

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

C. Bastin¹, N. Gengler¹, H. Soyeurt^{1,2}, S. McParland³, E. Wall⁴, M.P.L. Calus⁵

¹ Animal Science Unit, Gembloux Agro-Bio Tech, University of Liège, B-5030 Gembloux, Belgium

² National Fund for Scientific Research (F.R.S.-FNRS), B-1000 Brussels, Belgium

³ Animal and Grassland Research & Innovation Centre, Teagasc, Moorepark, Co. Cork, Ireland

⁴ Sustainable Livestock Systems Group, Scottish Agricultural College, Bush Estate, Penicuik, Midlothian, United Kingdom

⁵ Animal Breeding and Genomics Centre, Wageningen UR Livestock Research, PO Box 65, 8200 AB Lelystad, The Netherlands



www.robustmilk.eu

Contact: catherine.bastin@ulg.ac.be

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.

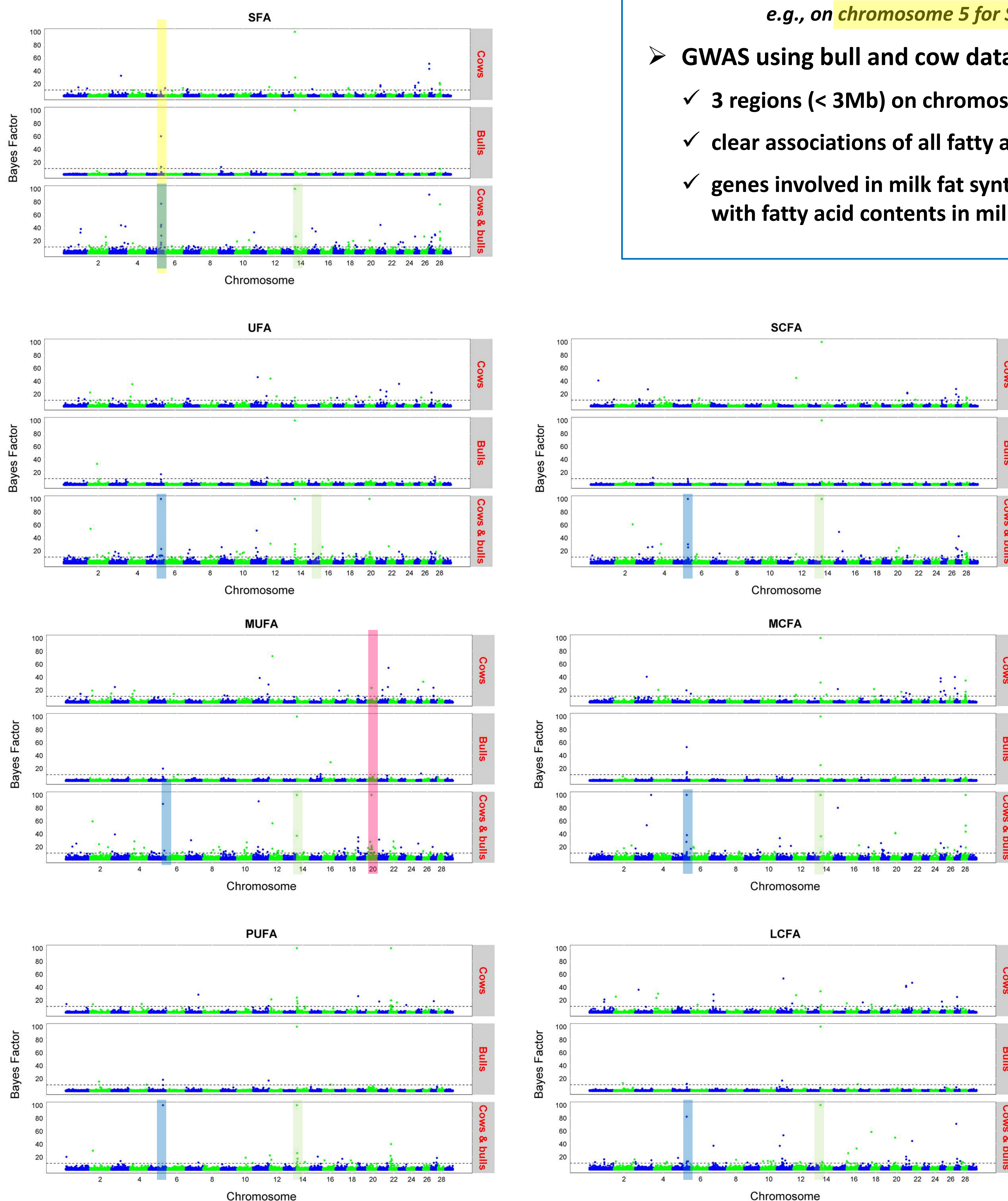
Objective: To perform a genome-wide association study for milk fat composition using either cow data, bull data, or both

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