Alternative haplotype construction methods for genomic evaluation

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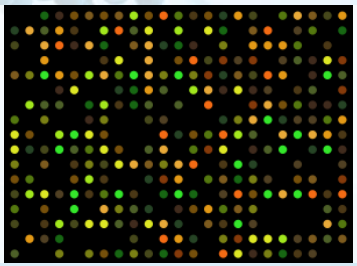

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Introduction

- 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**



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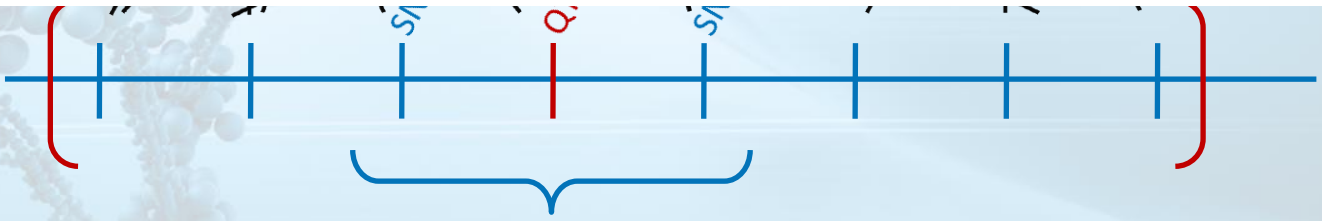
Materials and Methods

- Haplotype construction
  - Defining a combination of consecutive 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



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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

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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-GEBV 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

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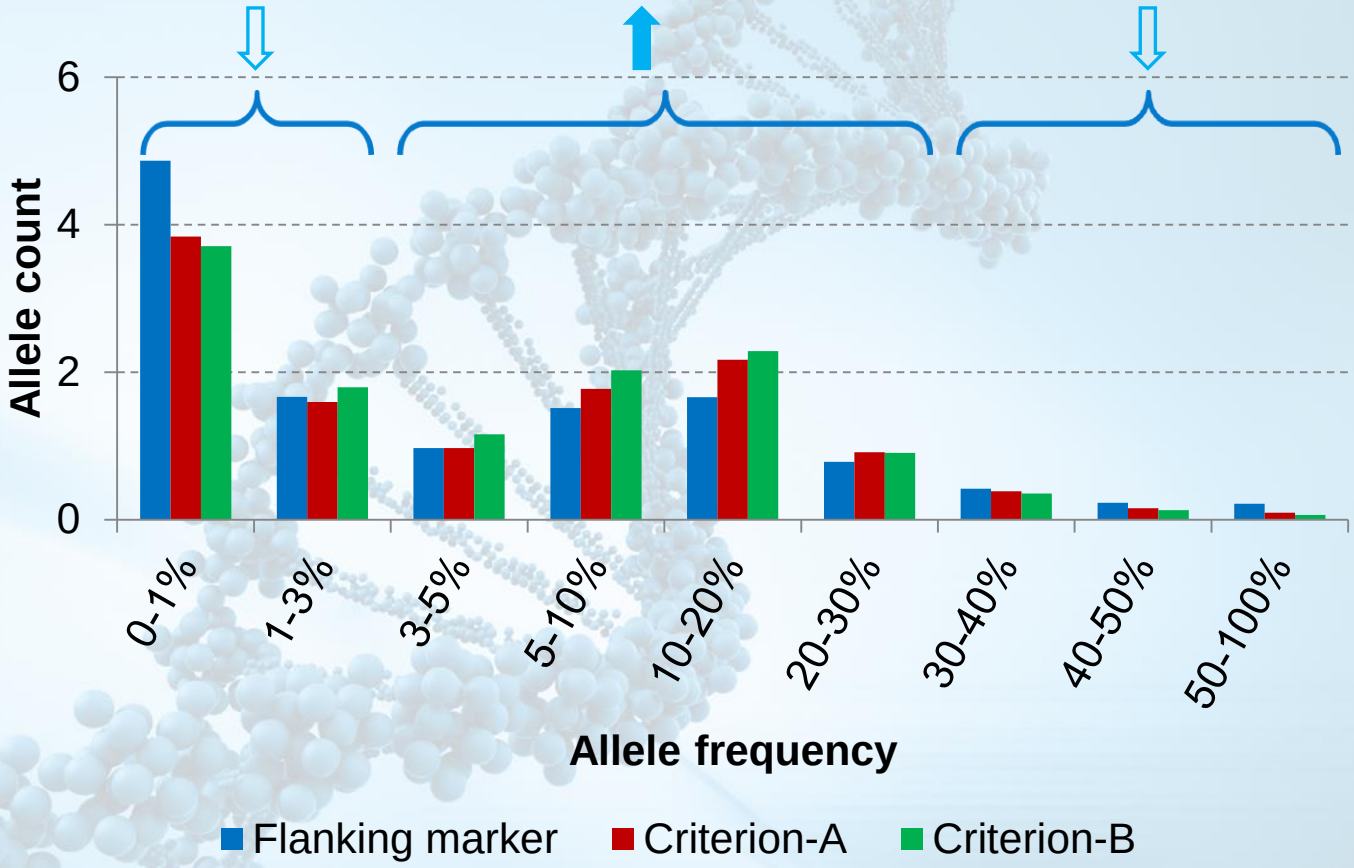
Average number of alleles per allele frequency group



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

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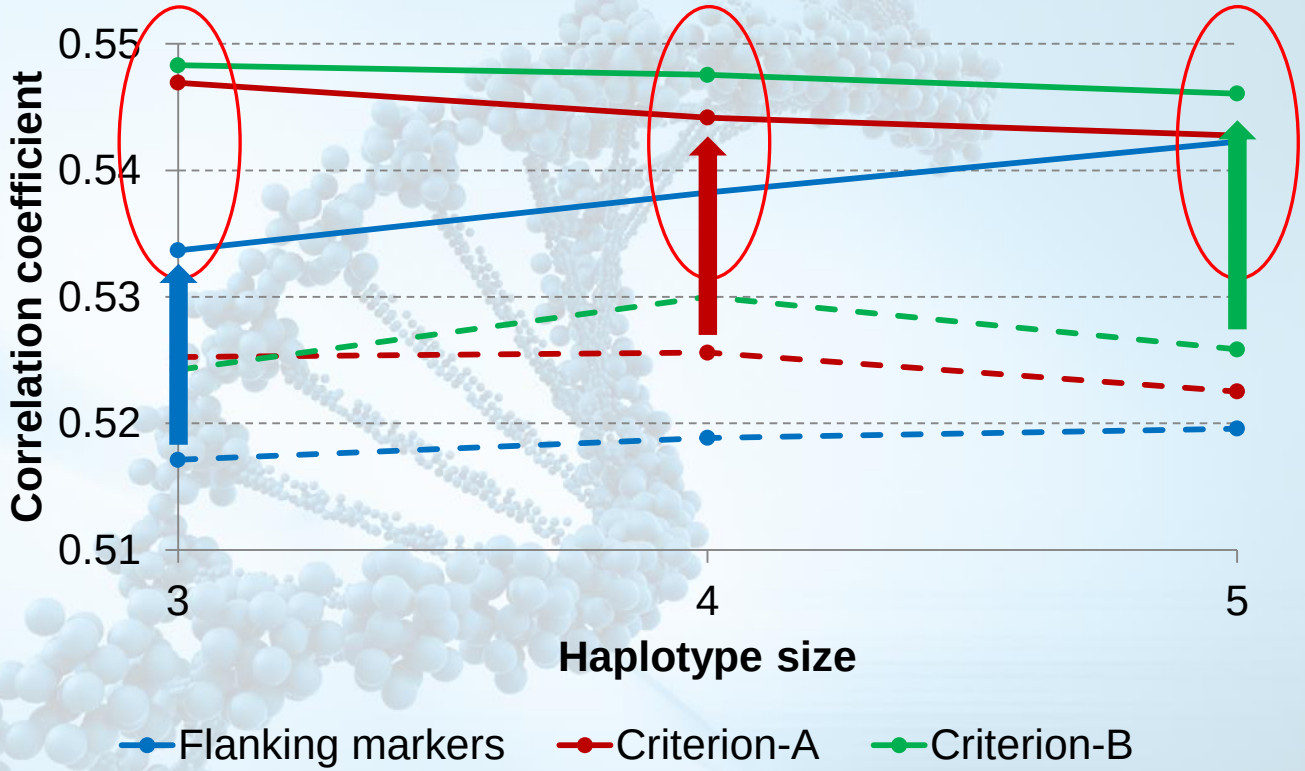
Correlations observed with the flanking- and selected SNP



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

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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**

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Thank you for your kind attention!

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