



**Federal Research Center  
for Animal Husbandry  
named after Academy  
Member L.K. Ernst**

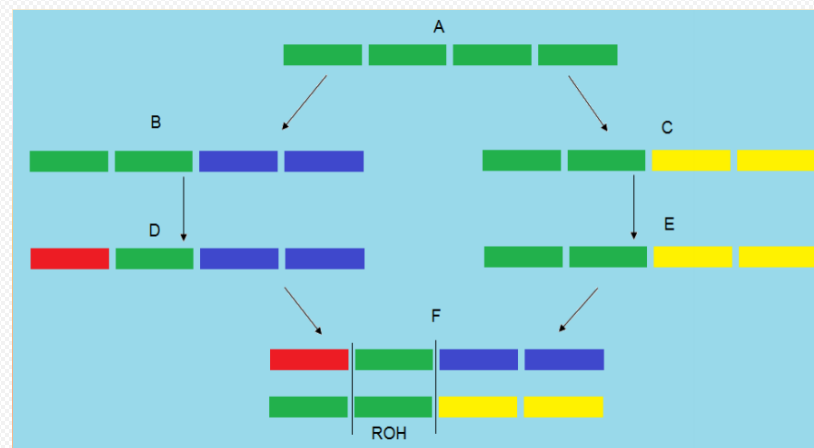


# **Identification of genomic regions in Large White pigs associated with climatic conditions**

*71st Annual Meeting of European Federation of Animal Science  
Porto, Portugal*

**EAAP-2020**

Runs of Homozygosity (ROH) are contiguous regions of the genome where an individual is homozygous across all sites



- Long ROH sites indicates a recent common ancestor
- Short ROH areas indicate a longer time interval from the common ancestor
- ROH has recently been increasingly used in the search for and identification of genomic sites associated with selection pressure. It is assumed that most of the genome is in the process of selection and that all functional sites in the genome are under pressure from selection or adaptive evolution, even in untranscribed areas.

The Large White pig is the mostly raised commercial pig breed around the world.

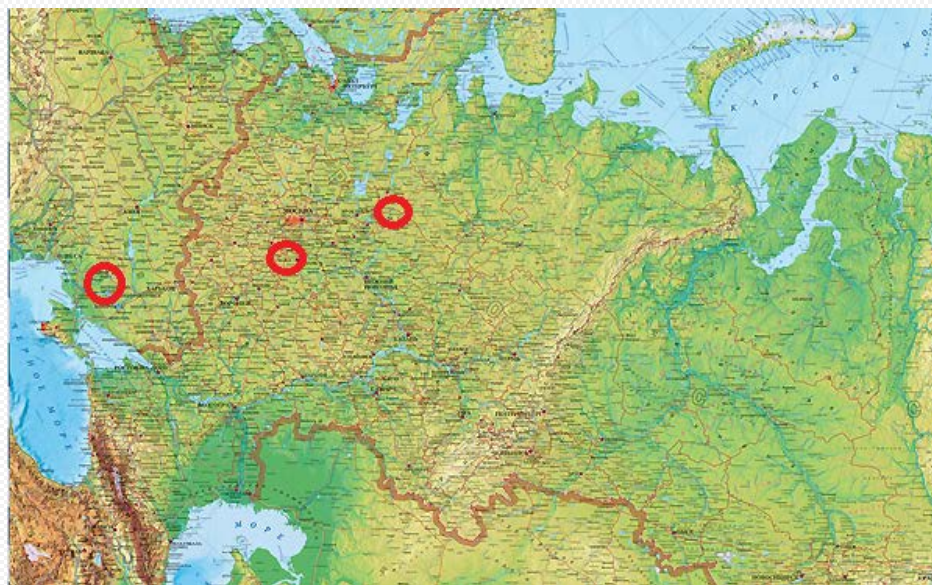
In 1923-1931 a livestock of Large White pigs was imported from England for developing domestic pedigree pig breeding.



The selection was aimed at adaptation of large white pigs to different ecological conditions in Russia due to different climatic conditions.

***In this connection, the hypothesis was advanced that in the process of formation of local type in Large White pigs and local breeds, one of the purposes of which was acclimatization, loci under pressure (signatures of selection) can be identified by ROH analysis.***

Research as conducted on pigs (n=210) of Large White breed of Russian selection or the breed created based on Large White breed.



According to the geographical location of the selected animals, they were distributed into three groups:

"Center" (Civil (n=33), LW\_Belorus (n=32), LW\_Konst (n=32))

"North" (LW\_UB (n=39), URZ (n=24), A4 (n=20))

"South" (UBS (n=30))

# Distribution of homozygosity areas in pigs of different breeds

Table 1. Distribution of homozygosity areas in pigs of different breeds

ROH	Civil	LW_A4	LW_Belorus	LW_Konst	LW_UB	UBS	URZ
<2	793	562	902	927	1182	854	1862
2-4	776	634	1108	1201	1278	1064	2081
4-8	355	363	653	592	760	625	906
8-16	97	193	360	327	338	339	239
>16	7	92	177	125	120	166	26
Total	2028	1844	3200	3172	3678	3048	5114

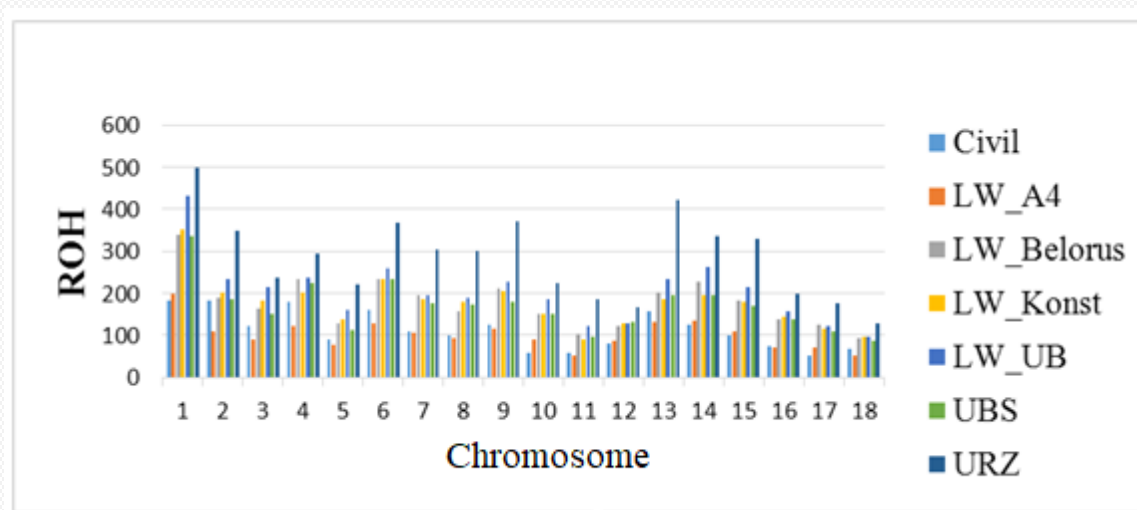


Figure 1. Distribution of ROH by chromosomes

## Distribution of ROH in groups "Center", "North", "South"

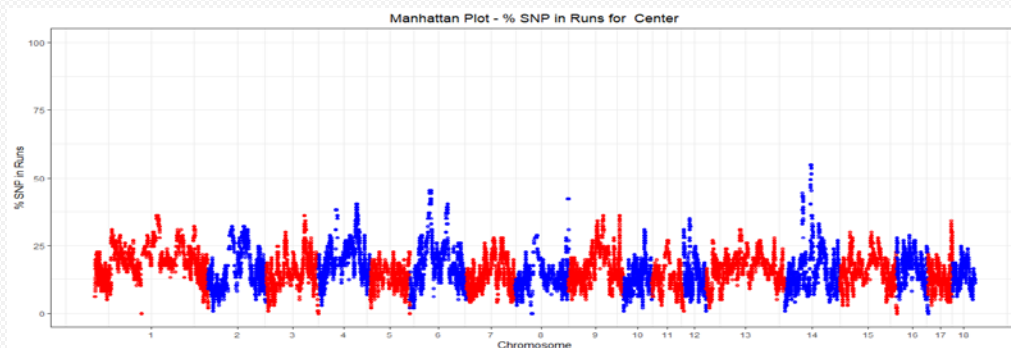


Figure 2.  
ROH distribution in the  
pigs of the "Center" group

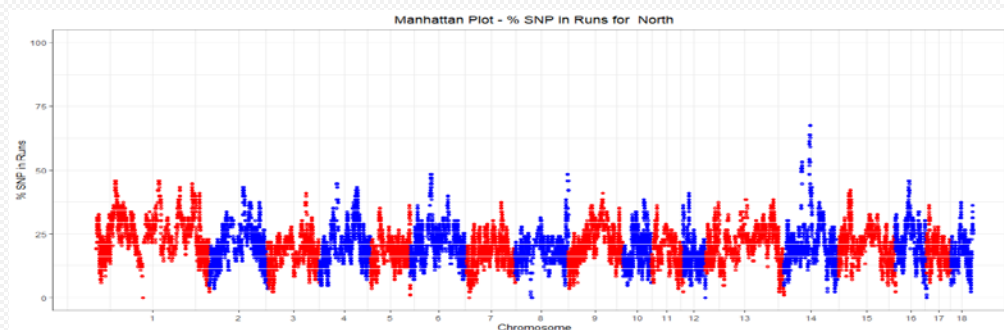


Figure 3.  
ROH distribution in  
the pigs of the  
«North" group

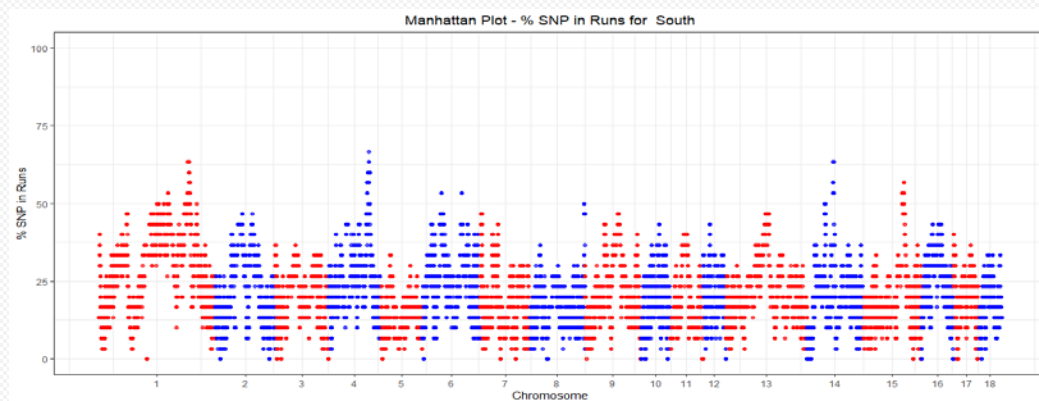


Figure 4.  
ROH distribution in the  
pigs of the "South" group

The X-axis represents the distribution of ROH across the chromosomes, while the Y-axis represents the amount of SNP (%) overlapping ROH common to the population

## Distribution of ROH in chromosomes SSC1, SSC4 and SSC14



Figure 5. ROH distribution in SSC1



Figure 6. ROH distribution in SSC4

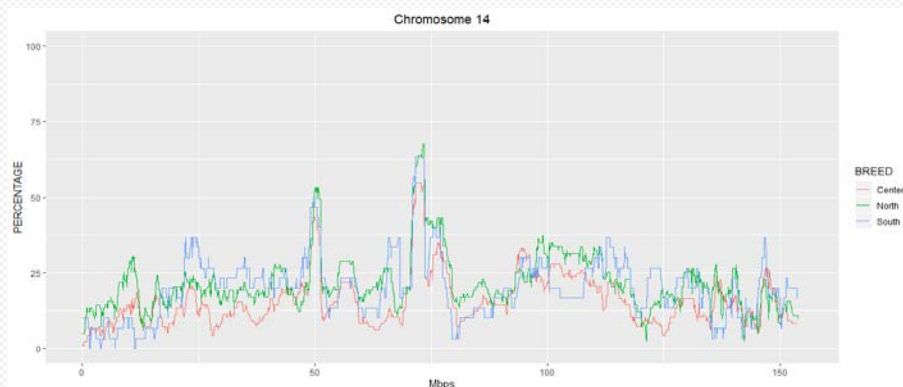


Figure 7. ROH distribution in SSC14

The X-axis represents the distribution of ROH across the chromosomes, while the Y-axis represents the amount of SNP (%) overlapping ROH common to the population

Long ROH (over 10 Mb) occur in more than 40% of the animals in the group

Table 2: Identified ROH over 10 Mb

Group	Start_SNP	End_SNP	Chr	nSNP	from	to	Mb
North	ALGA0002836	ALGA0003456	1	214	45342772	59292000	13,94923
<b>North</b>	<b>H3GA0002996</b>	<b>WU_10.2_1_180054118</b>	<b>1</b>	<b>123</b>	<b>163762514</b>	<b>180054118</b>	<b>16,2916</b>
North	ASGA0005568	WU_10.2_1_237432746	1	106	225825860	237432746	11,60689
North	ASGA0006218	WU_10.2_1_277756033	1	144	266185886	277756033	11,57015
South	ALGA0005754	DIAS0004572	1	72	132595455	144135159	11,5397
<b>South</b>	<b>WU_10.2_1_153717318</b>	<b>ASGA0093974</b>	<b>1</b>	<b>267</b>	<b>153717318</b>	<b>183880998</b>	<b>30,16368</b>
South	BGIS0003207	M1GA0001254	1	164	183948686	201473261	17,52458
South	H3GA0003484	ALGA0007561	1	68	213014666	223695380	10,68071
South	ALGA0007572	ALGA0008117	1	239	224937381	249045084	24,1077
South	MARC0008493	MARC0041502	13	149	99462031	116957243	17,49521
South	ALGA0086425	WU_10.2_15_115633164	15	126	105253199	115633164	10,37997
South	MARC0101455	WU_10.2_2_78468204	2	123	56469735	78468204	21,99847
South	MARC0051072	WU_10.2_2_105914959	2	131	95851681	105914959	10,06328
South	ALGA0026850	WU_10.2_4_113399137	4	231	101799859	113399137	11,59928
South	MARC0052953	6_59527435	6	131	46687771	59527435	12,83966
South	ALGA0053711	ALGA0054179	9	251	76479537	97314182	20,83465

ROH on SSC1 (163762514...180054118) in more than 40% of pigs in groups  
"South" and "North"

- ***CBLN2*** (cerebellin 2 precursor) NC\_010443.4 (167191334..167198494)
- ***CNDP2*** (carnosine dipeptidase 2) NC\_010443.4 (165529517..165548510)
- ***DOK6*** (docking protein 6) NC\_010443.4 (169782518..170053245, complement)
- ***FBXO15*** (F-box protein 15) NC\_010443.4 (165983435..166232074)
- ***TSHZ1*** (teashirt zinc finger homeobox 1) NC\_010443.4 (164830580..164837213)
- ***ZNF407*** (zinc finger protein 407) NC\_010443.4 (165164144..165186085, complement)
- ***ZNF516*** (zinc finger protein 516) NC\_010443.4 (163849431..163946769)

THANK YOU FOR YOUR ATTENTION

Getmanseva L., Bakoev S.,  
Kostunina O., Traspov A.,  
Bakoev N., Prytkov Y.

*ilonaluba@mail.ru*

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