

Alternative haplotype construction methods for genomic evaluation

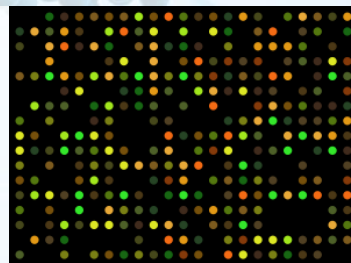
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Introduction

- Genomic selection
 - Improved breeding value estimation by exploiting knowledge on **DNA sequence variation**
 - Bi-allelic **SNP** markers
 - Requirement: large reference populations
- An alternative to SNP: **haplotypes**
 - A combination of N SNP
 - **Multi-allelic genetic marker**
 - Which haplotypes should be used?

Objectives

- Develop a method to *a priori* **construct** the **“best” haplotypes** for genomic selection
 - How to define the “best” haplotype?
 - Maximize the number of alleles
 - Consider the distribution of **allele frequencies**



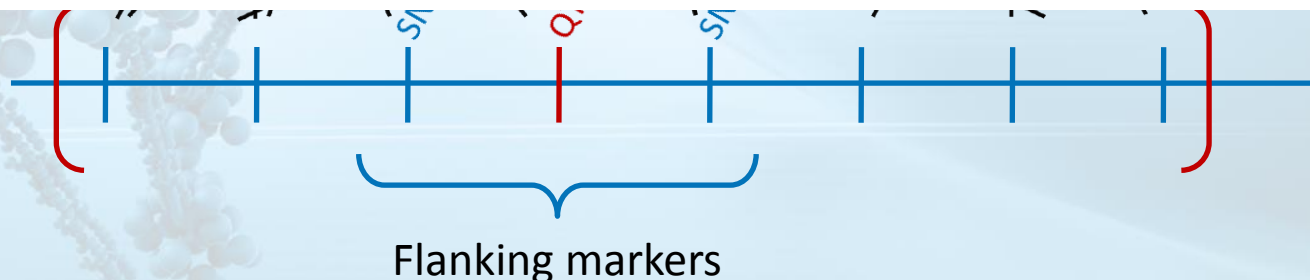
Materials and Methods

- Haplotype construction

- **Definition** a combination of **homozygous** SNP

An allele effect was considered “predictable”, if it had a sufficiently high allele frequency

- Tested haplotype sizes: 3-5 SNP
- Window size: 10 SNP
- Two, slightly different criteria
 - Termed as Criterion-A and Criterion-B
 - Difference: Criterion-B includes a constraint on the equilibrium of allele frequencies



Materials and Methods

- The dataset
 - Dairy cattle breed (Montbéliarde)
 - n=2,235 individuals (Training: 1,666; Validation: 569)
 - 5 dairy cattle production traits
Milk quantity, fat yield, fat content, protein yield, protein content
 - 43,801 SNP from the 50K chip
 - Assumed *a priori* information (QTL-SNP)
 - Represent **approximate** QTL positions
 - The most significant 1-, 3- and 6 thousand QTL-SNP

Materials and Methods

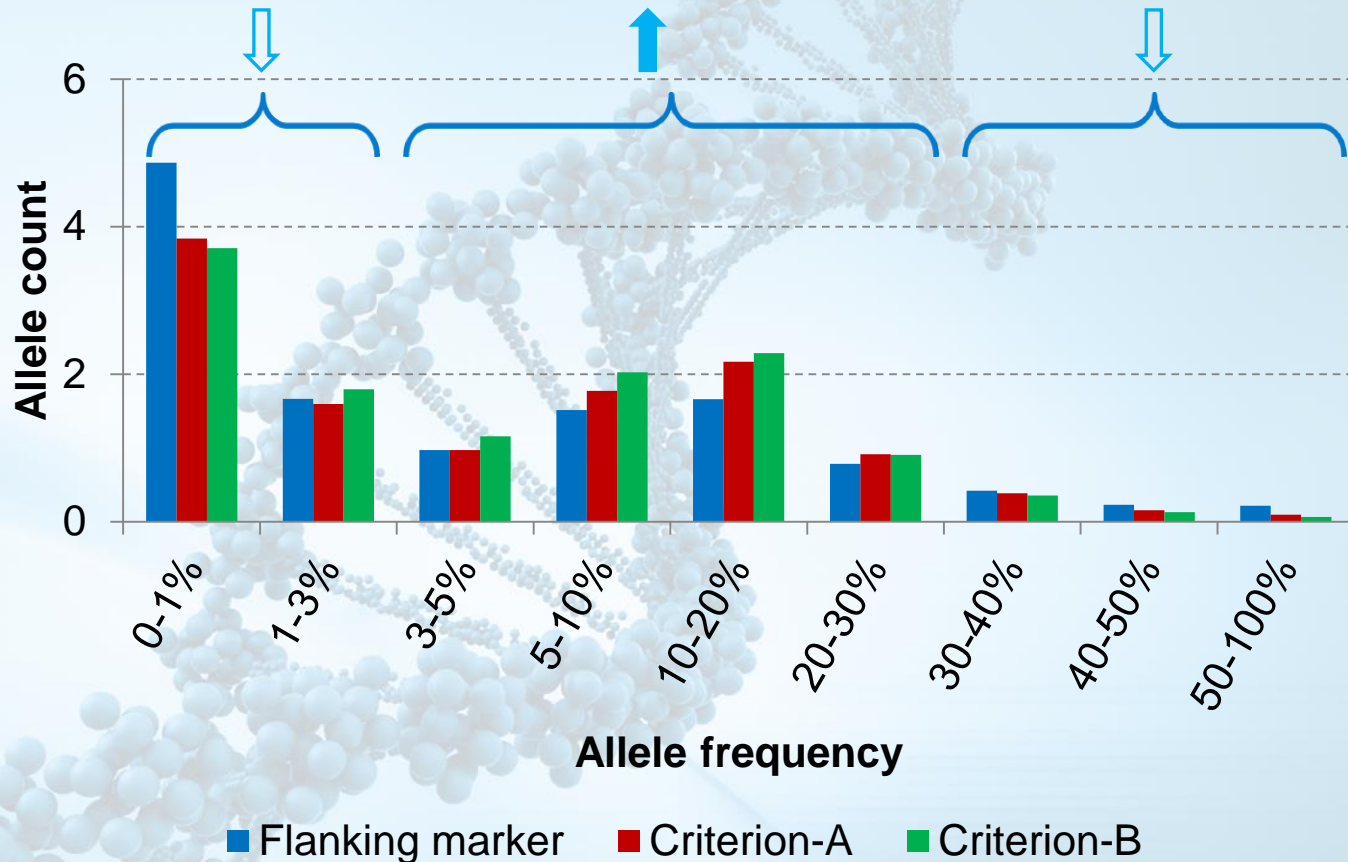
- Analyses based on different sources of genomic information (**Bayes-C**)
 - Only QTL-SNP
 - Haplotypes built from:
 - Flanking markers
 - Criterion-A
 - Criterion-B
- Comparison of the results
 - **Correlation** between phenotypes (DYD) and GEBV

DYD-GEV correlations observed with the flanking marker haplotypes

Number of QTL-SNP	QTL-SNP	Flanking marker haplotype		
		HS=3	HS=4	HS=5
1K	0.480	0.491	0.492	0.488
3K	0.499	0.523	0.526	0.528
6K	0.512	0.534	0.538	0.541
Optimal	0.512	0.534	0.538	0.542

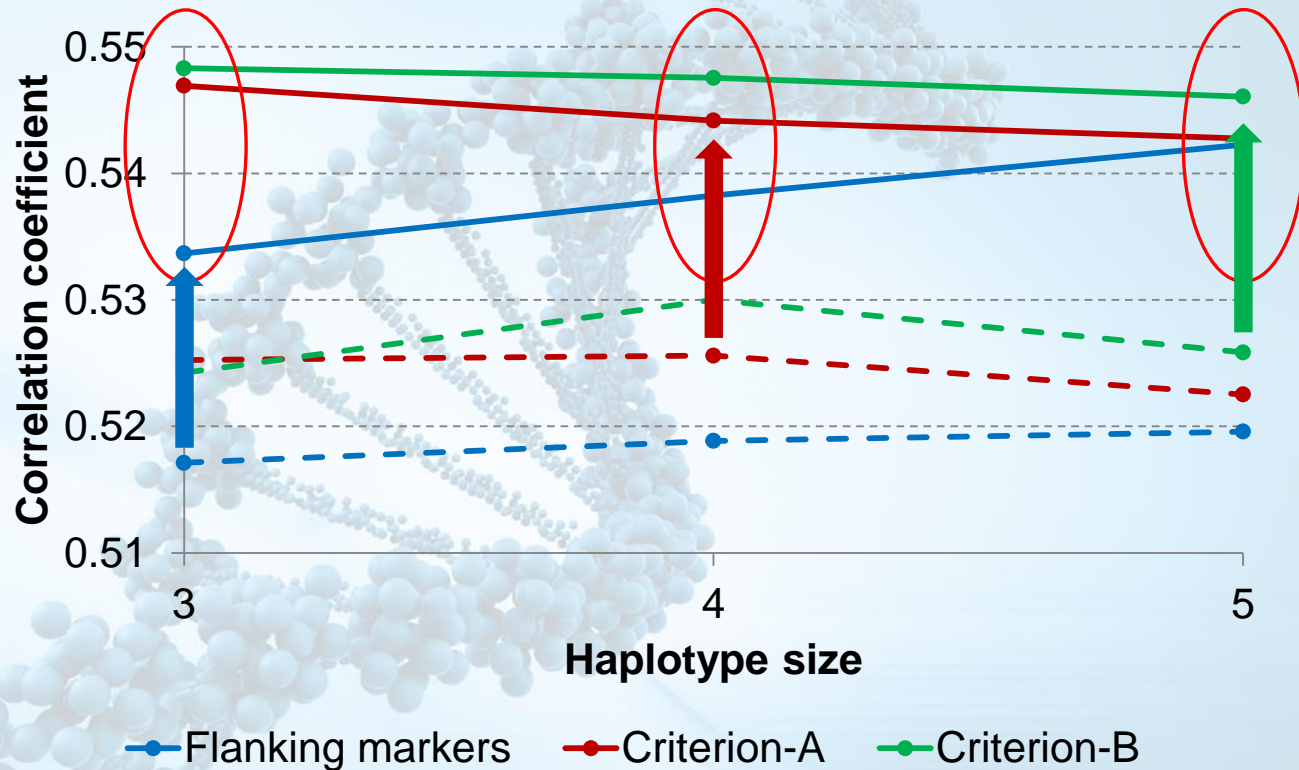
- **Optimal number of QTL-SNP:** for each trait separately, the number of haplotypes leading to the highest correlation coefficient is considered
- Average correlations of the 5 production traits are shown

Average number of alleles per allele frequency group



- Frequency of the rare alleles decreased with either of the 2 proposed criteria
- Similar results were observed with haplotypes of 3 and 5 SNP

Correlations observed with the flanking- and selected SNP



- Haplotypes built from the selected markers were superior in genomic selection
- Gain with the haplotype selection methods decreased as the haplotype size increased

Conclusions

- **Selection of SNP is beneficial** to build haplotypes for genomic selection
 - Reduced number of markers in the model
 - Larger number of alleles with proper frequencies
 - **Higher DYD-GEBV correlations**
- Decreasing gain with the increase of haplotype size
- Similar results with the **HD-chip**
- Similar results with **other breeds**

Thank you for your kind attention!

