

Genome-wide search for selection signatures in European wild boar

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INTRODUCTION: Searching of selection signatures in wild boar can help identify genomic regions associated with adaptation to environmental conditions.

The aim of our study was to search for selection signatures in European wild boars of Russia. We studied 66 wild boars from 20 different regions in four different climatic zones.

MATERIALS AND METHODS: DNA samples were genotyped using Porcine SNP60 BeadChips and GeneSeek SNP-chips (Illumina, San Diego, USA). Quality control procedures were carried out using PLINK v1.9; briefly, individuals with genotype call rates of < 0.8 and SNPs with call rates of < 0.3 or minor allele frequencies less than 0.99 were excluded. Also, we use “-LD” to make prune filtering in Plink. In total 37065 markers from full subset of SNPs were used for subsequent analysis. We remove close relatives with enabling option --rel-cutoff 0.75. After filtering 11271 SNPs remained and total genotyping rate of obtained dataset was 98.4%.

RESULTS: We subsequently identified SNPs, which had cross within log-likelihood ratio scores (LLRS) values > 2, in addition to integrated Haplotype Score (iHS) values > 2. After comparing 2 methods we detected 6 common elements in "iHS" and "LLRS" - ASGA0101898 – intergenic variant; H3GA0020102 – intergenic variant; ASGA0093835 - intron variant, RFX1 (RNA binding fox-1 homolog 1) is a Protein Coding gene, RNA-binding protein that regulates alternative splicing events by binding to 5'-UGCAUGU-3' elements, regulates alternative splicing of tissue-specific exons and of differentially spliced exons during erythropoiesis; ASGA0098807 - DSG3 (Desmoglein 3) is a Protein Coding gene, component of intercellular desmosome junctions, involved in the interaction of plaque proteins and intermediate filaments mediating cell-cell adhesion; MARC0064247 – non coding transcript exon variant ENSSCG00000035431, ASGA0020755 – intron variant, ARHGAP30 Rho GTPase activating protein 30).

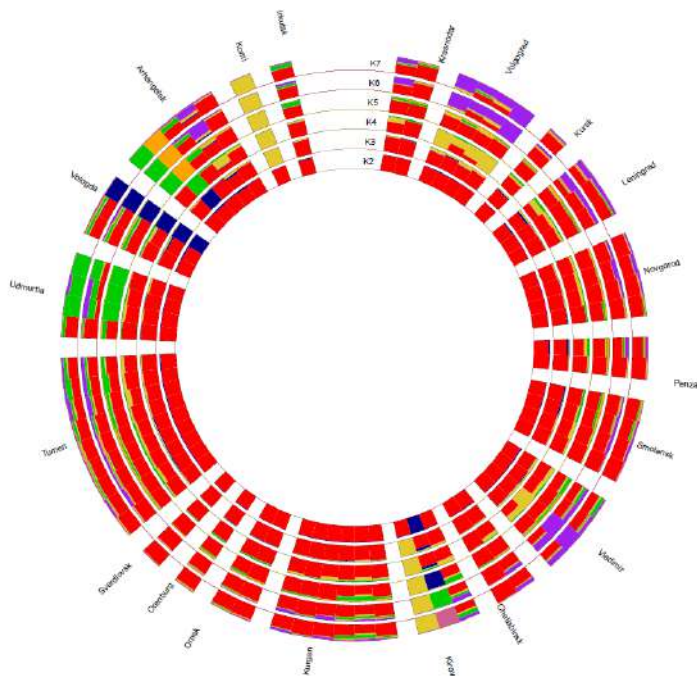


Fig 1. Admixture plot for Wild boars

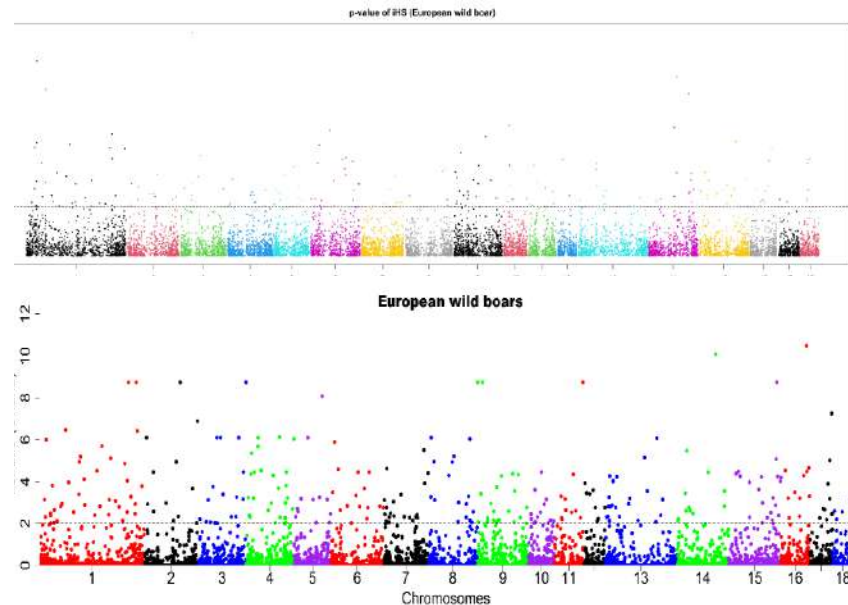


Fig.2. Manhattan plots for methods iHS and LLRS

Table 1. Common SNPs for methods iHS and LLRS

SNP	CHR	Sus scrofa build 10.2
ASGA0020755	4	97456653
ASGA0093835	3	36889519
ASGA0098807	6	107975607
ASGA0101898	6	60933494
H3GA0020102	7	16634919
MARC0064247	10	19258176

CONCLUSION: Our research result will help to reveal genetic regions associated with adaptation by the Russian wild boars.

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