



Detection of Selection Signatures in CIVIL and Large White pig breeds

Getmantseva L., Bakoev S., Kostyunina O., Traspov A., Prytkov Yu., Bakoev N.

L.K. Ernst Federal Science Center for Animal Husbandry, Podolsk, Russia.

Materials and methods

The research was carried out on Large White of three breeding centers (LW_1_New=16, LW_2_New=12, LW_3_New=15) and Civilskay (CIVIL=17), bred in the Chuvash Republic (Russia) on the basis of local pigs and Large White boars.

GeneSeek GGP Porcine HD BeadChip (San Diego, USA) was used.

A heatmap plot of genomic relationship matrix (GRM) was used to evaluate genetic variability between populations. The signals of diversifying selection were detected using Fst and Smoothing Fst (R package Lokern). QTLs and genes were identified and annotated in the Ensembl genome browser (Sscrofa 11.1) (<https://www.ensembl.org/index.html>), Panther 15.0 (<http://www.pantherdb.org/>) and QTLdb (<https://www.animalgenome.org/cgi-bin/QTLdb/index>).

Research objective

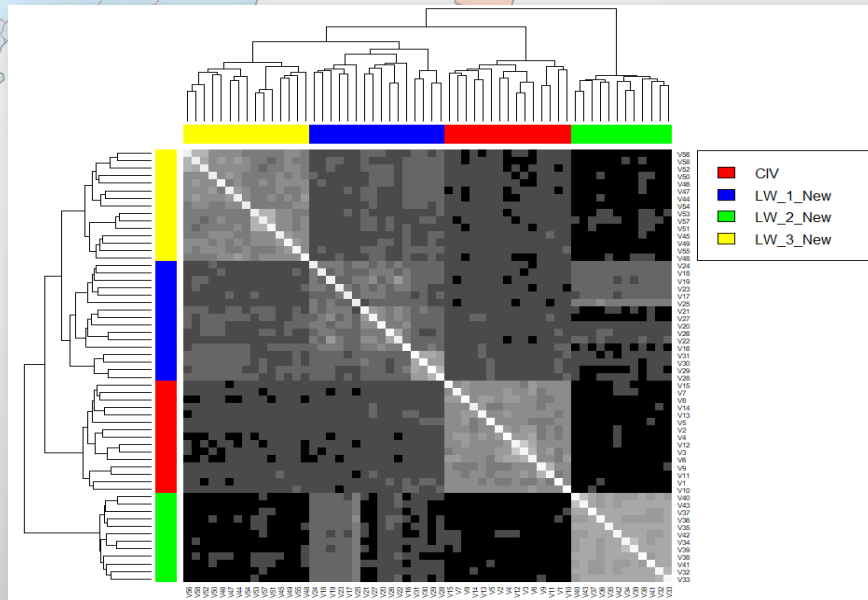
The purpose of this work is to determine the selection signatures in CIVIL pig relatively Large White breed.

Results

Data visualization from heatmapplot (Fig.) showed that all individuals are grouped in relation to their groups. However, the groups LW_1_New, LW_3_New and CIVIL were separated from LW_2_New. We have selected LW_1_New, LW_3_New and CIVIL to identify the selection signatures. After smoothing of the data by moving average, top 0.1% of the observations were considered as pinpointing CIVIL-specific selection signals. As a result, genome regions with strong selection signals on SSC1:214634036-217738857, SSSC2:137533941-138048506, SSC4:24655041-30832595, SSC7:27386432-28655399 and SSC8:55806826-56299366 were found.

In these areas, 535 QTLs have been identified, including 347 QTLs for Meat and Carcass Traits (the majority related to Backfat), 67 QTLs Production (Average daily gain or Body weight), 62 QTLs Health (Mean corpuscular volume, Actinobacillus pleuropneumoniae susceptibility et al.), 32 QTLs Reproduction (Teat number) and 27 QTLs Exterior (Leg conformation). In general, 32 genes are defined in these regions (SSC1-11; SSC2-5; SSC4-10; SSC7-3; SSC8-3) (Table). They are mainly involved in the following biological processes: metabolic (GO:0008152), cellular (GO:0009987) and biological regulation (GO:0065007).

Data visualization from heatmapplot



This research was supported by the Russian Scientific Foundation (RSF) within Project No. 19-16-00109.