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Comparative analysis of linkage disequilibrium in Fleckvieh and Brown Swiss cattle

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Introduction

- Hayes et al. (2009): Accuracy of genomic breeding values depending on:
  - Heritability
  - Genetic architecture
  - Size of the reference population
  - Linkage disequilibrium (LD) between markers and QTL

- LD depends on:
  - Population structure
  - Distance between marker and QTL

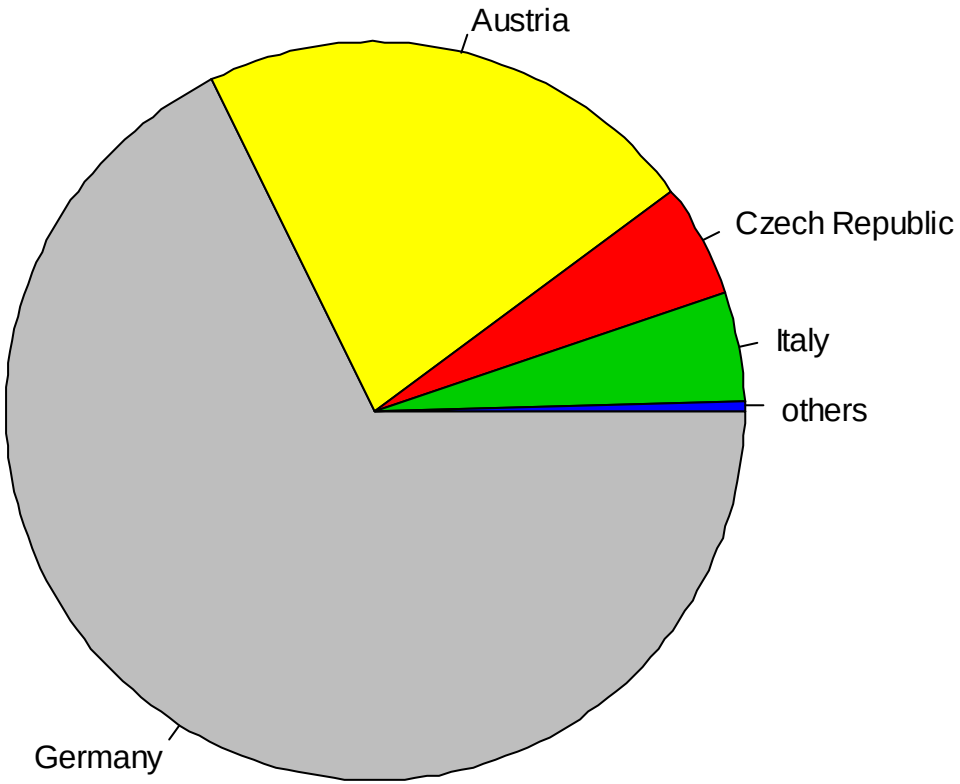
⇨ **Analysis of LD in Fleckvieh and Brown Swiss**

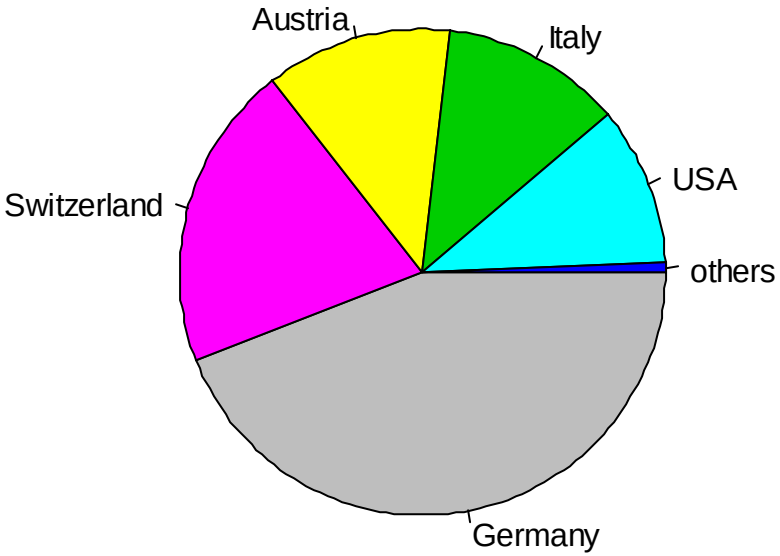
Aims

- Extent of LD in Fleckvieh and Brown Swiss
- Impact of population structure
  - Persistency of LD phase
  - F_{ST}
  - Difference of allele frequencies
  - Effective population size from SNPs

Material & Methods

- Illumina 54K genotypes
- Fleckvieh: 9.387 bulls
- Brown Swiss: 4.068 bulls

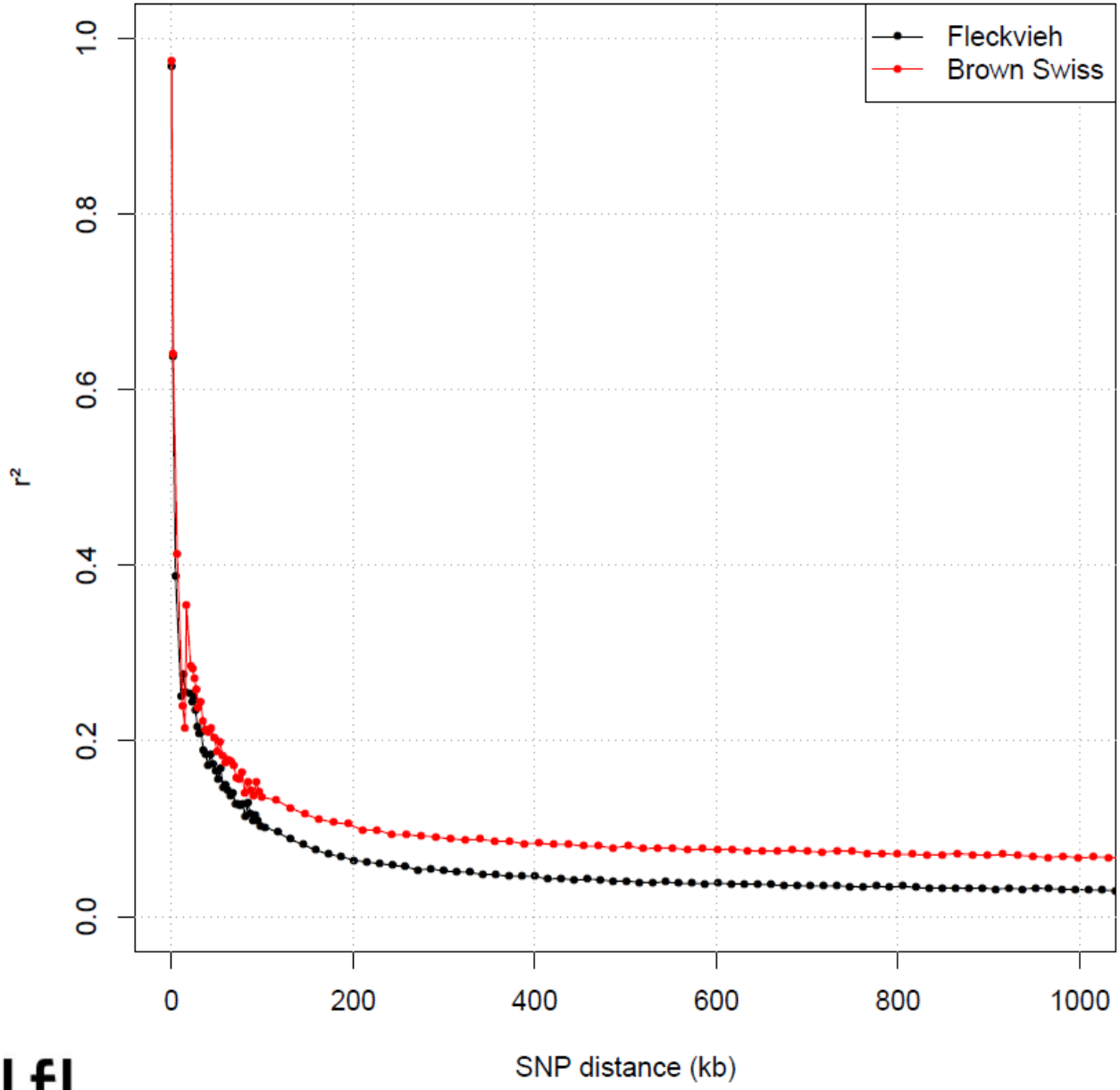




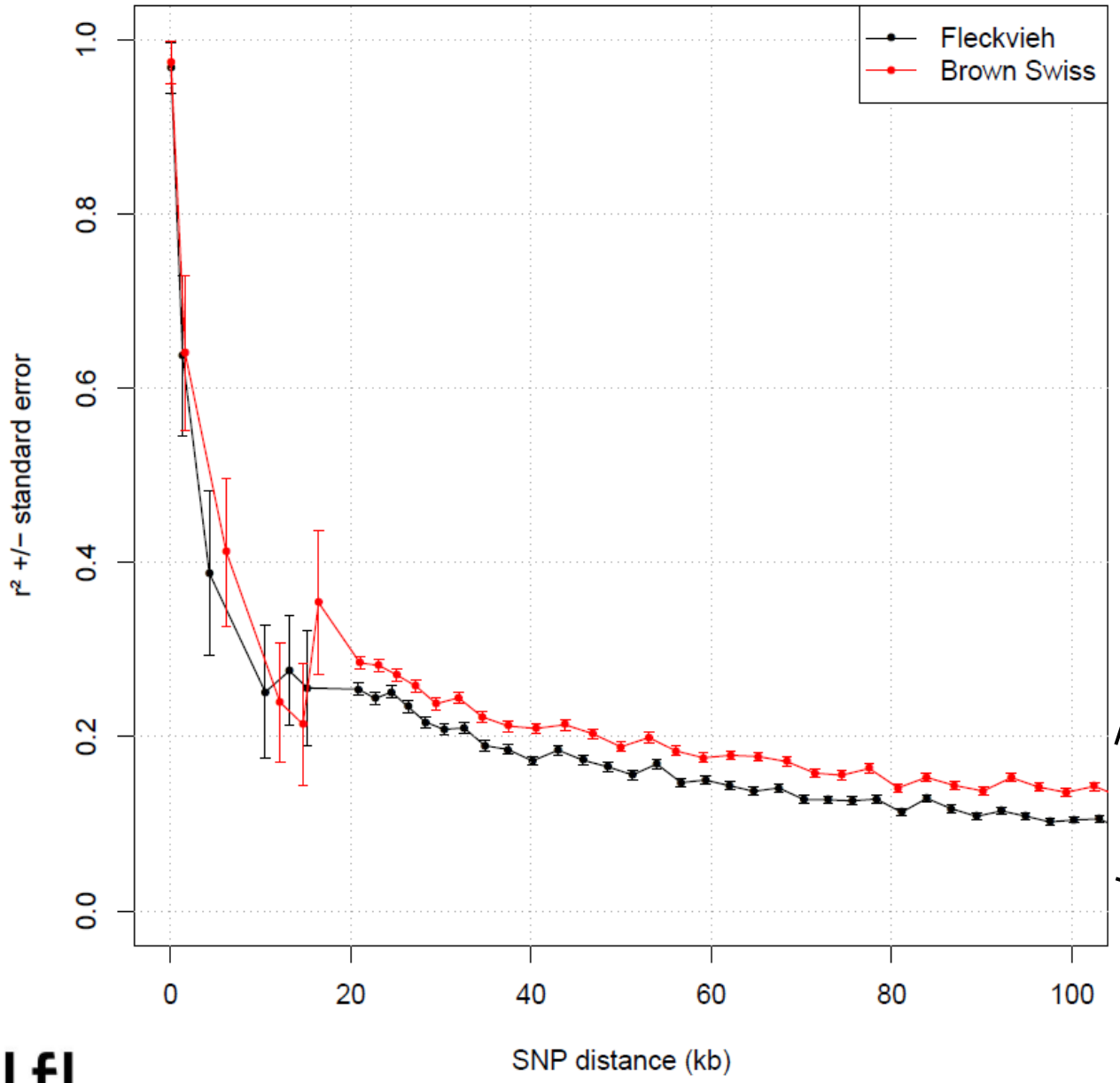
Material & Methods

- SNP quality checks
  - Call rate >95%
  - Minor allele frequency >0.5%
  - Deviation from HWE ($p<10^{-5}$)
- Conflicts with pedigree
- Calculation of r and r^2 between syntenic SNPs
  - Genotypes coded as allele counts (0,1,2)
  - r: pairwise correlation of SNP genotypes

LD Fleckvieh–Brown Swiss



LD Fleckvieh–Brown Swiss



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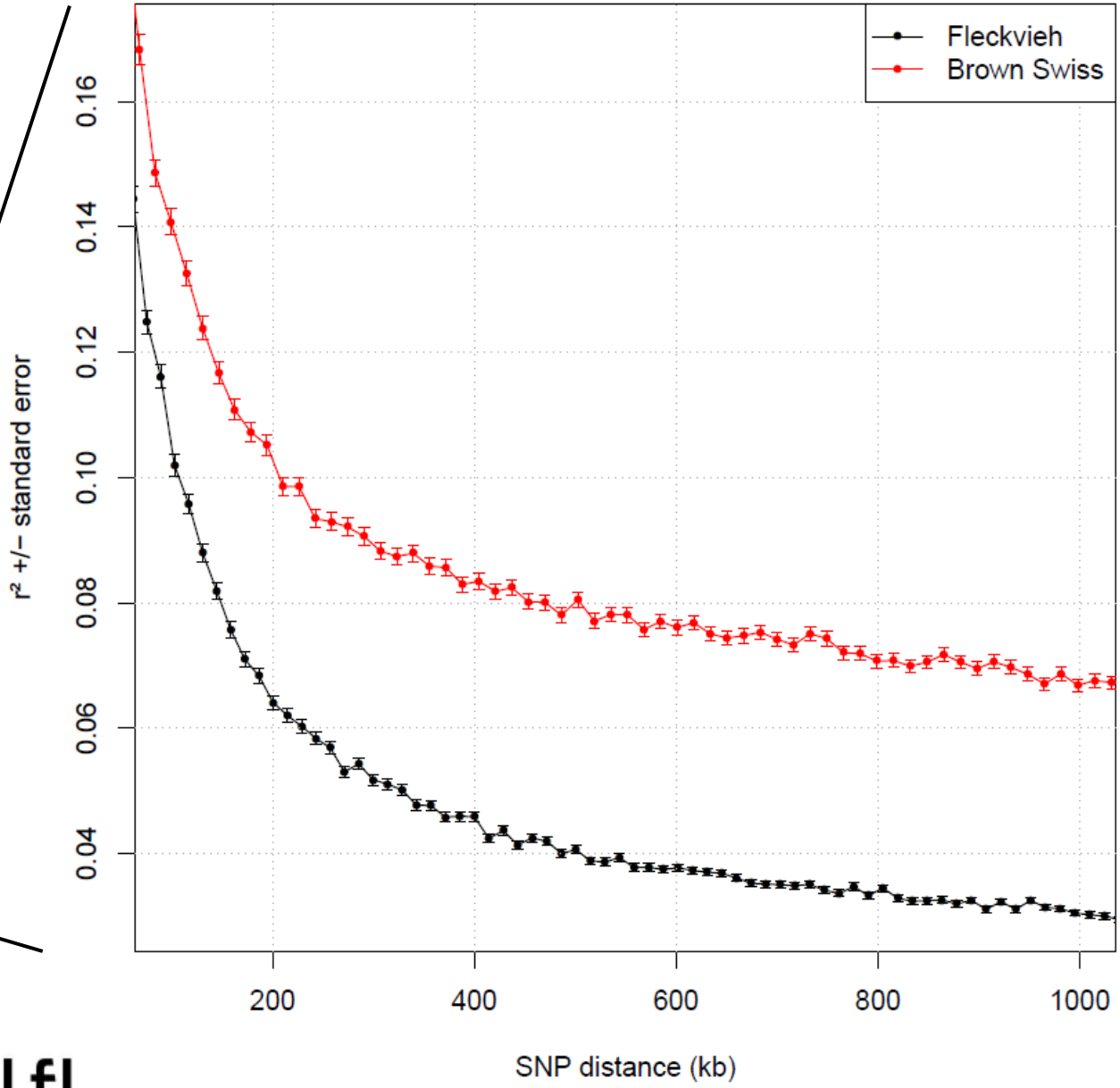
LD Fleckvieh–Brown Swiss



LD Fleckvieh–Brown Swiss

- SNP distance ⇑ → LD ⇓

- <20 kb: LD Fleckvieh ≈ LD Brown Swiss
- >500 kb: LD Brown Swiss ≈ 2·LD Fleckvieh

- LD Fleckvieh as observed by Pryce et al. (2011)
- LD Brown Swiss comparable with LD in
  - Dutch Holstein (de Roos et al., 2008)
  - North American Holstein (Bohmanova et al., 2010)
  - German Holstein (Habier et al., 2010; Qanbari et al., 2010)
  - Australian Holstein and Jersey (Pryce et al., 2011)

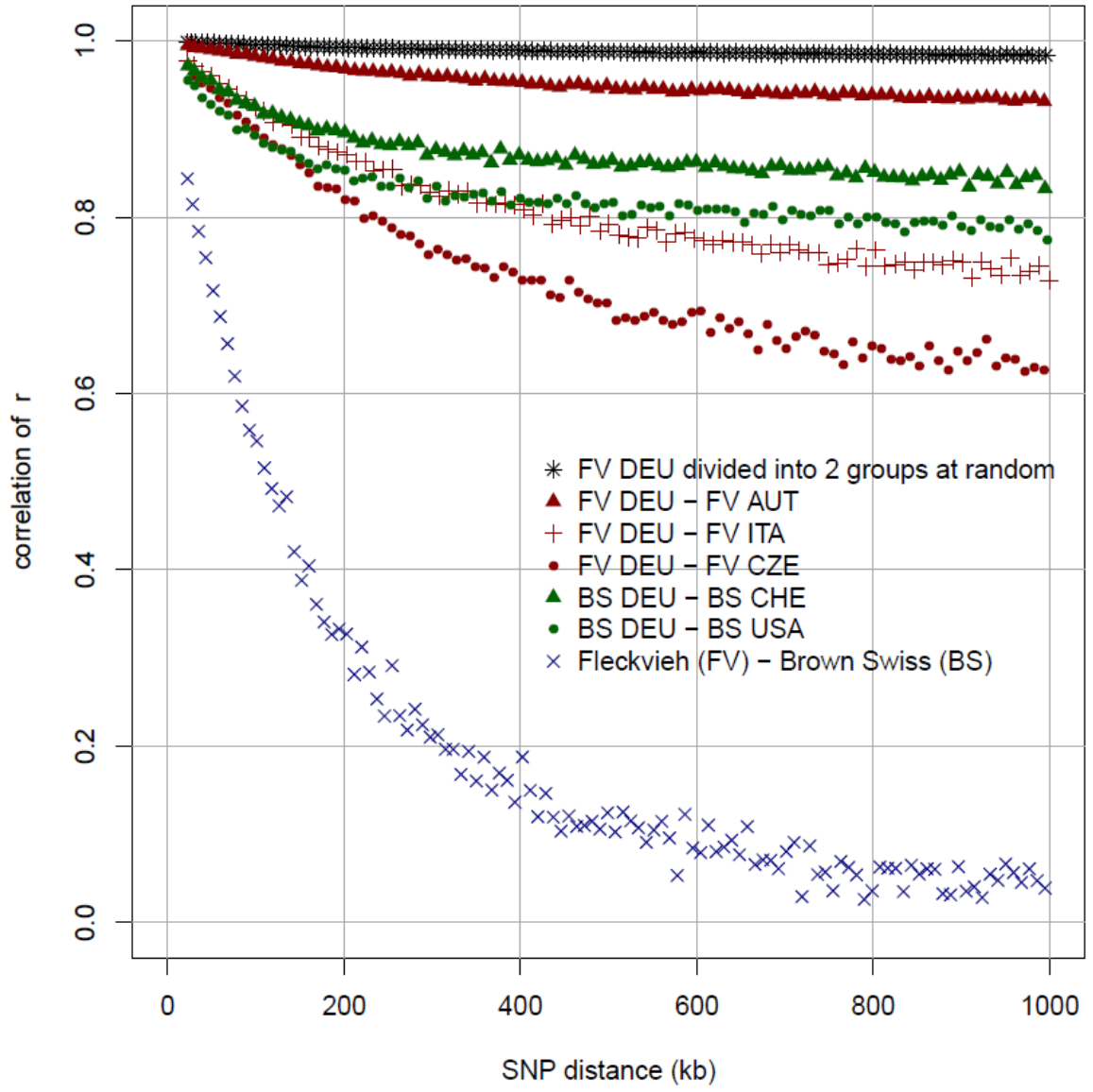
LD Fleckvieh–Brown Swiss

⇨ Fleckvieh genetically more diverse than Brown Swiss, Holstein and Jersey

- e.g. $r^2 = 0.2$:
  - Fleckvieh: ~30 kb
  - Brown Swiss: ~50 kb

Persistency of LD phase

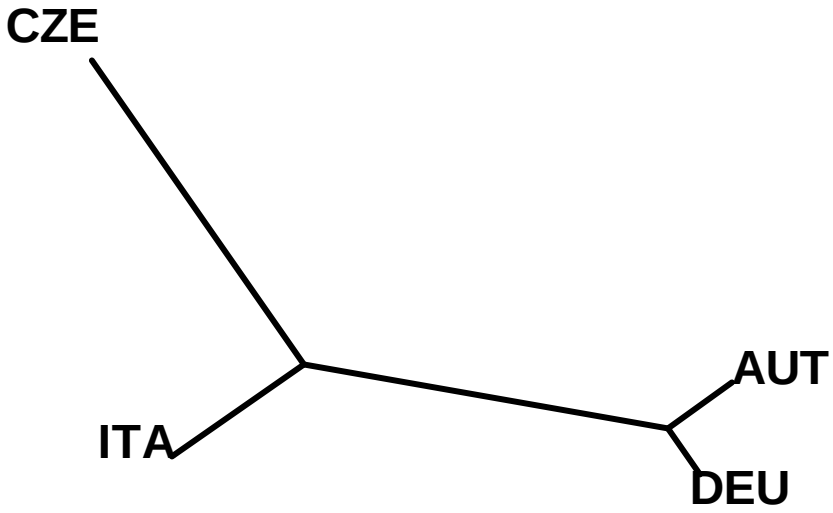
- Correlation of r values for the same SNP pairs (de Roos et al., 2008)

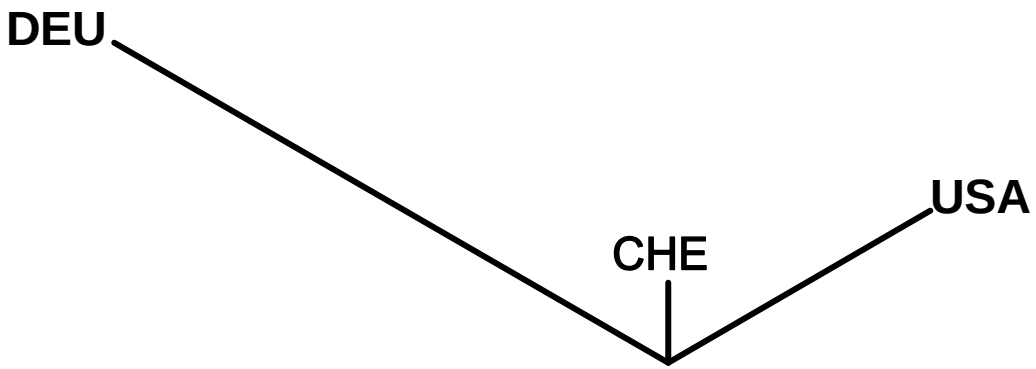


Pairwise F_{ST} between subpopulations

(Wright, 1951; Weir & Cockerham, 1984)

Fleckvieh ⟵ 0.103 ⟶ **Brown Swiss**

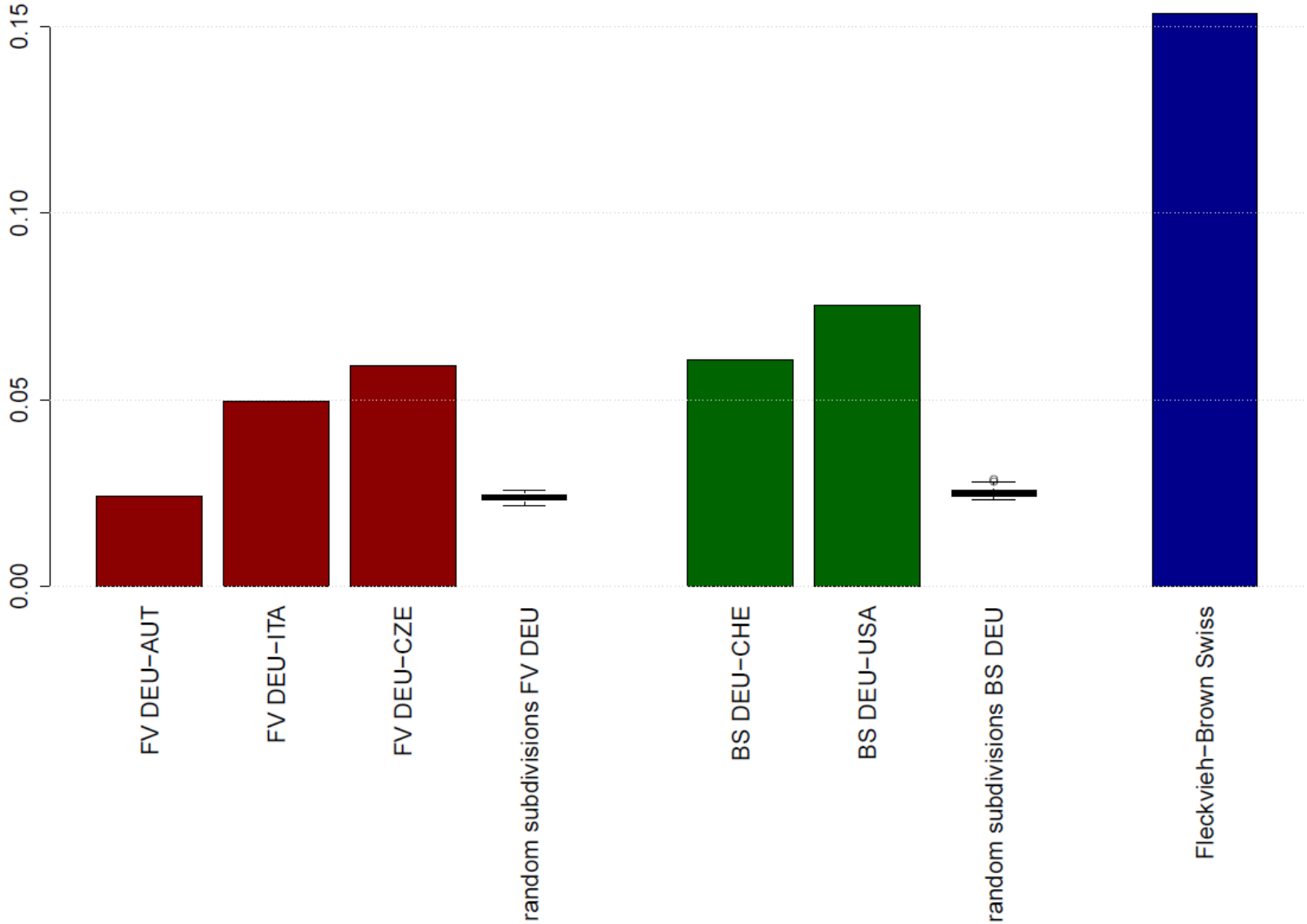




	DEU	AUT	ITA
AUT	0.003		
ITA	0.011	0.012	
CZE	0.016	0.016	0.010

	DEU	CHE
CHE	0.016	
USA	0.028	0.007

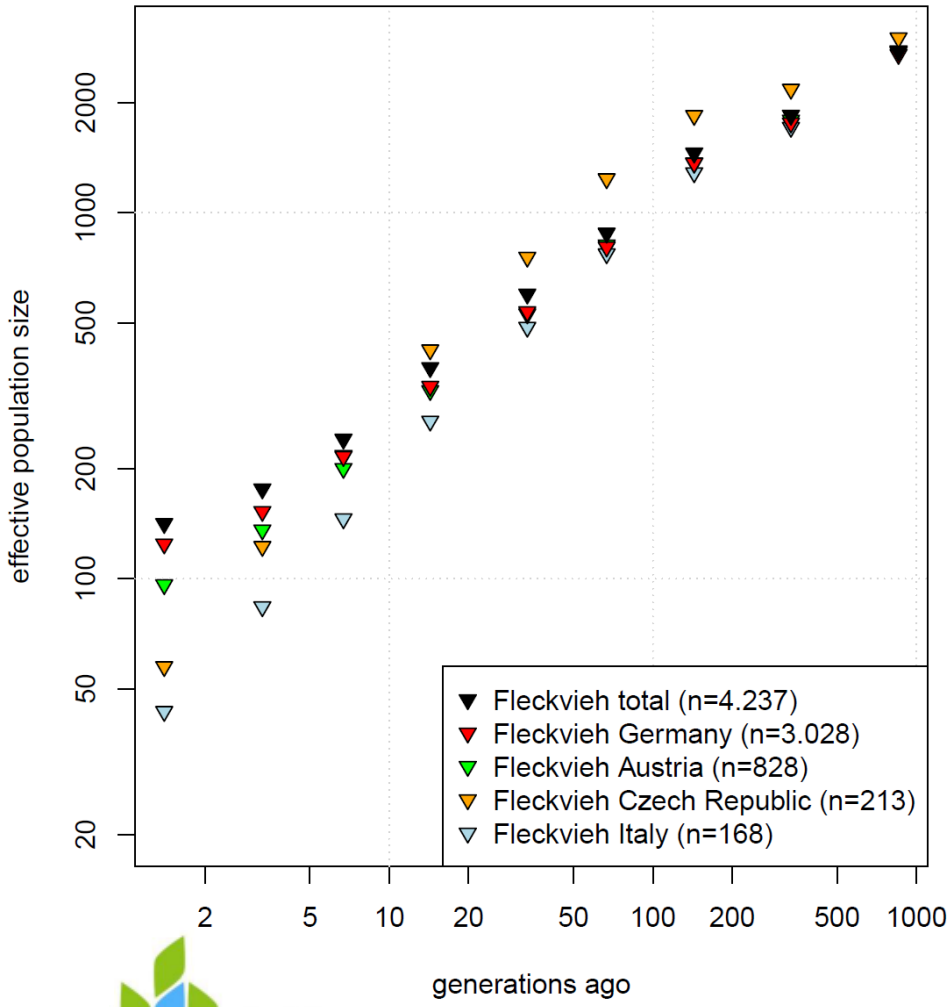
Mean difference of allele frequencies



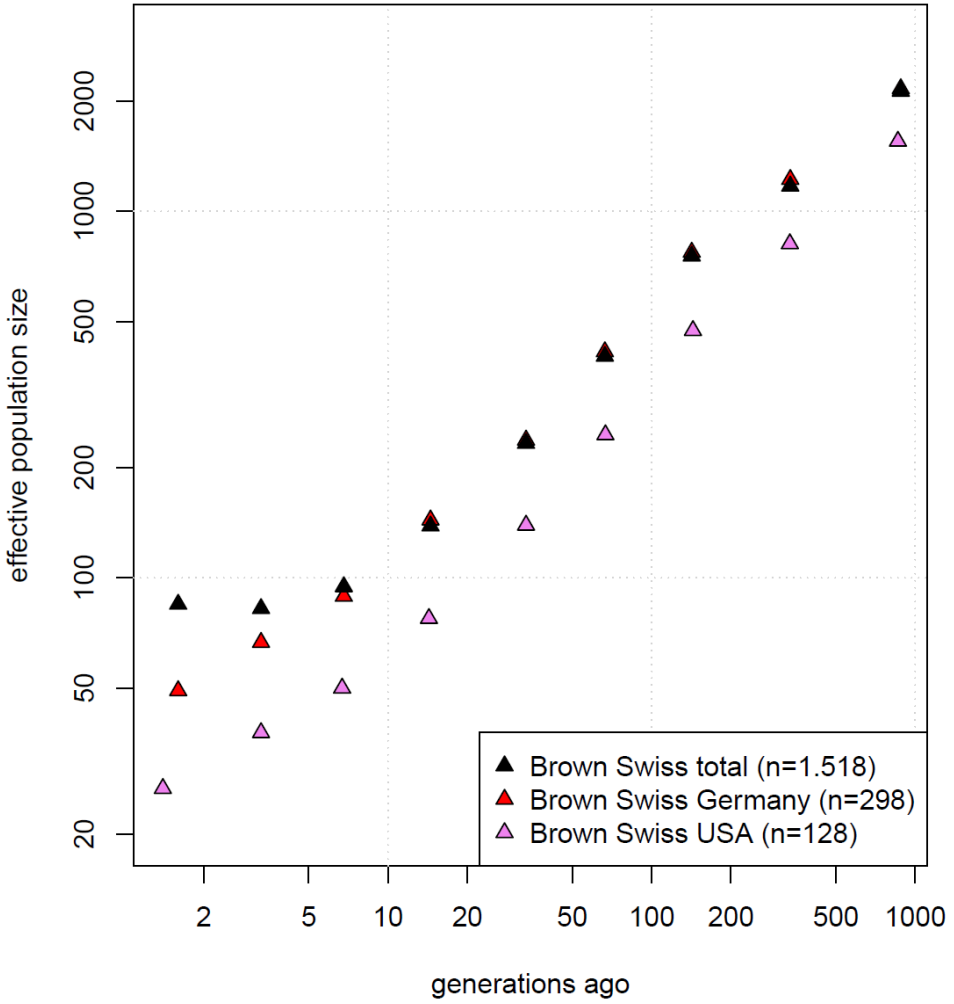
Effective population size

(Sved, 1971; Hayes et al., 2003)

Fleckvieh



Brown Swiss



Conclusion

- Fleckvieh:
  - Close connections: Germany and Austria
  - Larger differences: Italy, Czech Republic
- Brown Swiss:
  - Unidirectional gene flow from USA to Europe
  - Higher distance between original subpopulations from Germany and USA
- Fleckvieh–Brown Swiss:
  - Fast decay of persistency of LD phase:

    comparable with Holstein–Angus (de Roos et al., 2008)
- Good accordance of different measures of population structure

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Synbreed

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Thank you for your attention!

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