

Differences in genomic structure between two cattle breeds

Kosinska-Selbi B. * 1, Fraszczyk F. 1, Suchocki T.^{1,3}, Egger-Danner Ch.^{2,‡}, Schwarzenbacher H. ‡², Szyda J. ^{1,3}
Biostatistics group,, Wrocław University of Environmental and Life Sciences, Kozuchowska 7, 51-631 Wrocław, Poland
ZuchtData EDV-Dienstleistungen GmbH, Dresdner Straße 89/19, 1200 Vienna, Austria
National Research Institute of Animal Production, Krakowska 1, 32-083 Balice, Poland
* barbara.kosinska@upwr.edu.pl



Cows → 1999 Fleckvieh, 985 Braunvieh

SNP → Geneseek Genomic Profiler HD BeadChip
→ 76932 SNPs per animal

Conclusions Material

- Overall linkage disequilibrium (LD) patterns are similar in both breeds
- Local changes exist.
- Changes in LD stracial can be explained by changes of principal components in 2-dimensional space.
- Regions with high value of statistics (S) show clusters in cattle population.
- 50% of SNPs mapped to intron regions, 35% were intergenic and one 1% mapped to non-coding transcript regions.
- 1% of SNPs mapped to coding sequence of 48 genes, which have different metabolic function. ADCY8, PLCB1 and PDE4A take part in calcium signalling pathway.

Methods

1. Editing raw SNP data.
2. Removal of SNPs with a call rate below 95% and a minor allele frequency below 5%.
3. LD estimation with Beagle 4.0 (R²).
4. Calculating statistics (S) expressing changes LD structure.
5. Calculating PCA from genotype matrices of two cattle breeds.
6. Selected region with high value of statistics (S) were chosen for genomic annotation to ARS_UCD1.2 genome for *Bos taurus*.

$$S1 = 2 \sum_{i=1}^n (v_{i11} - v_{i21})^2 + (v_{i12} - v_{i22})^2$$

S1 – general measure of changes

$$S2 = \sum_{i=1}^n [(v_{i11} + v_{i22}) - (v_{i12} + v_{i21})]^2$$

S2 – measure of changes in orientation → express LD decay with bp distance

S3 – measures changes in variability → express LD variation

$$S3 = \sum_{i=1}^n [(v_{i11} + v_{i12}) - (v_{i21} + v_{i22})]^2$$

v_{ij} - product of multiplying covariance matrix the first sample by own matrix of eigenvectors or matrix of eigenvectors from the second sample

Results

BSW – Braunvieh, FLV - Fleckvieh

