



University of Ljubljana



Genomic analysis of diversity and population structure of baroque horse breeds in Czech Republic and Slovakia

Vostra-Vydrova Hana, Moravcikova Nina, Kasarda Radovan,
Shihabi Mario, Brajkovic Vladimir, Hofmanova Barbora, Ferme Tamara,
Dovč Peter, Zorc Minja, Rogić Biljana, Cubric-Curik Vlatka, Curik Ino,
Vostry Lubos

Czech University of Life Science Prague - Slovak University of Agriculture in Nitra
- University of Ljubljana - University of Zagreb, Faculty of Agriculture - University of Banja
Luka - Hungarian University of Agricultural and Life Science

History of Baroque horse in Central Europe



Habsburg monarchy



Old Kladruuber horse
the carriage horse



Lipizzaner horse
the riding horse

Regeneration of Old Kladrub horse

Serious reduction in 1925-1931

Black variety - tree stallions - half-siblings and two mares - preserved by 1941

Used breeds:

Lipizzaner (1946, Dakovo - CHR), Frisian horses (1966, NL), Lusitano horse (1968, PT)

Regeneration successfully completed 1974



Genesis of Baroque horses



Analysed breeds



Old Kladruber horse

355 individuals; 53k SNP

Gray: 284

Black: 71



Lipizzaner horse

362 individuals; 53k SNP

BiH: 42; Slo: 235; SK: 62; CZ: 23



Andalusian horse

18 individuals 49k SNP

Petersen et al. (2013)



Lusitano horse

39 individuals, 38k SNP

CZ: 15, Petersen et al. (2013): 24



Friesian horse

20 individuals, 66k SNP

Aims of the study

Analysis of **genetic diversity and admixture** in **Baroque horse populations** using high-throughput **genomic data**.

1. To estimate population structure and admixture
2. To estimate genomic inbreeding (F_{ROH})
3. To estimate current LD effective population size
4. To estimate the historical LD effective population size & the change observed in the last 10 generations

Methods: ROH genomic inbreeding level

Ferenčaković et al. *Genetics Selection Evolution* 2013, 45:42
<http://www.gsejournal.org/content/45/1/42>

GSE Genetics
Selection
Evolution

RESEARCH

Open Access

Estimating autozygosity from high-throughput information: effects of SNP density and genotyping errors

Maja Ferenčaković¹, Johann Sölkner^{2*} and Ino Curik¹

$$F_{ROH} = \frac{\sum_{j=1}^n L_{ROH_j}}{L_{total}}$$

F_{ROH} 2-4Mb

F_{ROH} 4-8Mb

$F_{ROH} > 8$

detectRUNS



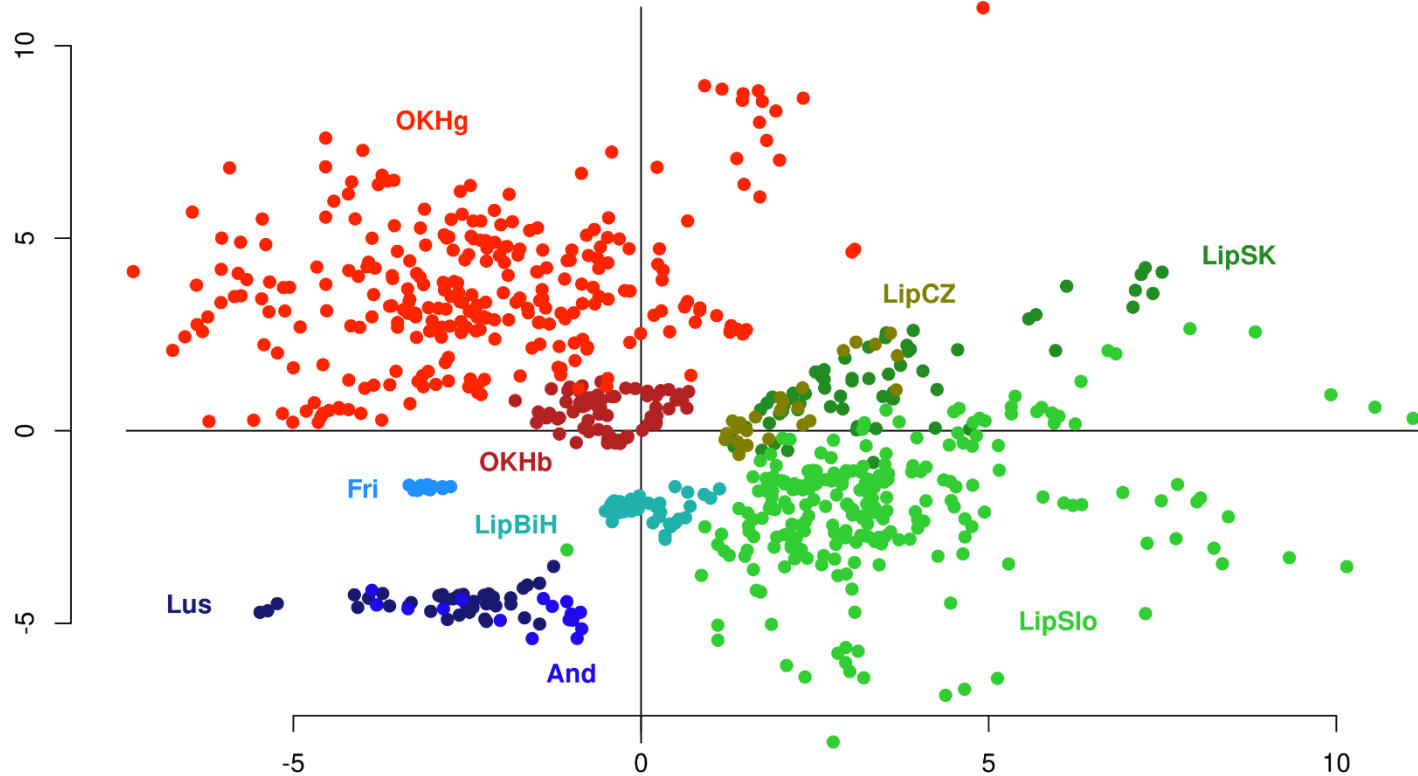
Methods: Population structure and admixture

- Variational autoencoder (VAEs) implemented in the POPVAE software (Battey et al., 2021)
- Population structures were assessed with Admixture 1.3.0 (Alexander et al., 2009)

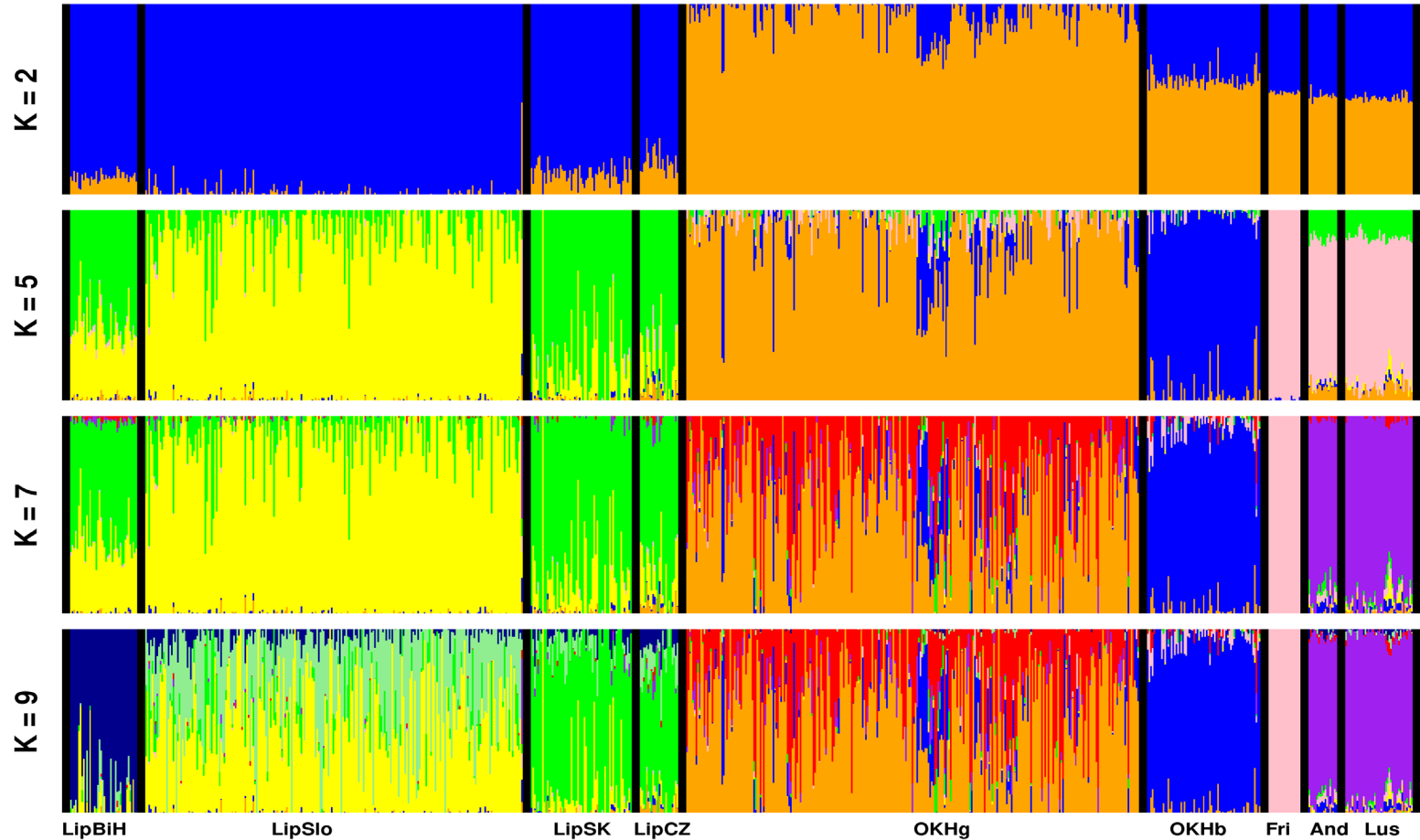
Methods: Current and historical effective population size

- Linkage disequilibrium, GONE & currentNe -> softwares (Santiago et al., 2021, 2024)

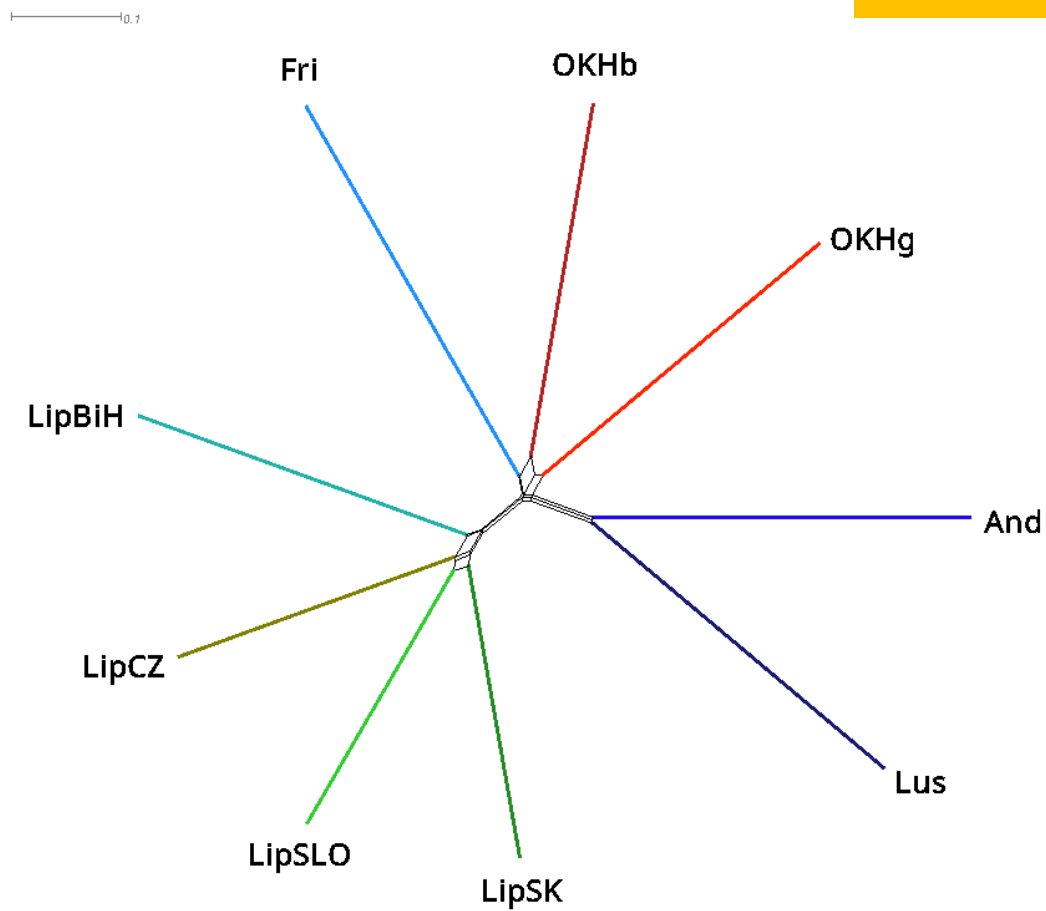
Results: Relatedness between horse populations



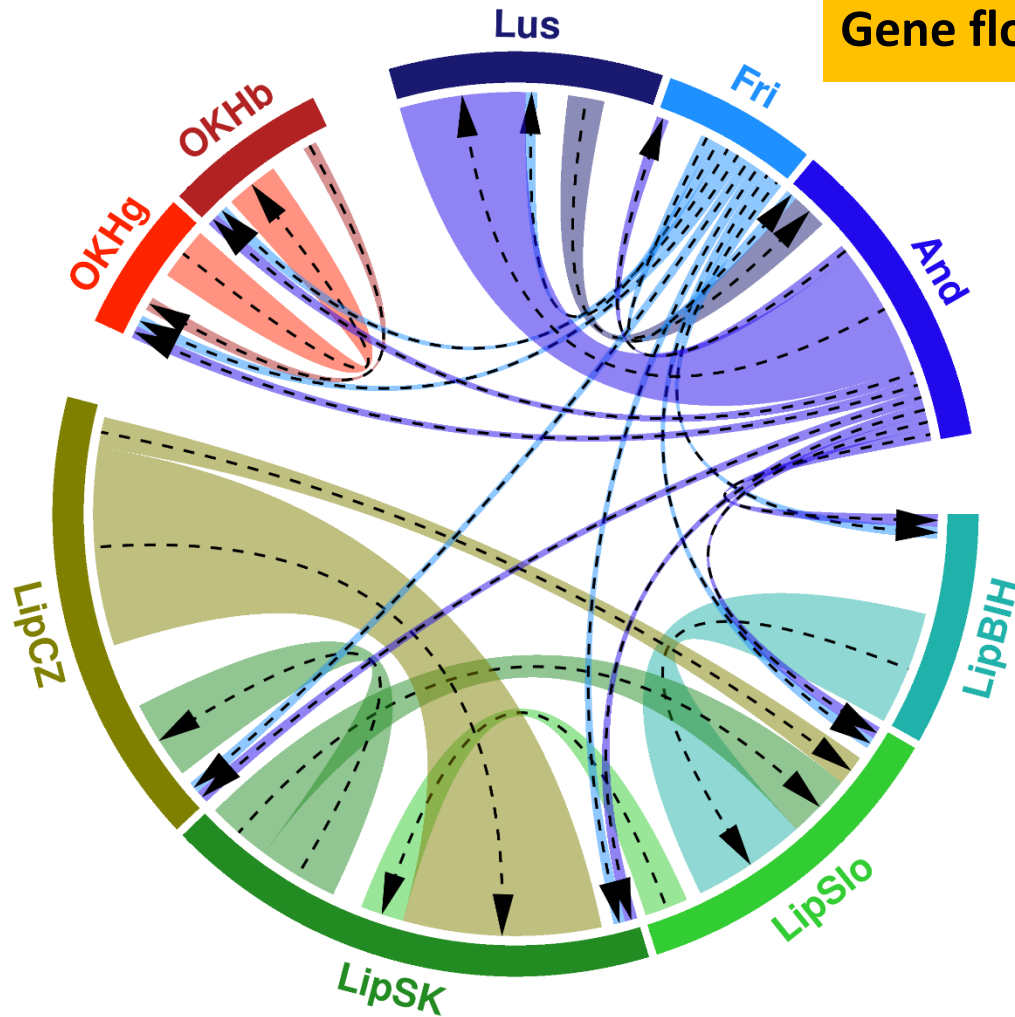
Results: Bayesian clustering approach



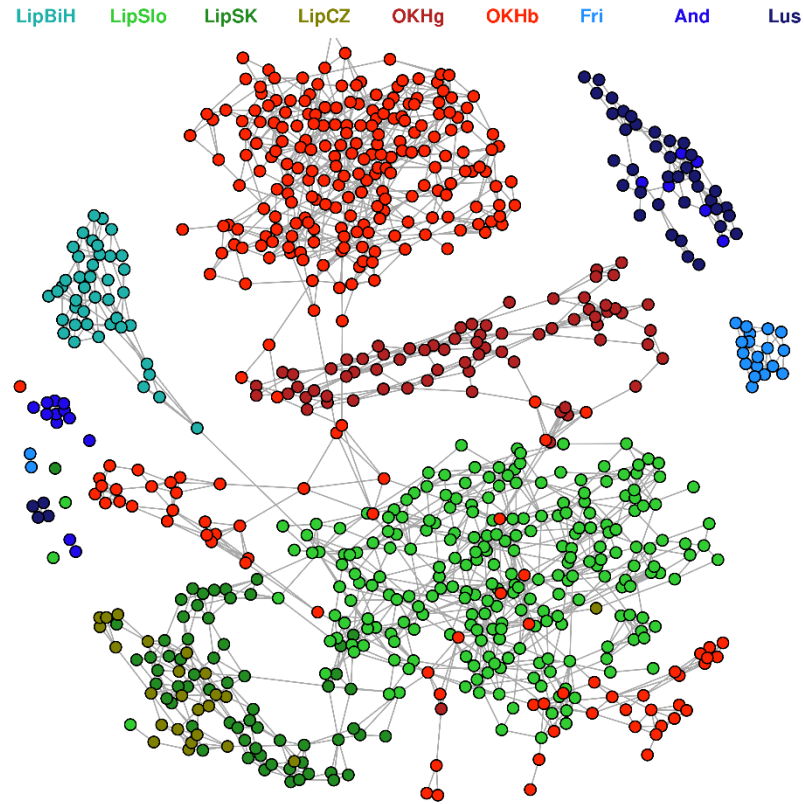
NeighborNet network



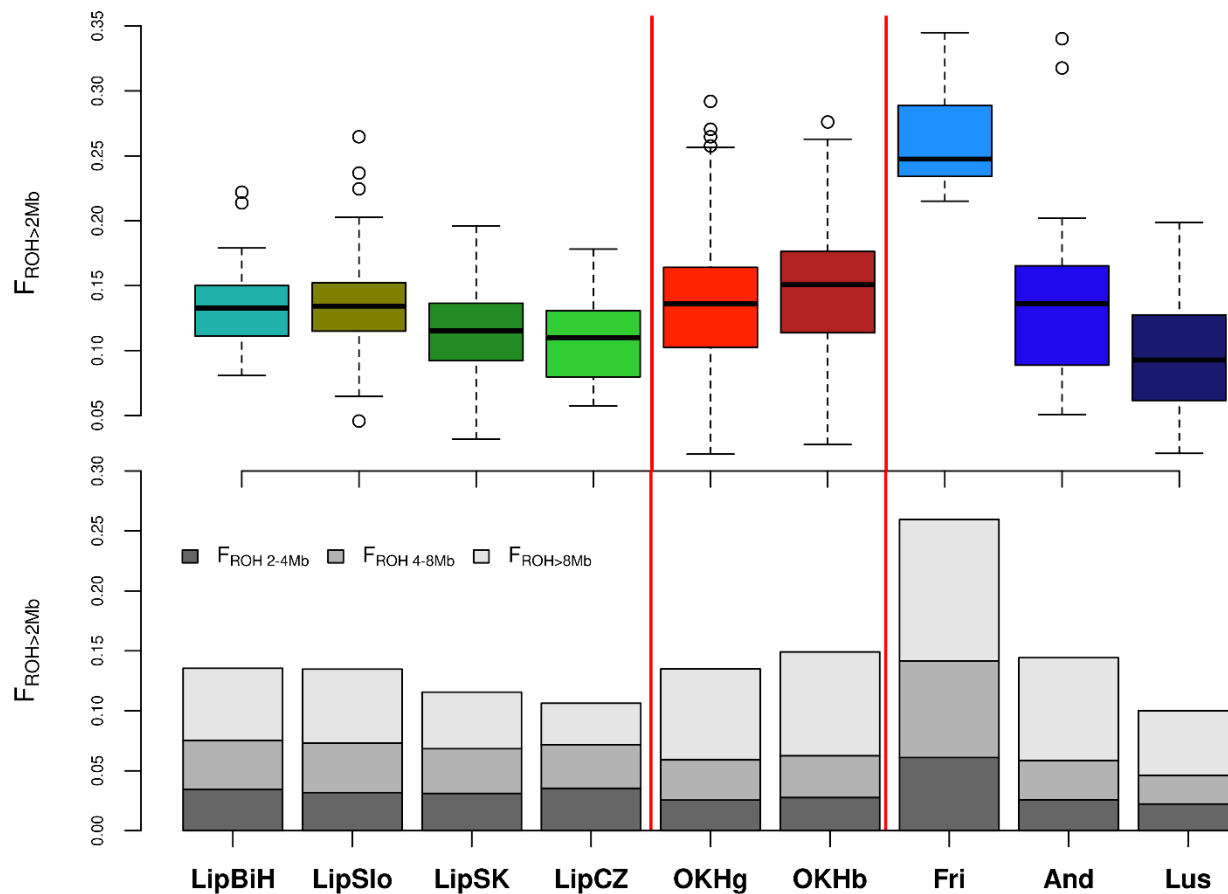
Gene flow between horse breeds



Network visualisation



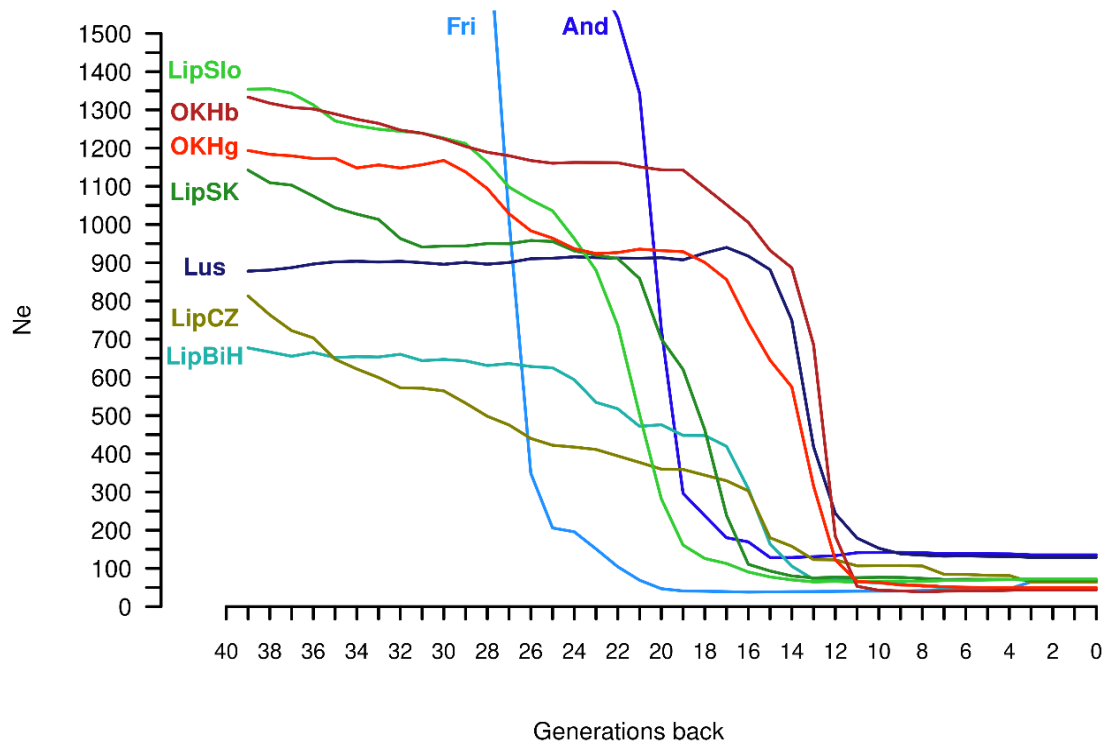
Results: Genomic inbreeding



LD - effective population size (GONE)

Breed	N _{eLD} (GONE)	N _{eLD} (currentNe)
LipBiH	46 (33-57)	33 (27 -39)
LipCZ	64 (37-55)	19 (15-24)
LipSK	69 (59-81)	37 (32-41)
LipSlo	72 (68-77)	70 (67-74)
OKHb	44 (38-51)	56 (49-63)
OKHg	49 (48-53)	58 (56-58)
Fri	65 (47-87)	85 (57-126)
Lus	129 (97-172)	107 (81-144)
And	135 (85-214)	64 (41-58)
OKH	53 (51-55)	32(32-32)
Lip	100 (95-105)	88 (85-90)

Historical N_{eLD}



Conclusions

- ✓ Hight admixture among populations (migrations)
- ✓ OKG shows the same genetic population parameters as other breeds
- ✓ Relatively high inbreeding ($F_{ROH>2Mb} > 0.10$) observed in all populations
- ✓ N_{eLD} ranging from 43 (LipBiH) to 129 (Lus) - all breeds are sustainable
- ✓ In last 18 - 12 generations all breeds have gone through a significant Bottleneck



It would be of interest to analyse larger number of animals (And, Fri) or subpopulations (Lip: AT, HUN)

Acknowledgments

**any
Questions ?**

**Thanks for
your
attention!**



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