Genome-wide association study for milk fatty acid composition using cow *versus* bull data

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Background

➢ Genome-wide associations studies (GWAS) are of interest to explore underlying molecular mechanisms behind SNP effects in usual genomic prediction.

➢ Few GWAS were performed on milk fat composition of dairy cows. Those studies used single SNP models applied to cow data.

Objective: To perform a genome-wide association study for milk fat composition using either cow data, bull data, or both

Conclusion

➢ Great interest of combining cow and bull data for GWAS
➢ Many regions associated with fatty acids
➢ Fatty acid contents in milk strongly influenced by *DGAT1* gene

Results & Discussions

Figure 1. Bayes factors across the genome for the 7 studied traits (SFA, UFA, MUFA. PUFA, SCFA, MCFA, LCFA), using cow, bull, or cow & bull data
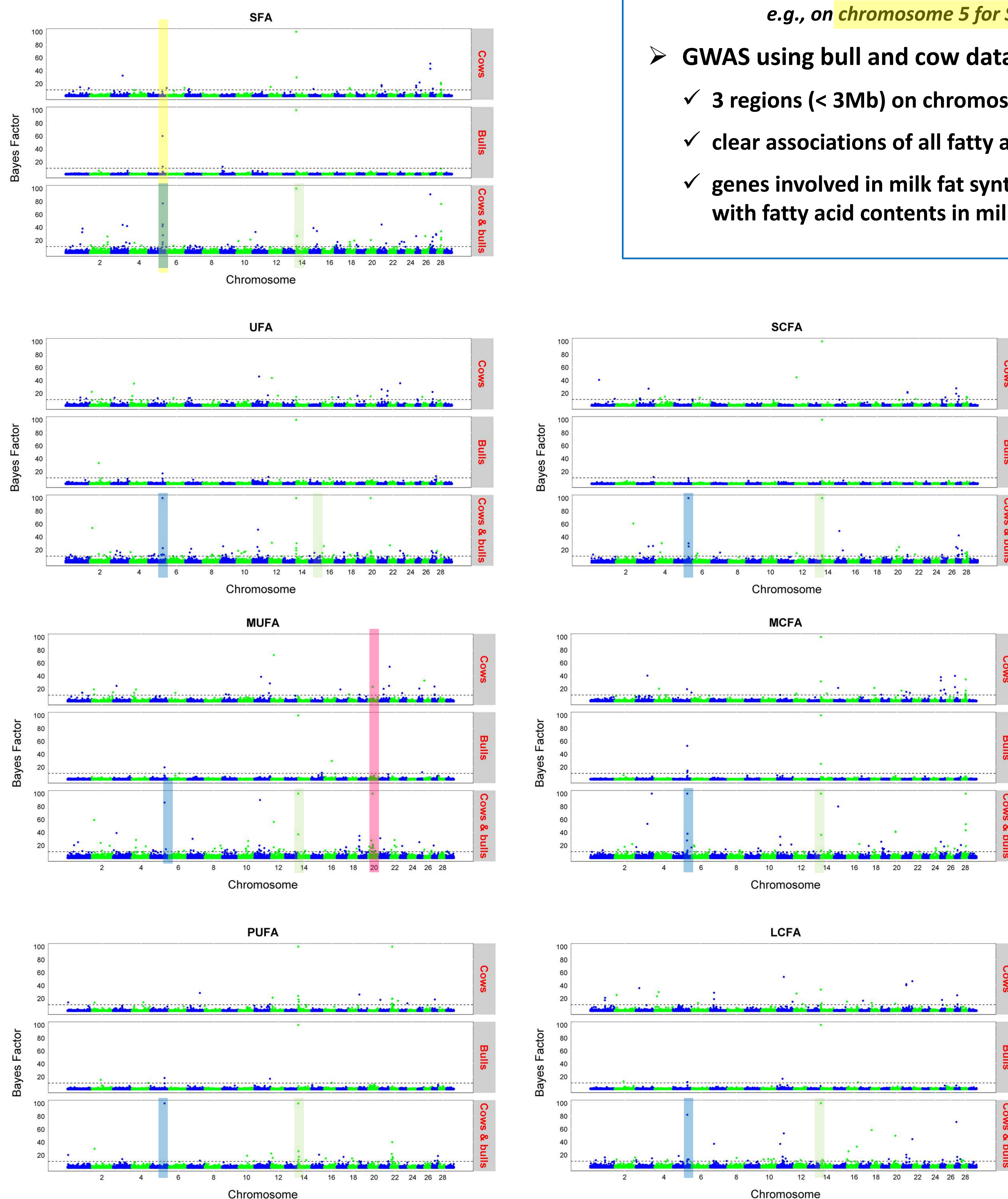
➢ Combining cow and bull data

✓ genetic correlations between cow and bull data ranged from 0.5 – 0.7 (except for PUFA)

✓ some QTL peaks displayed by the combined analyses but not by the separate analyses (1 or both)
e.g., on chromosome 5 for SFA, *on* chromosome 20 for MUFA

➢ GWAS using bull and cow data

✓ 3 regions (< 3Mb) on chromosomes 2, 5 & 14 were associated with all traits

✓ clear associations of all fatty acids with *DGAT1* gene

✓ genes involved in milk fat synthesis are present in some regions significantly associated with fatty acid contents in milk *e.g., on* chromosome 5 (OLR1 gene)

Table 1. Genetic correlations between bull and cow data

SFA	UFA	MUFA	PUFA	SCFA	MCFA	LCFA
0.67	0.47	0.50	0.19	0.65	0.63	0.61

Model

➢ Bayesian stochastic search variable selection (Bayes-SSVS)

➢ Univariate: 1 cow or 1 bull trait

➢ Bivariate: 1 cow and 1 bull trait

➢ One QTL-indicator sampled for both traits per locus

➢ Zero residual correlation between (cow & bull) traits

Data

➢ 7 groups of fatty acids predicted by mid-infrared spectrometry *(Soyeurt et al.,2011, J. Dairy Sci. 93:1657-1667)*

✓ saturated (SFA), unsaturated (UFA), monounsaturated (MUFA), polyunsaturated (PUFA), short chain (SCFA), medium chain (MCFA), long chain (LCFA)

➢ genotypes available for 36,346 SNPs after edits

➢ 226 genotyped bulls with estimated breeding values (EBV)

✓ EBV obtained from a dataset including 345,723 Walloon Holstein cows using a series of 4-trait 3-lactation random regression models

✓ reliabilities ≥ 0.44

➢ 370 genotyped cows with phenotypes