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**Feasibility of genomic prediction of fatty acids
composition in milk of dairy cattle of
Luxembourg using single-step procedure**

P. Faux^{*,1}, V. M-R. Arnould^{1,2}, H. Soyeurt^{1,3}, N. Gengler¹

¹University of Liège, Gembloux Agro-Bio Tech, Belgium
²CONVIS s.c., Ettelbruck, Luxembourg
³National Fund for Scientific Research, Brussels, Belgium

fnls
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Introduction

- Milk composition in fatty acids (FA)
 - Focus on oleic acid C18:1*cis*9
 - Lactation heritability : 0.48
 - Observed range from ~ 8 to 165 mg/l
- Routinely recorded in Luxembourg (and Wallonia) since 2007
- Two main control methods: S and T
 - T: AM or PM alternatively, S: AM and PM

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The Luxembourg context

- Dairy cattle population
 - Approximately 30,000 cows under milk recording
 - 369,944 animals in pedigree
- Phenotypes
 - 29 FA routinely recorded
 - Prediction using MIR spectrometry (Soyeurt et al., 2009)
 - Spectral data from 87,368 cows (from 690 different herds) have been recorded (May 2012)

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The Luxembourg context

- Genotypes
 - No genotypes available so far
 - BUT, breeders in Luxembourg use a lot of foreign AI bulls (e.g., USA, CAN, DEU, FRA, NLD)
 - many bulls possibly genotyped
- Interest of Luxembourg:
 - availability of estimated breeding values on new traits
 - sharing genotypes of young bulls allows genomic selection for these new traits also foreign bulls

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Objectives

- To assess the impact of genomic prediction on a new trait (milk composition in C18:1*cis*9)
- To compare the gain in accuracy by adding genomic information in the traditional evaluation for milk composition in FA, for:
 - recorded cows
 - genotyped sires of these cows
 - genotyped sons of these sires, candidates to selection in another country

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Materials & Methods: Population

- **7,946** cows with records (REC) on C18:1*cis*9 (first lactation; S-method)
- **47,227** records (average: ~5.94 records/cow)
- **1,666** sires and maternal grand-sires (S-MGS)
- **233** sires (out of 1,666) may be sires of young bulls candidates to selection (CS)
- **10** sons simulated for each of these 233 sires
- Pedigree extracted up to 1950: **62,141** animals

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Materials & Methods: Genotypes

- Simulation of 29,000 SNP markers:
 - 29 autosomes
 - 1,000 SNPs uniformly distributed
- Simulation of genotypes for the whole pedigree, 2 steps:
 - Simulation of founders population using QMSim (Sargolzaei and Schenkel, 2009)
 - Simulation of others animals with real pedigree as mating plan (average crossing-over: 1.6/chromosome)

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Materials & Methods: Phenotypes

- Real data modeled by a RR-TD model, with 3 fixed effects, permanent environment and animal effect (both modeled with 3 Legendre polynomials)
- Simulation of true breeding values (TBV):
 - Polygenic TBV (TBV_p) obtained by using Van Vleck (1994) simulation algorithm:

$$TBV_p = \mathbf{L}_A \begin{bmatrix} \mathbf{v}_1 & \mathbf{v}_2 & \mathbf{v}_3 \end{bmatrix} \mathbf{L}'_{VG}$$
 with:
 - \mathbf{L}_A , factorization of the additive genetic relationship matrix
 - \mathbf{L}'_{VG} , factorization of the Legendre polynomials covariance matrix
 - $\mathbf{v}_1, \mathbf{v}_2, \mathbf{v}_3$, random vectors out of normal distributions $N(0,1)$

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Materials & Methods: Phenotypes

- Regressing TBV_p on Z_c (SNP matrix of recorded cows) to estimate snp effects $\hat{\mathbf{u}}$:

$$\hat{\mathbf{u}} = (\mathbf{Z}'_c \mathbf{Z}_c)^{-1} \mathbf{Z}'_c \cdot TBV_{p,c} \times 0.8$$
- Genomic TBV (TBV_g) obtained by the product of Z (SNP matrix for all animals) and $\hat{\mathbf{u}}$:

$$TBV_g = \mathbf{Z}\hat{\mathbf{u}}$$
- TBV obtained by blending genomic and polygenic TBV as follows:

$$TBV = TBV_p \times 0.2 + TBV_g$$

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Materials & Methods: Phenotypes

- Simulation of permanent environments (PE) following the same process (in that case, $\mathbf{L}_r = \mathbf{I}$)
- Simulation of random residuals (R)

→ Construction of phenotypes:
phenotype = fixed effects + TBV + PE + R

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Evaluations

- Two genetic evaluations
 - without any genomic information → EBV
 - with genotypes of S-MGS and CS → GEBV
- Reliabilities (R²) obtained by computation of correlations between:
 - Breeding values: TBV vs. EBV and GEBV
 - Parent averages: based on TBV (PA_{TBV}) vs. based on EBV (PA_{EBV}) and based on GEBV (PA_{GEBV})

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Results: Breeding values

Group	N	Reliability EBV	Reliability GEBV	Gain in reliability(%)
REC	7,946	0.43	0.43	0.09
S-MGS+CS	3,996	0.21	0.24	2.17
S-MGS	1,666	0.38	0.41	2.17
CS	2,330	0.10	0.12	2.01
ALL	62,141	0.12	0.13	0.45

REC = recorded cows; S-MGS = sires and maternal grand-sires of recorded cows; CS = sons of S-MGS candidates to selection; ALL= all animals in population.

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Results: Parent Averages

Group	N	Reliability PA _{EBV}	Reliability PA _{GEBV}	Gain in reliability(%)
REC	7,946	0.51	0.52	0.35
S-MGS+CS	3,996	0.27	0.30	2.5
S-MGS	1,666	0.41	0.43	1.74
CS	2,330	0.18	0.21	2.8
ALL	62,141	0.19	0.20	0.86

REC = recorded cows; S-MGS = sires and maternal grand-sires of recorded cows; CS = sons of S-MGS candidates to selection; ALL = all animals in population.

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Results: Details for S-MGS

Number of daughters*	N	Reliability EBV	Reliability GEBV	Gain in reliability(%)
1	735	0.25	0.28	2.34
2→10	700	0.38	0.42	2.56
11→50	200	0.67	0.68	0.83
>50	31	0.84	0.84	0.20

* Number of daughters (for sires) and grand-daughters (for grand-sires) is computed with 1 accounting for daughters and 0.5 for grand-daughters.

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Discussion

- Reliabilities increase when using genotypes
 - Low increase
 - Highest increase for young bulls candidates to selection
- May be due to the amount of phenotypic information vs. amount of genomic information
- Next steps:
 - extension to all sampling methods
 - extension to lactations > 1
 - collaboration with Walloon Region

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Conclusions

- Use of genotypes may enhance slightly reliabilities of prediction of breeding values of C18:1 *cis*9 milk composition
 - Upcoming studies will assess more accurately these results
- Nevertheless, sharing genotypes of bulls with Luxembourg (and Walloon Region) is worthwhile
 - Provides breeding value for new traits of interest
 - Reliability: up to 41% for sires of recorded cows

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