Population structure and recent migration in closely related Old Kladruber and Lipizzan populations

Nina Moravčíková[1], Luboš Vostrý[2], Hana Vostrá-Vydrová[2], Ondrej Kadlečík[1], Radovan Kasarda[1]

[1]Department of Animal Genetics and Breeding Biology, Slovak University of Agriculture in Nitra, Tr. A. Hlinku 2, 949 76 Nitra, Slovak Republic

[2]Department of Genetics and Breeding, Czech University of Life Sciences Prague, Kamycka 129, 165 21 Praha 6-Suchdol, Czech Republic

67th Annual Meeting of the European Federation of Animal Science
Belfast UK, 29 Aug – 2 Sept 2016

Outline

- Analysis of the genetic substructure of Old Kladruber horse population in relation to the historically related Lipizzan breed based on microsatellite data:

  ➢ Assessment of genetic variability

  ➢ Analysis of populations subdivision

  ➢ Determination of genetic relationships

  ➢ Estimation of migration events

Material and methods

Analysed individuals
- **270 Old Kladruber horses**
(175 grey, 95 black variety)

- **418 Lipizzan horses**
(61 Slovak, 357 Slovenian)

Genetic variability
- Heterozygosity, PIC, F-statistic
- AMOVA (analysis of molecular variance) using 10,000 permutations

Material and methods

Populations subdivision and genetic relationships
➢ DAPC (discriminant analysis of principal components)

➢ Bayesian clustering method implemented in **STRUCTURE**
  ▪ 100,000 burn-in period
  ▪ 1,000,000 MCMC replication

➢ Nei,s genetic distance

Migration events
➢ recent migration rates
➢ construction of the ancestry graph

Results

Genetic variability analysis

Population	H_O	Gene diversity	MNA	F_{IS}
Old Kladruby grey (OKg)	0.673	0.673	5.615	-0.004
Old Kladruby black (OKb)	0.652	0.654	7.000	0.008
Slovakian Lipizzan (LSK)	0.685	0.669	6.385	0.081
Slovenian Lipizzan (LSLO)	0.654	0.705	7.077	-0.021

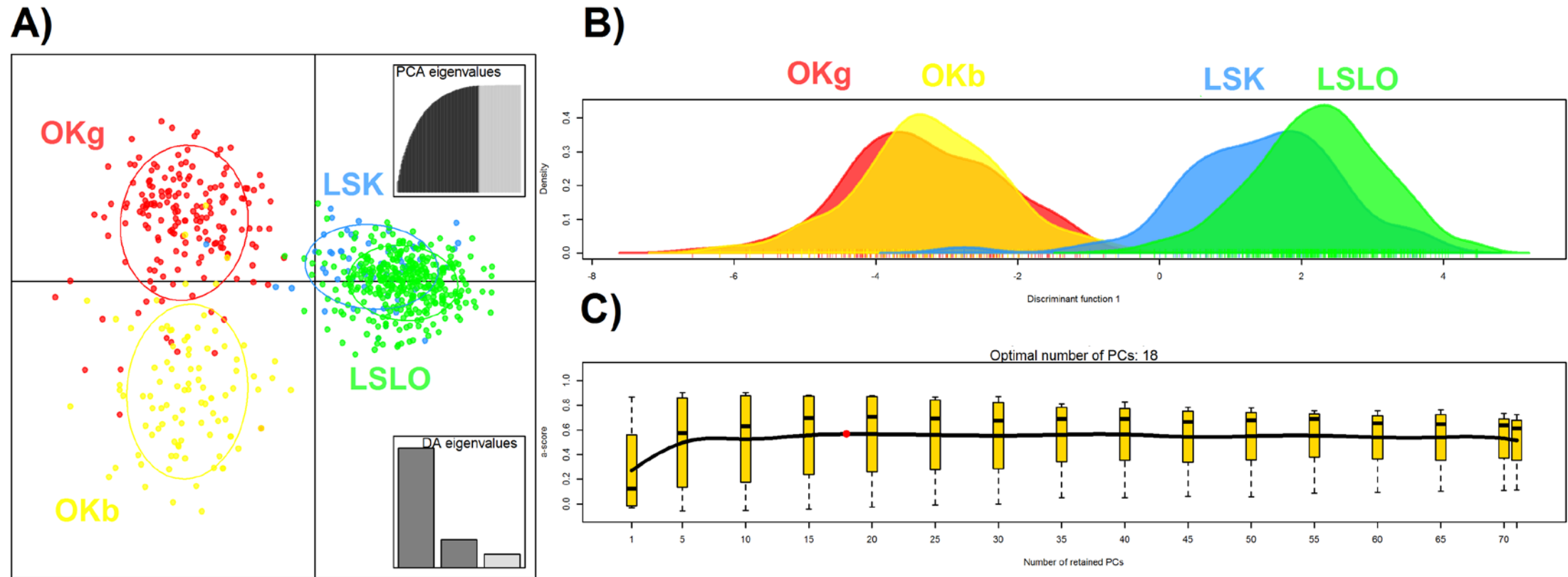# Populations subdivision and genetic relationships

Figure 1. Genetic clusters determined using discriminant analysis of principal components (A), based on first discriminant function (B) and optimal number of PCs for successful reassignment of individuals (C).
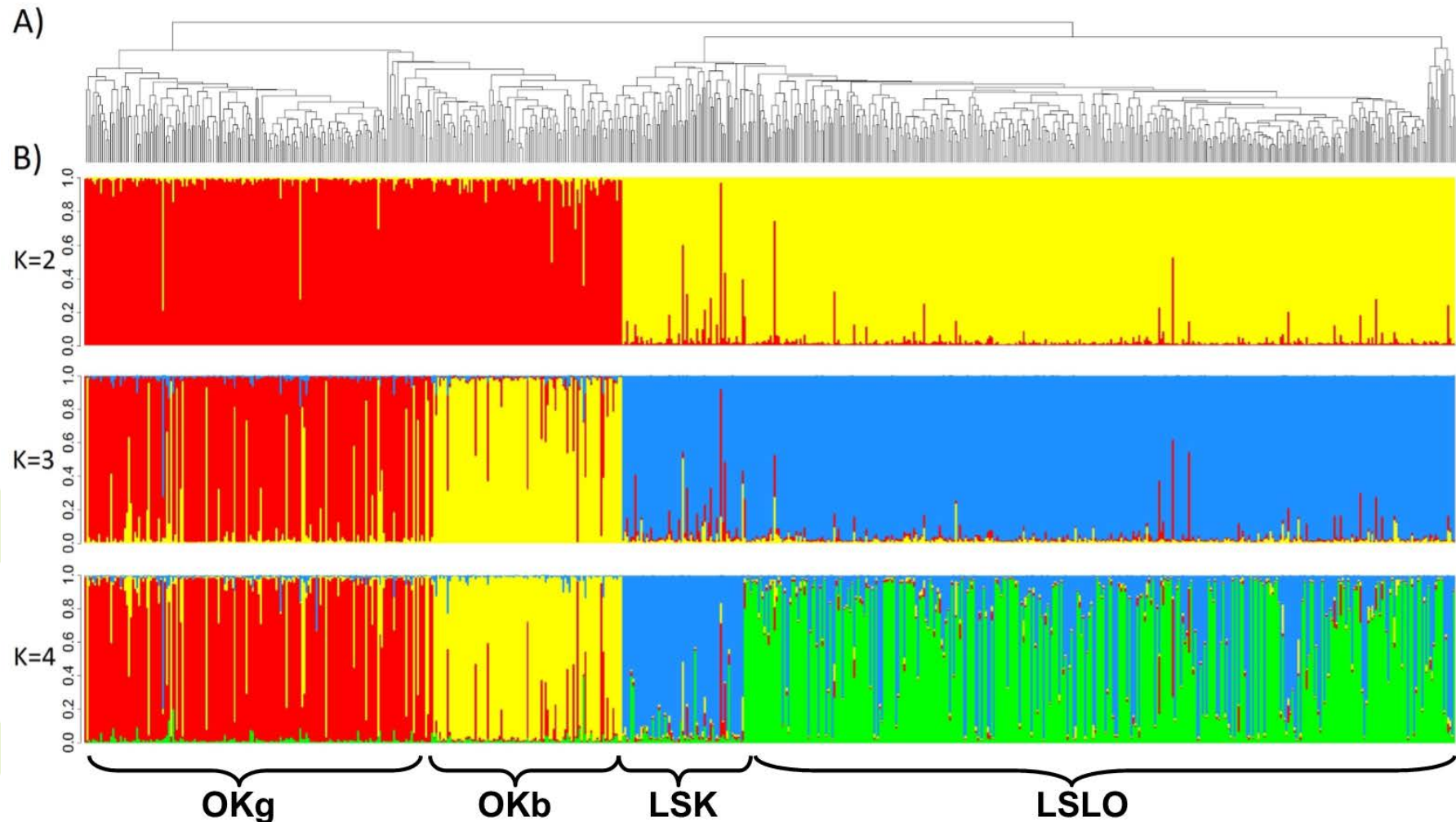
Populations subdivision and genetic relationships

Figure 2. Hierarchical plot showing inferred relationships between individuals (A) and representative results from Bayesian assignment analysis implemented in STRUCTURE (B).

Migration events

- ➢ low migrations rate across all populations
- ➢ higher migration rates was found at intra-population levels of analysed groups
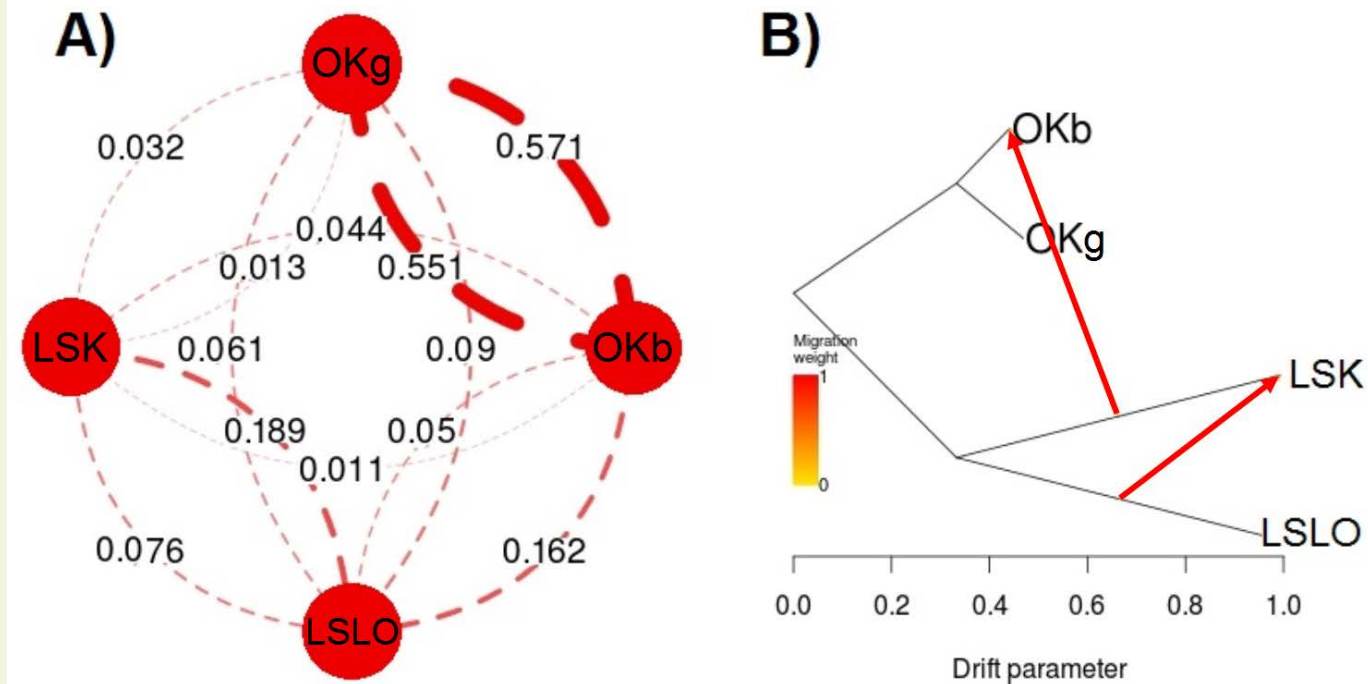

Figure 3. Relative migration network (A) and maximum likelihood tree showing inferred relationship between among analysed horse subpopulation (B).

Conclusion

➢ The sufficient proportion of heterozygotes within the populations for sustainable future development of the breeds was found.

➢ All of the applied methods for estimation of population structure showed clear genetic distinction between the Old Kladruber and the Lipizzan populations.

Conclusion

- ➢ The genetic differentiations among populations reflected the formation of separate clusters with respect mainly to the breeding history and strategy of studs.

- ➢ The evidence of admixture between Lipizzan and Kladruber horses that can be due to the common breeding history and remaining genetic connectedness was not found.

Thank you for your attention!