



Analysis of genomic heterozygosity-rich regions in selected local horse breeds

Vostra-Vydrova Hana, *Moravcikova Nina, R. Kasarda Radovan,*
Halvonik Adrian, Hofmanova Barbora,

Vostry Lubos

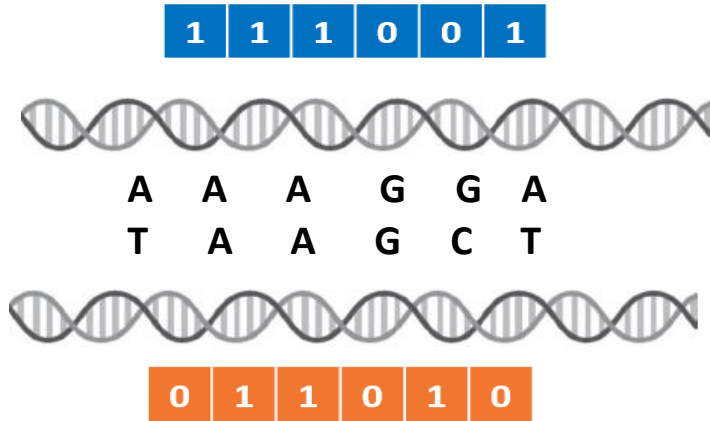
Czech University of Life Science Prague - Slovak University of Agriculture in Nitra

Introduction

Heterozygosity-rich regions (HRR) are genomic regions with high heterozygosity.

The heterozygosity-rich regions complement homozygosity measure.

The analysis of heterozygosity in livestock is less frequent than homozygous patterns.



-AT-AA-AA-GG-GC-AT-TA-CG-GC

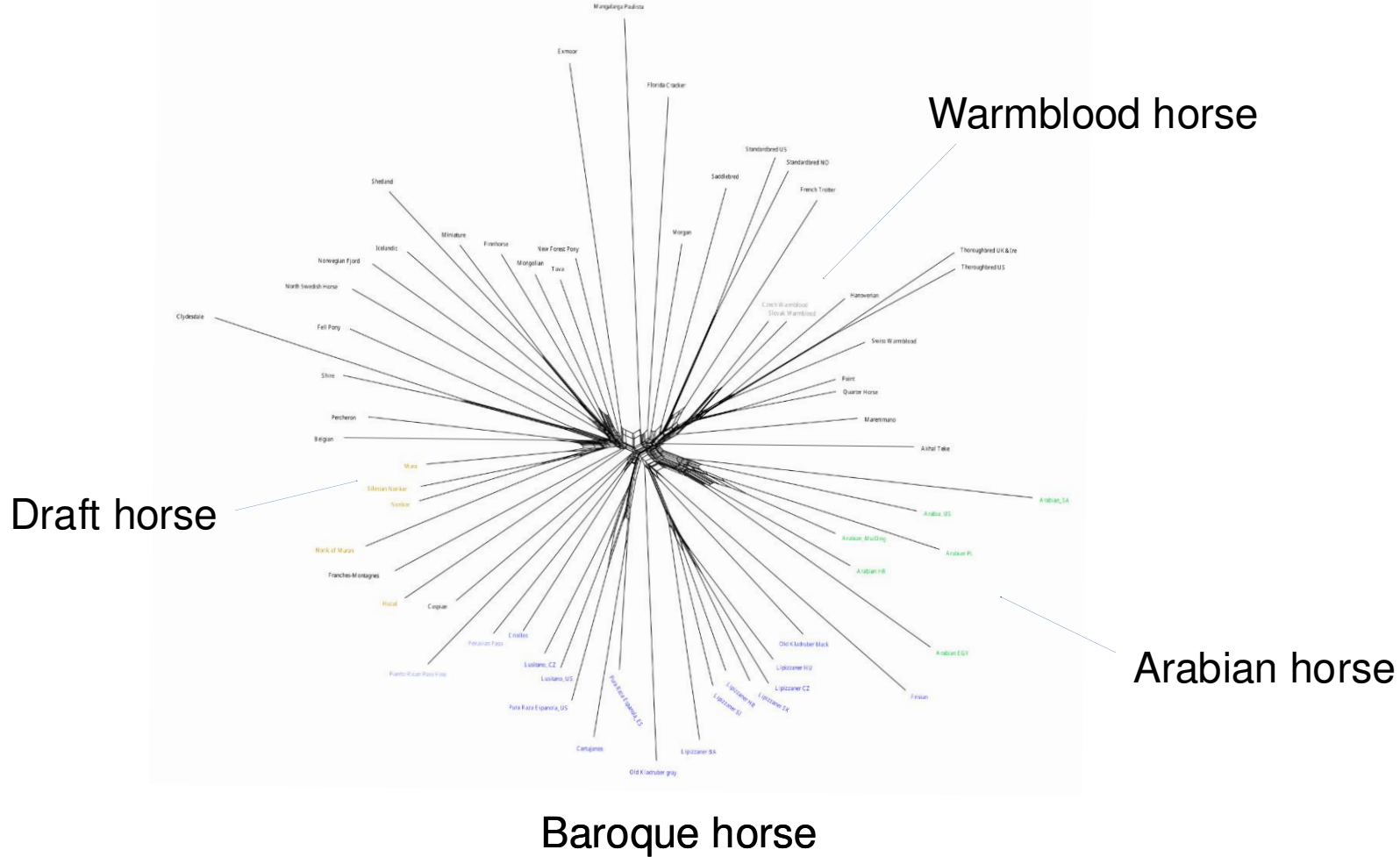
1 2 2 0 1 1 1 1 1

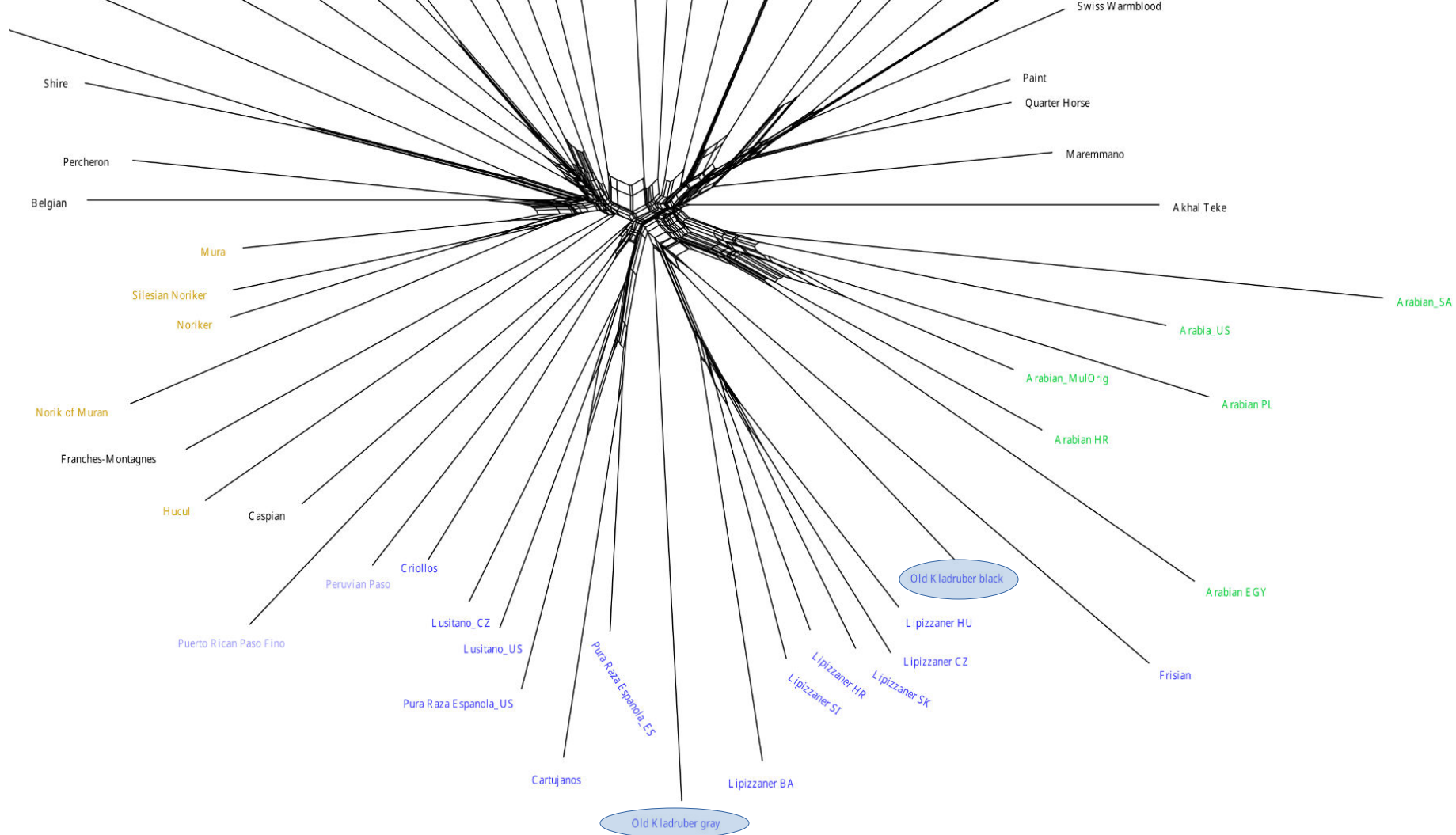


ROH



HRR





Analysed breeds



Old Kladruber horse

Gray: 284



Black: 119



Lipizzaner horse

362 individuals



Arabian

71 individuals



Warmblood

54 individuals



Mura

24 individuals



Noriker of Muran

24 individuals



Silesian Noriker

174 individuals,

Aims of the study

Analysis of **genomic heterozygosity-rich regions** in selected **local horse breeds** using **high-throughput genomic data**.

1. investigate and characterize the patterns of heterozygosity in seven horse breeds
2. identification specific islands based on different type of analysed breeds



DetectRUNS – consecutive methods

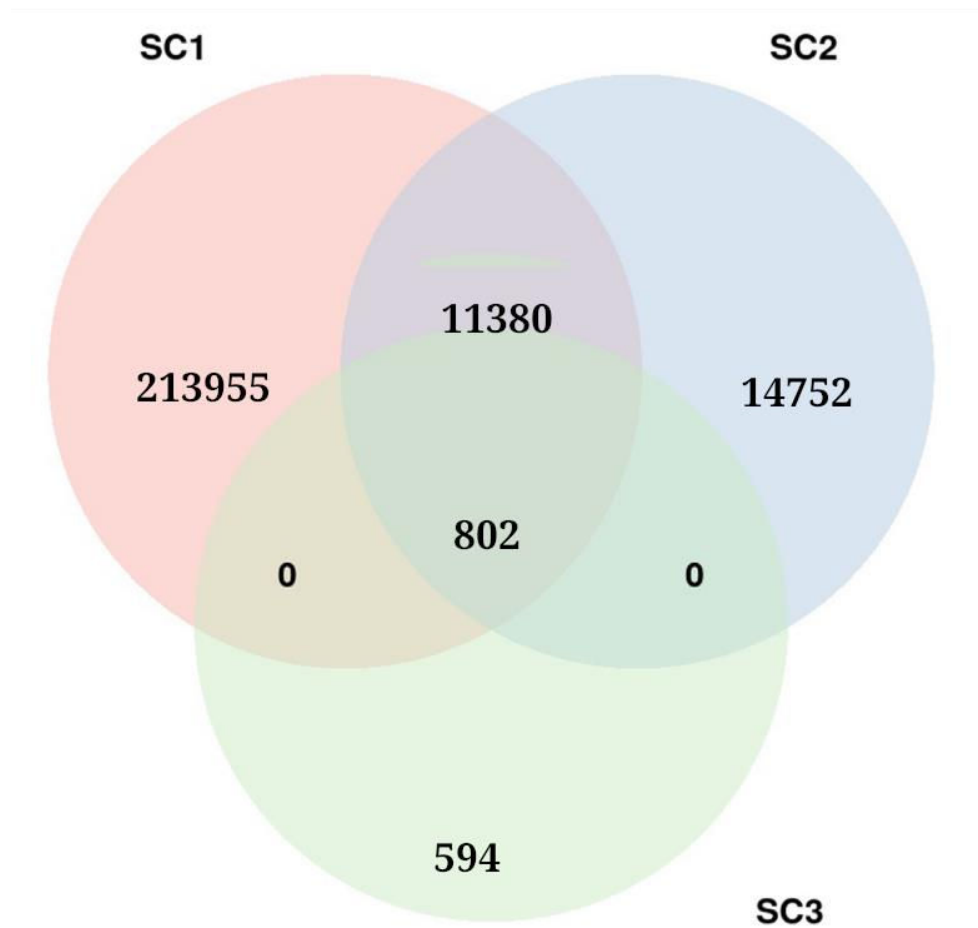
three scenarios

Scenario 1 (SC1): the minimum number of SNP in an HRR set to 10
1 missing SNP and 2 homozygous SNPs

Scenario 2 (SC2): the minimum number of SNP in an HRR set to 15
1 missing SNP and 2 homozygous SNPs

Scenario 3 (SC3): the minimum number of SNP in an HRR set to 15
no missing SNP and **no** homozygous SNPs

Results: HRR genomic regions



Results: HRR genomic regions

Breed	No. HRR	Mean No. HRR	No. individual	% of genome coverd by HRR	Longest HRR
Arabian	1909	26.89	71	0.82	1582554
Warmblood	2437	45.13	54	1.42	1988834
Silesian noriker	1464	8.41	174	0.25	2119295 
Noriker of Muran	250	10.41	24	0.29	1472695
Mura	350	10.94	32	0.36	1446890 
Old Kladruber - gray	5404	15.62	346	0.45	1717081
Old Kladruber – black	1673	14.06	119	0.42	1679732
Lipizzaner	3472	15.50	224	0.46	1655437

Results: HRR genomic regions

Breed	No. HRR	Mean No. HRR	No. individual	% of genome coverd by HRR	Longest HRR
Arabian	1909	26.89	71	0.82	1582554
Warmblood	2437	45.13	54	1.42	1988834
Silesian noriker	1464	8.41	174	0.25	2119295
Noriker of Muran	250	10.41	24	0.29	1472695
Mura	350	10.94	32	0.36	1446890
Old Kladruber - gray	5404	15.62	346	0.45	1717081
Old Kladruber – black	1673	14.06	119	0.42	1679732
Lipizzaner	3472	15.50	224	0.46	1655437

Results: HRR genomic regions

Number of Heterozygous-Rich Regions (HRRs) for class of length for each breed

Mbps	Arabian	Warmblood	Silesian noriker	Noriker of Muran	Mura	OKH - gray	OKH – black	Lipizzaner
0 - 0.5	325	458	301	55	70	1106	321	702
0.5 - 1	1405	1706	1043	168	198	3959	1181	2443
1 - 2	179	273	119	27	26	339	171	327
2 - 4	0	0	1	0	0	0	0	0

Results: HRR genomic regions

Number of Heterozygous-Rich Regions (HRRs) for class of length for each breed

Mbps	Arabian	Warmblood	Silesian noriker	Noriker of Muran	Mura	OKH - gray	OKH – black	Lipizzan er
0 - 0.5	325	458	301	55	70	1106	321	702
0.5 - 1	1405	1706	1043	168	198	3959	1181	2443
1 - 2	179	273	119	27	26	339	171	327
2 - 4	0	0	1	0	0	0	0	0

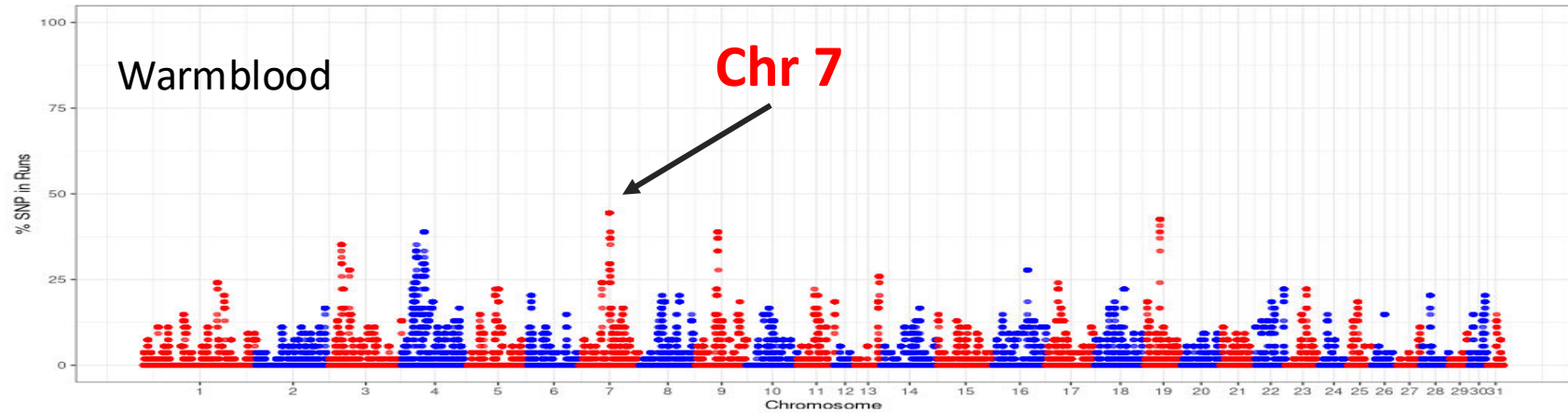
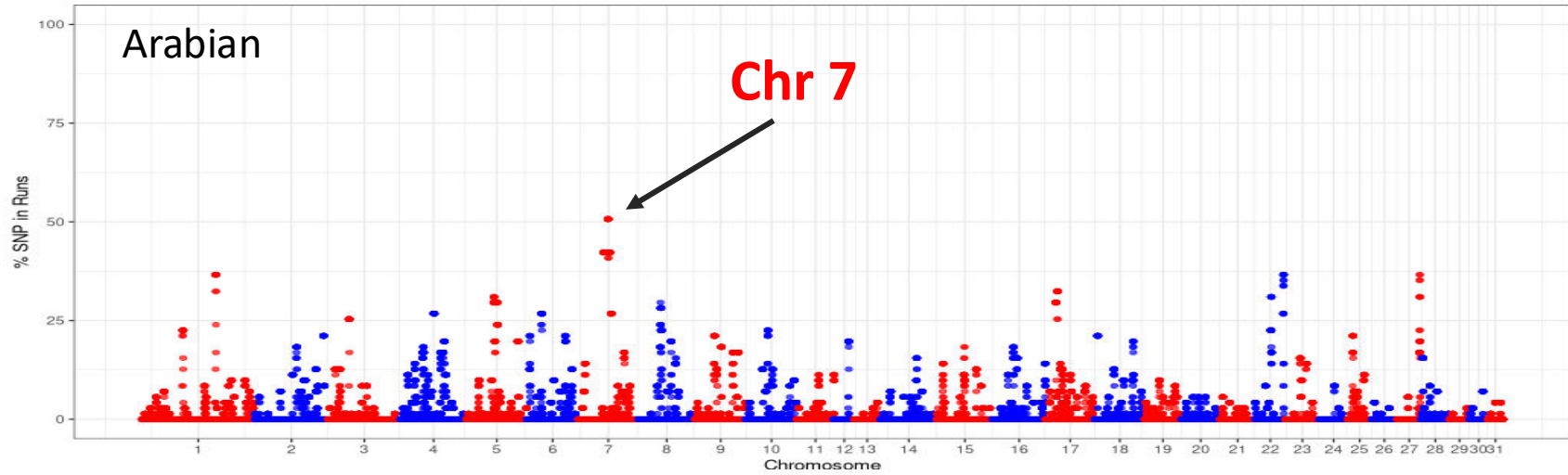


Results: HRR genomic regions

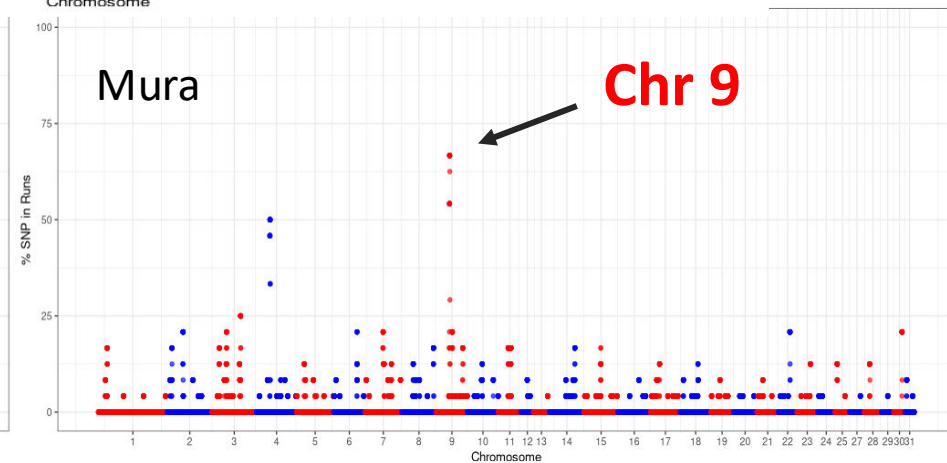
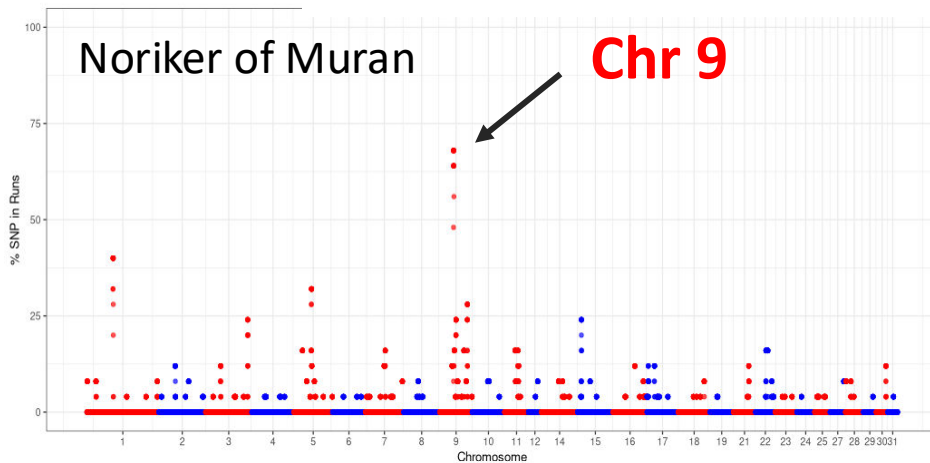
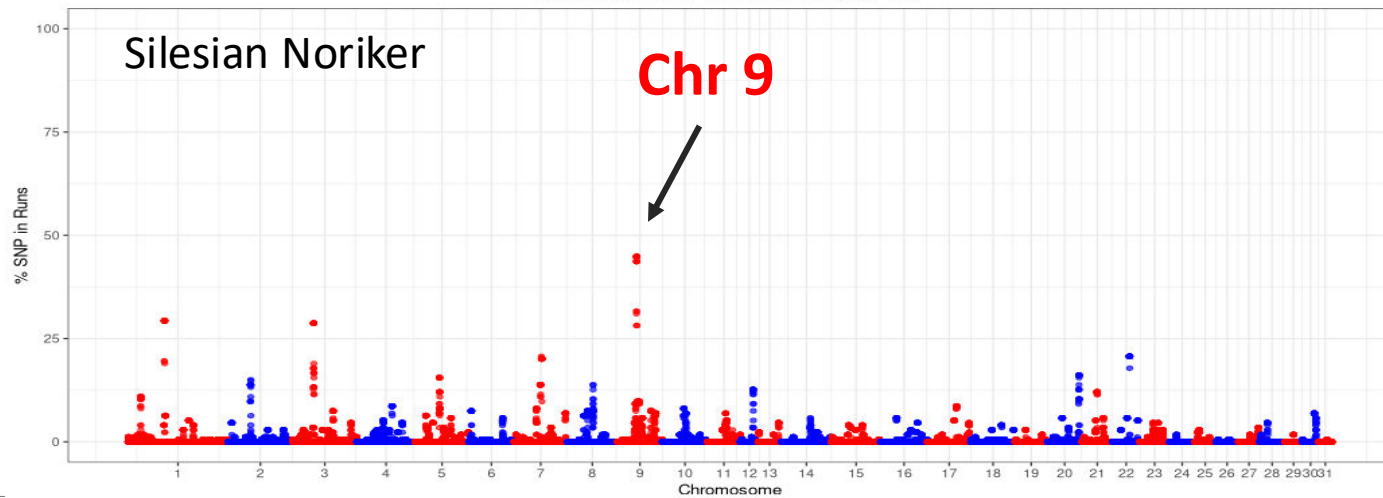
Number of Heterozygous-Rich Regions (HRRs) for class of length for each breed

Mbps	Arabian	Warmblood	Silesian noriker	Noriker of Muran	Mura	OKH - gray	OKH - black	Lipizzaner
0 - 0.5	325	458	301	55	70	1106	321	702
0.5 - 1	1405	1706	1043	168	198	3959	1181	2443
1 - 2	179	273	119	27	26	339	171	327
2 - 4	0	0	1	0	0	0	0	0

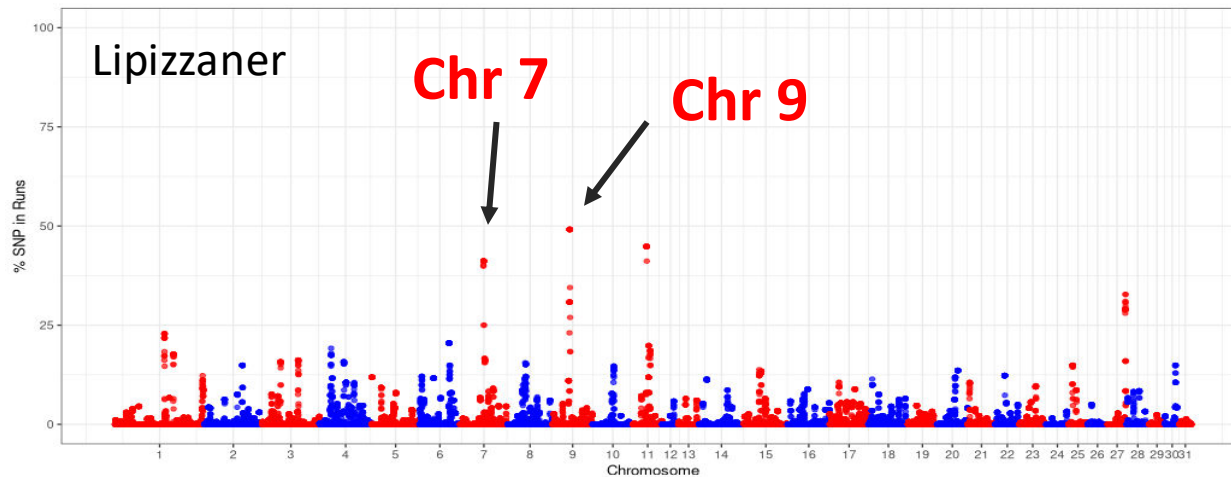
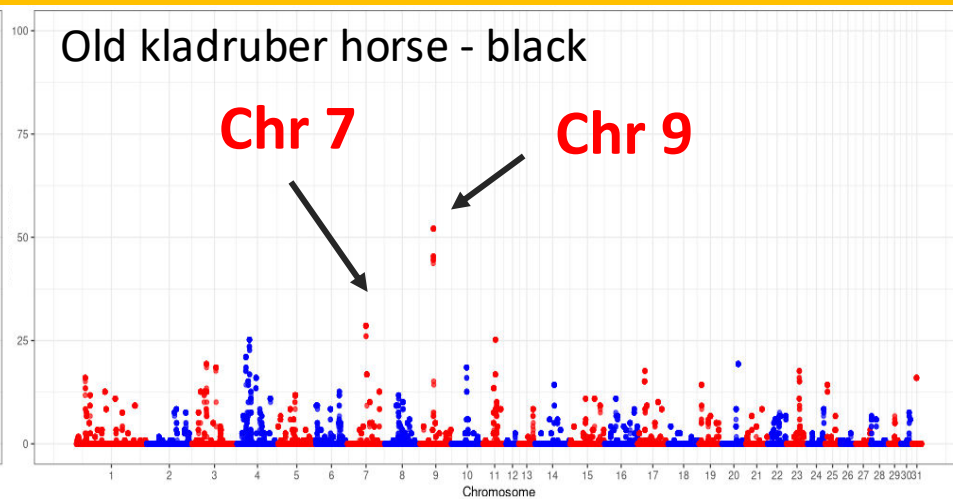
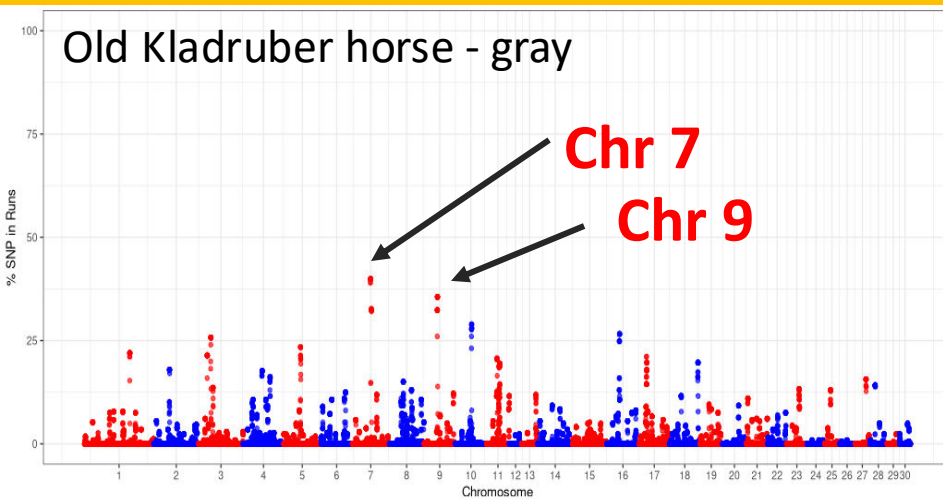
Results: HRR genomic regions



Methods: HRR genomic regions



Methods: HRR genomic inbreeding level



Conclusions

- ✓ The highest proportion of HRR was found in Warmblood horses
- ✓ The lowest proportion of HRR was found in draft horses
- ✓ HRRs with lengths from 0.5 to 1 Mbps showed the highest frequency
- ✓ Different HRR were found in different groups of horses
- ✓ OKH showed common HRR islands as draft and warm-blooded horses.



Acknowledgments

**any
Questions ?**

**Thanks for
your
attention!**



The study was supported by projects *GACR 24-14325L, QL25020022, and APVV-20-0161, APVV-17-0060*