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Genomic relationship among InterGenomics populations

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Introduction

- Brown Swiss - longevity, functionality, adaptability, calving ease, strength, disease resistance, docility
- Brown Swiss - very popular in Europe - the highest number - top selective
- Brown Swiss -USA - the source of new blood lines - renewed the original European Alpine Brown Breed

The aim

- to found out the genomic relationship among nowadays InterGenomics populations
- despite the fact that Brown Swiss cattle were widespread from its homeland through the World and it was used for improving local populations

Materials

- SNP genotypes (BovineSNP50 BeadChip, Illumina)
- 5755 Brown Swiss bulls (Intergenomics project)
- 7 countries
 - Austria (487)
 - France (115)
 - Germany (1642)
 - Italy (1151)
 - Slovenia (181)
 - Switzerland (1347)
 - United States of America (832)

Methods

- Sires divided by countries (country code)
- SNPs considered if :
 - marker call rate higher than 95%
 - minor allele frequencies higher than 0.05
 - the departure from the Hardy-Weinberg equilibrium at a threshold of $P < 0.0001$
 - Excluded: not mapped SNPs and on the X chromosome,
 - Final set of 55172 SNPs.
- The imputation method proposed by VanRaden et al. (2010) and its associated program (FindHap; VanRaden, 2010).
- The *Bos taurus* genome assembly UMD 3.1 was used to determine the SNP position within each autosome.
- Genome-wide relationships between individuals were estimated using the PLINK software (Purcell et al. 2007) as genome-wide identity-by-descent (IBD) estimates for all pairs of individuals.

Results

- Identity-by-descent (IBD) is a fundamental concept in genetics and refers to alleles that are descended from a common ancestor in a base population.
- In modern applications, IBD relationships are estimated from genetic markers for individuals without any known relationship

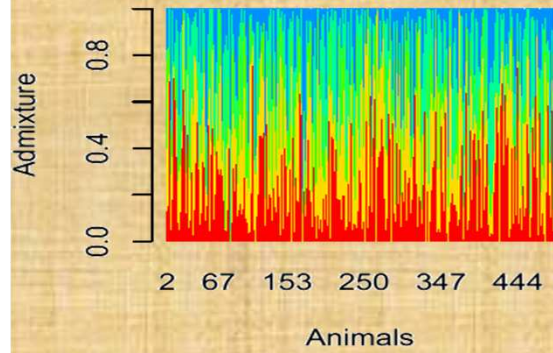
Average IBD (above diagonal) and maximum IBD (below diagonal) among Brown cattle “Intergenomics” populations

	AUT	CHE	DEU	FRA	ITA	SVN	USA
AUT		0.05	0.05	0.05	0.05	0.06	0.06
CHE	0.59		0.04	0.05	0.05	0.05	0.06
DEU	0.55	0.59		0.05	0.05	0.05	0.05
FRA	0.59	0.54	0.52		0.06	0.06	0.07
ITA	0.55	0.59	0.60	0.54		0.06	0.06
SVN	0.50	0.50	0.53	0.50	0.52		0.06
USA	0.58	0.60	0.59	0.59	0.59	0.52	

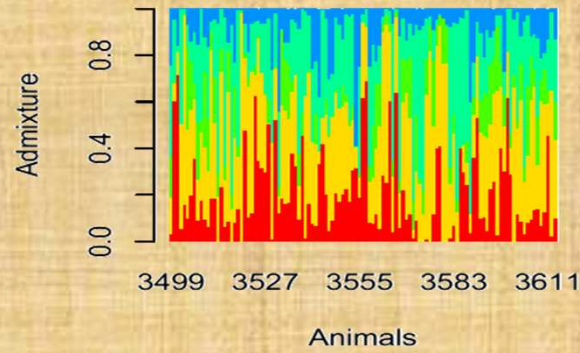
K=5; related animals by genomic data

ADMIXTURE ANALYSIS PRELIMINARY RESULTS

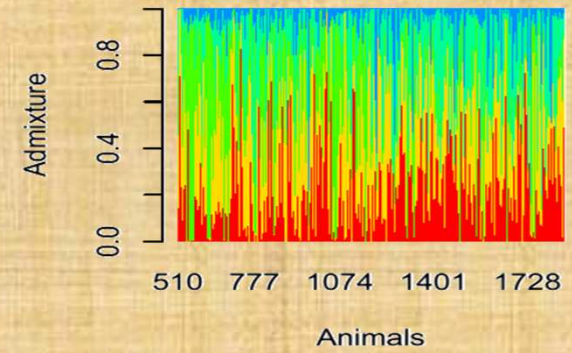
Admixture bsw AUT n=487



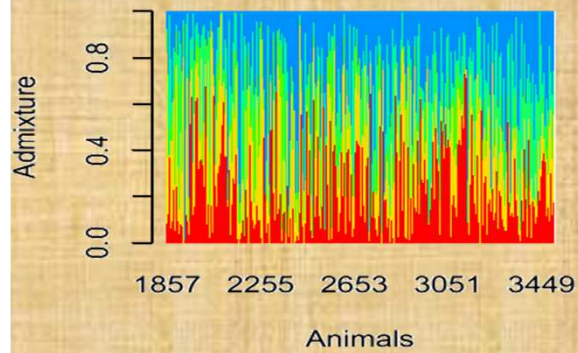
Admixture bsw FRA n=115



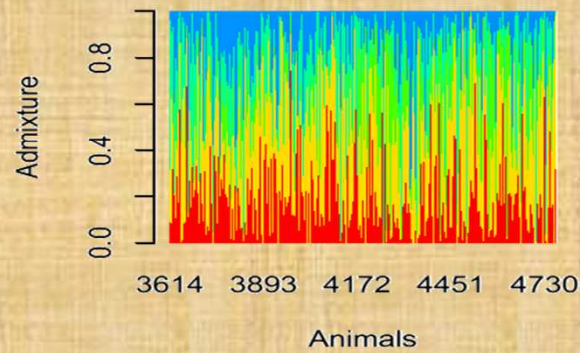
Admixture bsw CHE n=1347



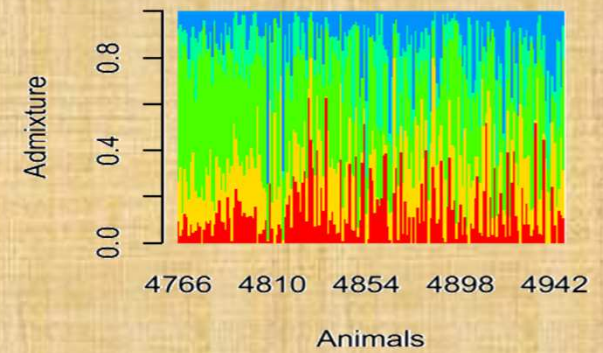
Admixture bsw DEU n=1642



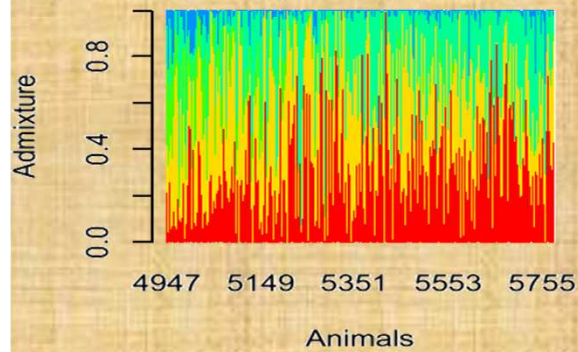
Admixture bsw ITA n=1151



Admixture bsw SVN n=181

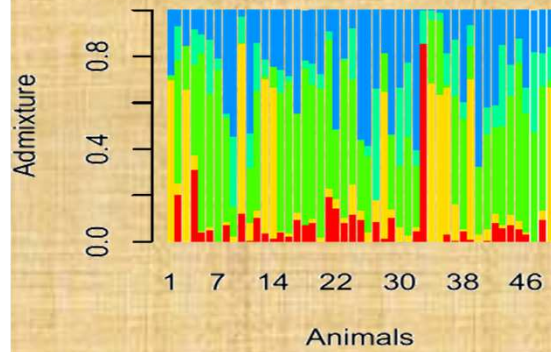


Admixture bsw USA n=833

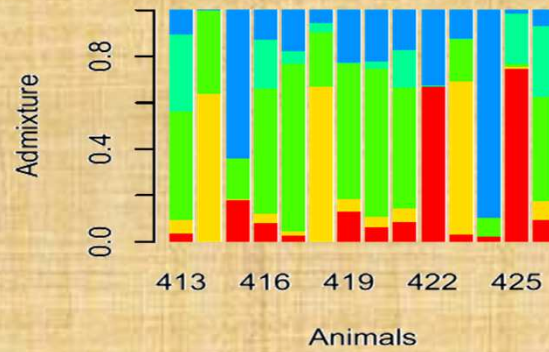


- N=5755
- Countries: 7
- K=5

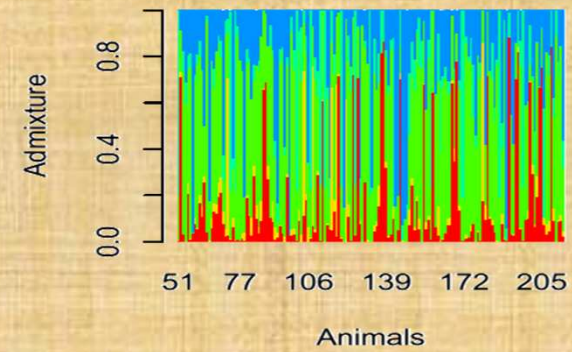
Admixture bsw AUT n=49



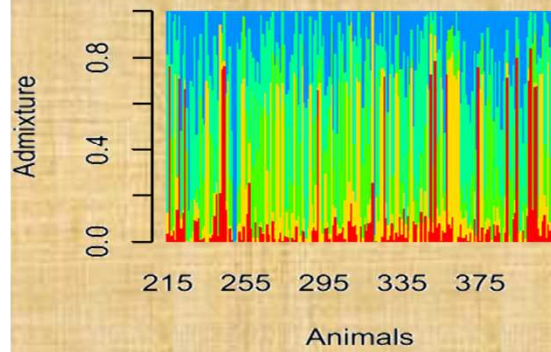
Admixture bsw FRA n=14



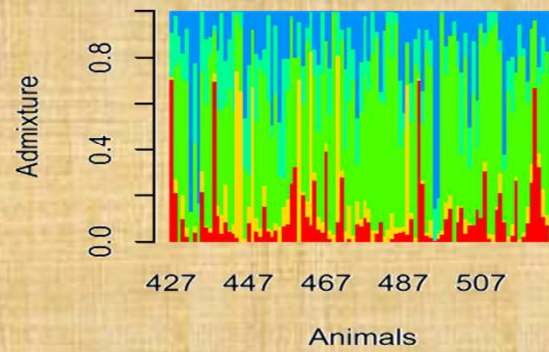
Admixture bsw CHE n=164



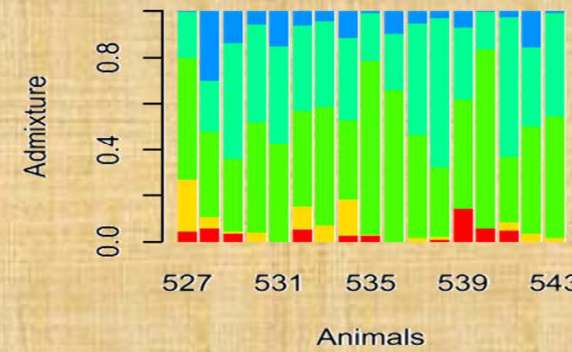
Admixture bsw DEU n=198



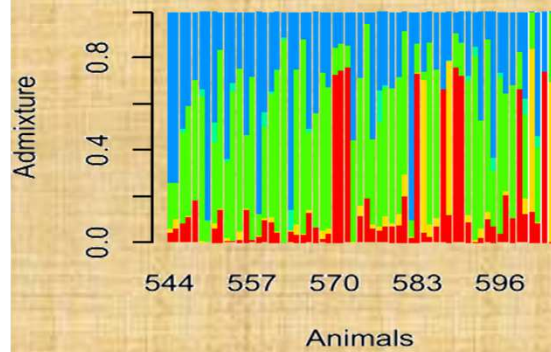
Admixture bsw ITA n=100



Admixture bsw SVN n=17



Admixture bsw USA n=61



- N=596
- Birth years
 - 2006-07
- Countries: 7
- K=5

Conclusions

- Preliminary results of this study support the idea:
 - Sires from all included countries (populations) are related based on genom information (IBD)
 - Genetic structure by countries is more or less similar
- Future investigation need to be done
 - Relationship among sires have to be considered
 - Outgroups (breeds) need to be included

Thank you for your attention!

