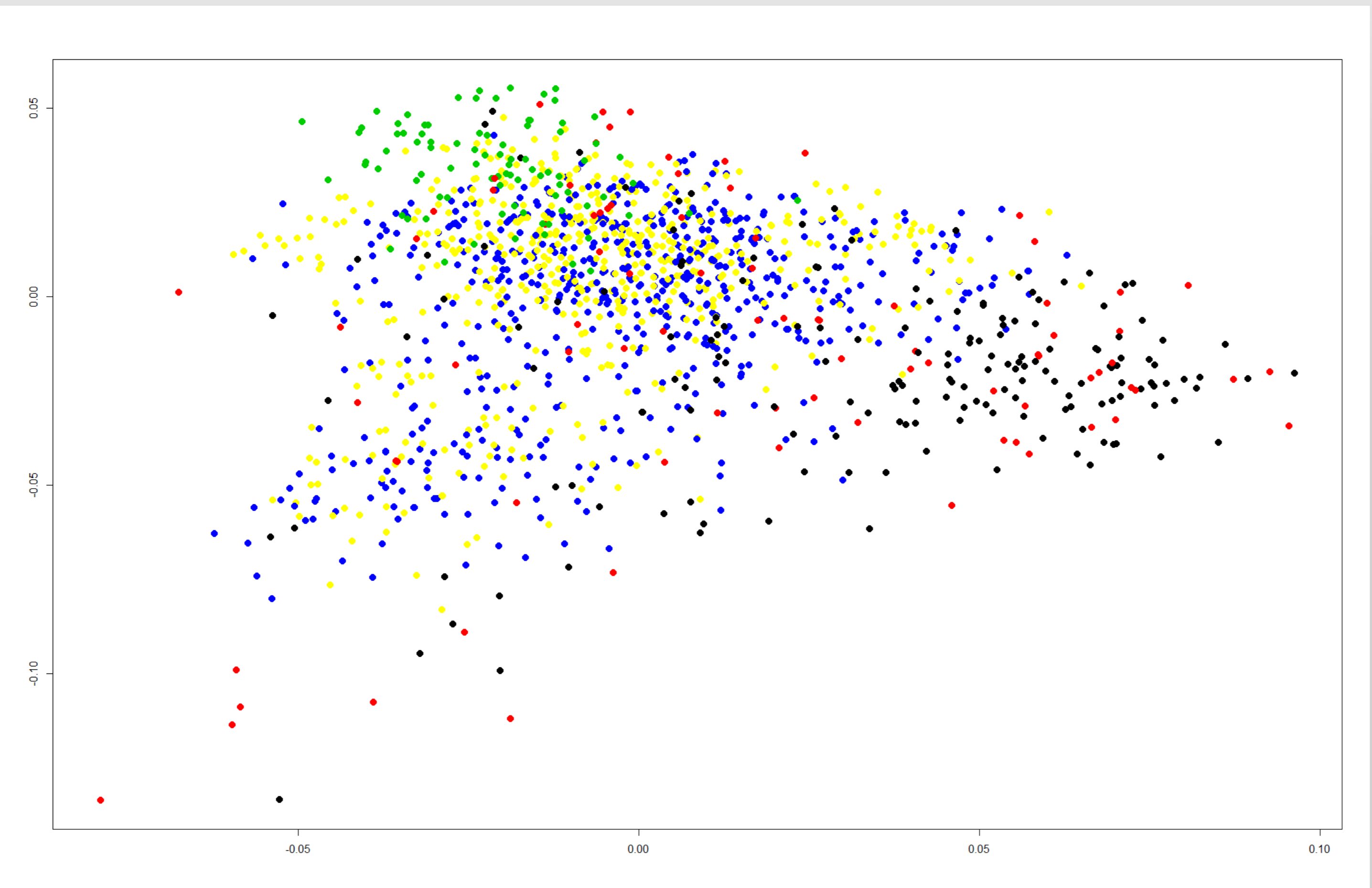
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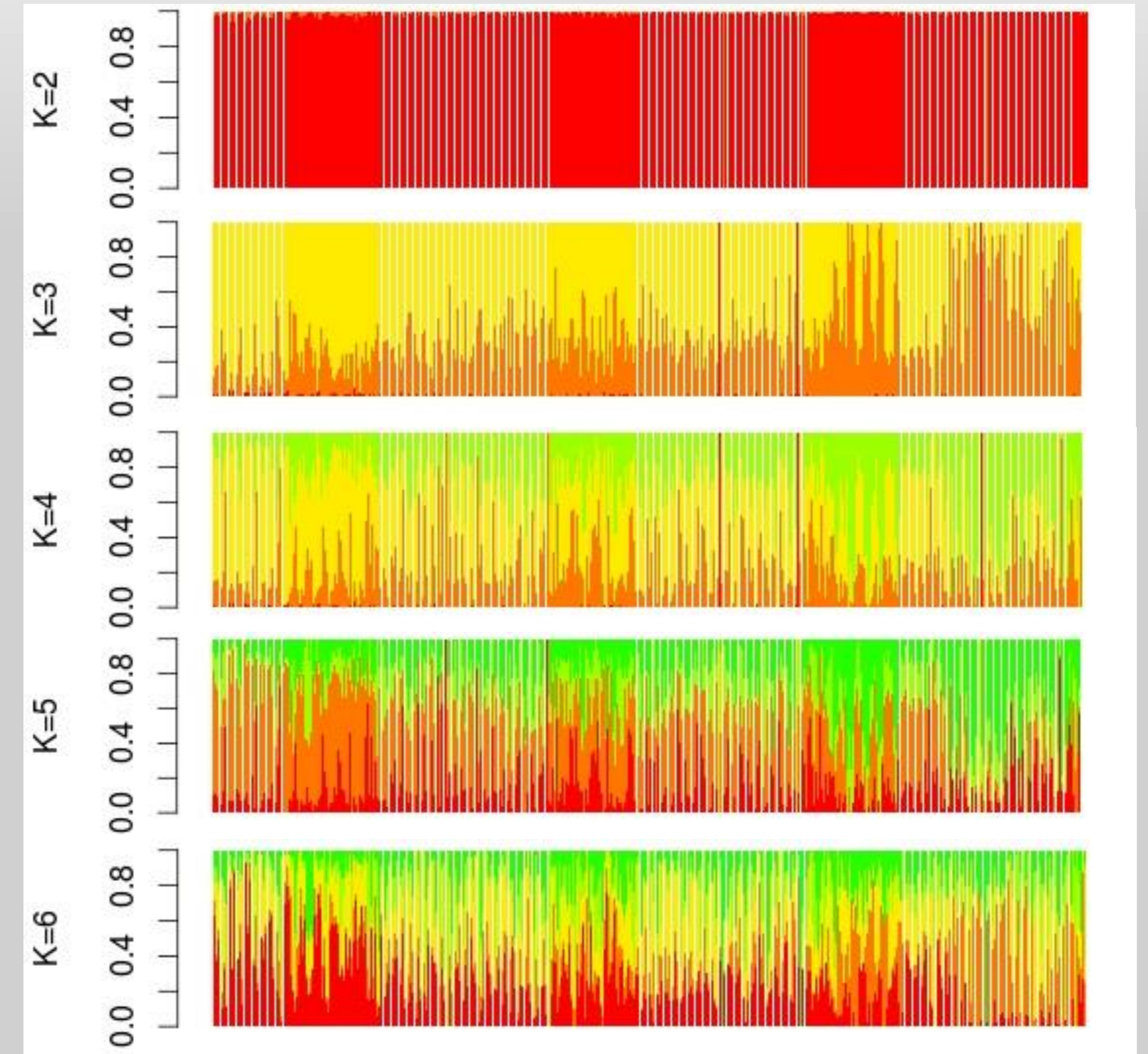
Principle component analysis



PCA analysis using Eigenvector 1 & 2, x & y axes respectively.

- US and CAN Holstein sires
- Europe (DEU, NDL) HOL sires
- Russian sires
- Russian HOL cows
- Russian BW cows

Structural analysis



Analysis for different K values.



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Quite high homogeneity of RBW and HOL populations can be considered from PCA and Structural analysis. Despite on some separation between Russian and North American bulls on PCA plot, cows of RBW and HOL breed stay in high admixture. All cows generally are placed between groups of sires and can be treated as mixture of their genetics. Neither no contrast clusters are standing out in shown Structure (Admixture) analysis using K from 2 to 6. Using this evidence we decide to use mixed model equation published by Kudinov (Kudinov et al. 2018) for single step genomic evaluations. Shown in paper mix model containing Herd – Year – Season fixed effect, which accounting difference between herds. This effect is enough for eliminating possible breeds difference.

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