



TOWARDS IMPROVEMENT OF **RUMINANT** BREEDING
THROUGH **GENOMIC** AND EPIGENOMIC APPROACHES

Genetic correlation: a parameter or a latent phenotype in genetic evaluations?

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Interbull & ICAR Meeting - Bled, SI
May 21, 2024



This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 101000226

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Are genetic correlations identical for all selection candidates?

French Montbéliarde data

- ▶ \approx 800,000 cows with complete records from first lactation on PROD/FERT:
 - ▶ PROD (MY305d)
 - ▶ FERT (CR at first insemination after the start of lactation)
- ▶ \approx 4 million animals in pedigree.

Model for variance components estimation and genetic evaluation

$$\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \text{AI bull} + \mathbf{g} + \mathbf{e} \longrightarrow \mathcal{N}(\mathbf{0}, \mathbf{R}\sigma_e^2)$$

\downarrow fixed effects \downarrow $\mathcal{N}(\mathbf{0}, \mathbf{A}\sigma_g^2)$ \downarrow (het. variance by HY group)

FERT only: $\mathcal{N}(\mathbf{0}, \mathbf{I}\sigma_{\text{bull}\times\text{year}}^2)$

Fixed effects:

- overall mean, age, HYS
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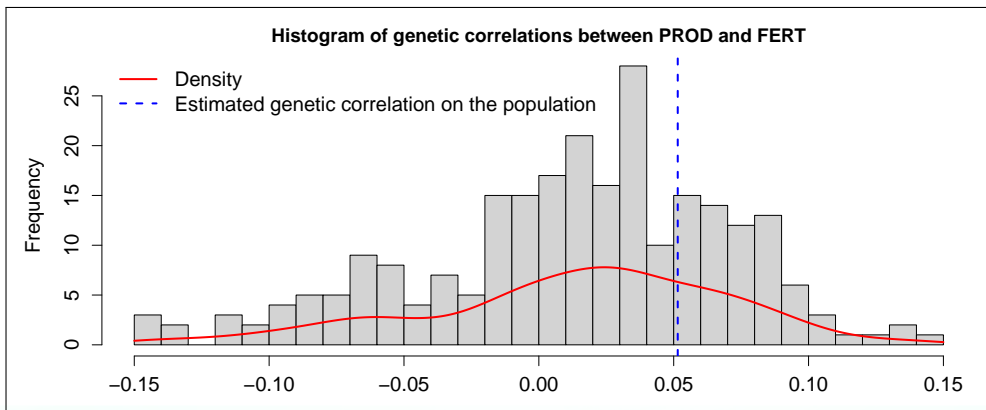
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- ▶ REML estimated genetic correlation: 0.051
- ▶ Subset of 207 sires with at least 500 daughters evaluated,
- ▶ Genetic correlation between PROD and FERT among their daughters.

- Sires expressed different genetic correlations through their daughters.



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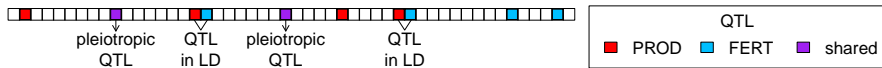
- ▶ Because the consequences of these two hypothesis are very different in the medium to long-term of a breeding program.

- ▶ Base population with 2,000 individuals,
- ▶ 50k SNPs in 29 chromosomes, resembling the cattle genome,
- ▶ Two traits: PROD ($h^2 = 0.3$) and FERT ($h^2 = 0.04$),
- ▶ Genetic correlation of -0.2,
- ▶ Created genetic correlations as either a parameter, or as a latent regulatory phenotype,
- ▶ Selection on sires only (top 20%), similar to dairy cattle system,
- ▶ Evolved the population over at least 40 generations.

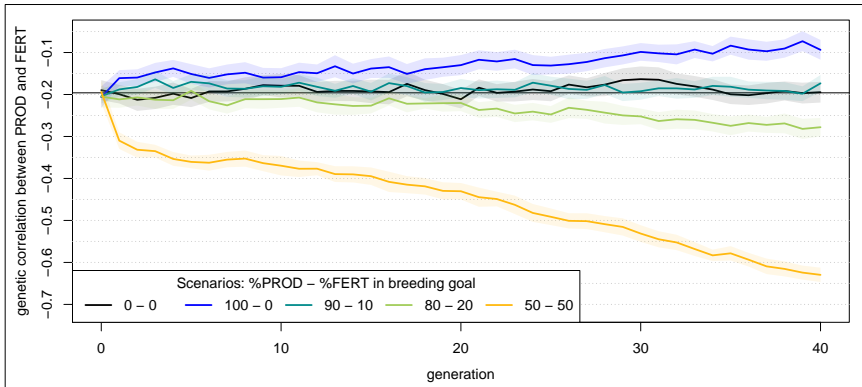
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- ▶ Part of genetic correlation was due to pleiotropy:
1k QTL shared by both traits, with correlated effects,
- ▶ Part of genetic correlation was do to LD:
Each trait had 1k specific QTL that were nearby so that they were in LD
- ▶ Each trait had extra 1k independent QTL.



- ▶ Dual selection inevitably leads to an intensification of negative genetic correlation.

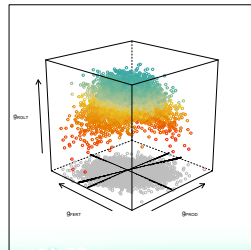
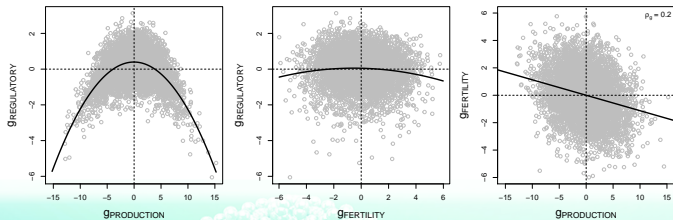


(results based on 100 replicates)

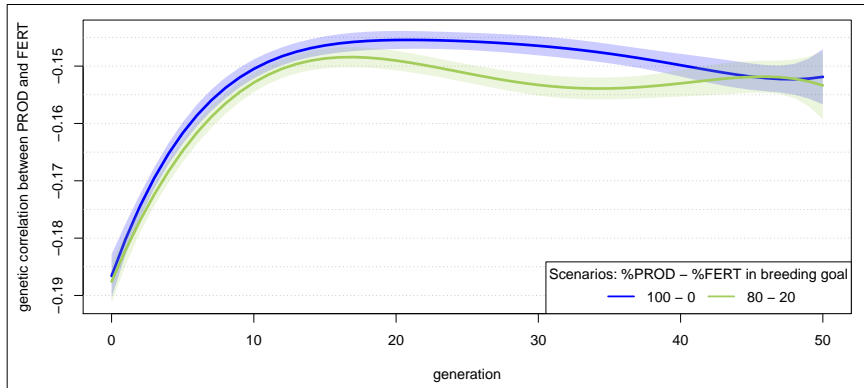
- ▶ Results are mathematically and statistically sound,
- ▶ Biologically, these results raised a lot of questions.

Genetic correlation was the consequence of a concealed regulatory trait, which balances the trade-off between PROD and FERT

- ▶ Three traits: RGLT ($h^2 = 0.1$), PROD ($h^2 = 0.3$), and FERT ($h^2 = 0.04$),
- ▶ Both PROD and FERT had a concave parabolic relationship with RGLT,
 - ▶ simulation of non-linear related traits as in Shokor et al (pre-print available at <https://doi.org/10.1101/2024.03.23.585208>),
- ▶ Genetic correlation between PROD and FERT of -0.2,

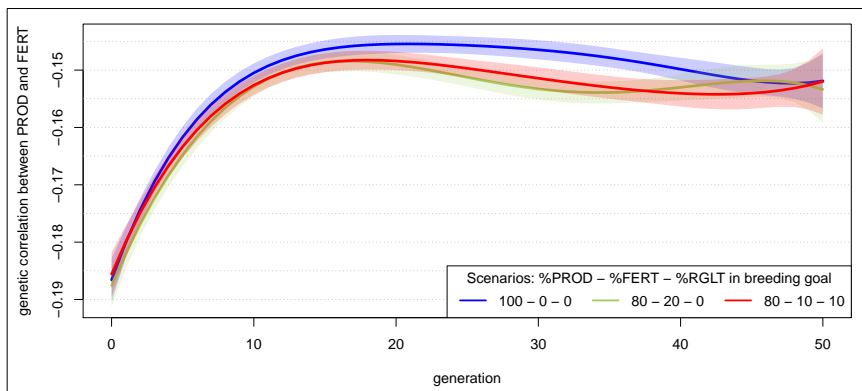


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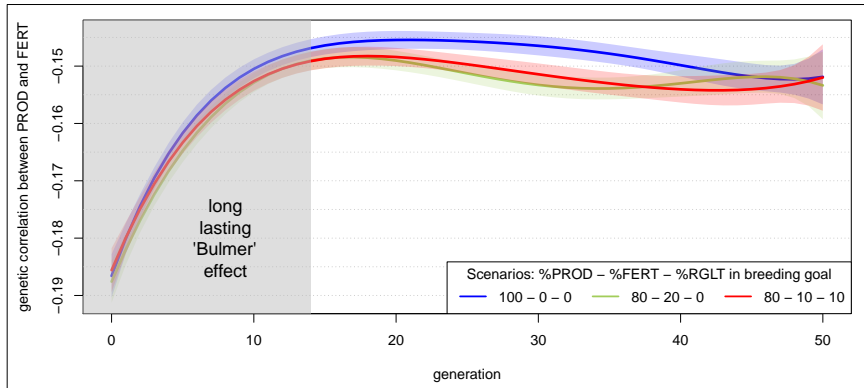
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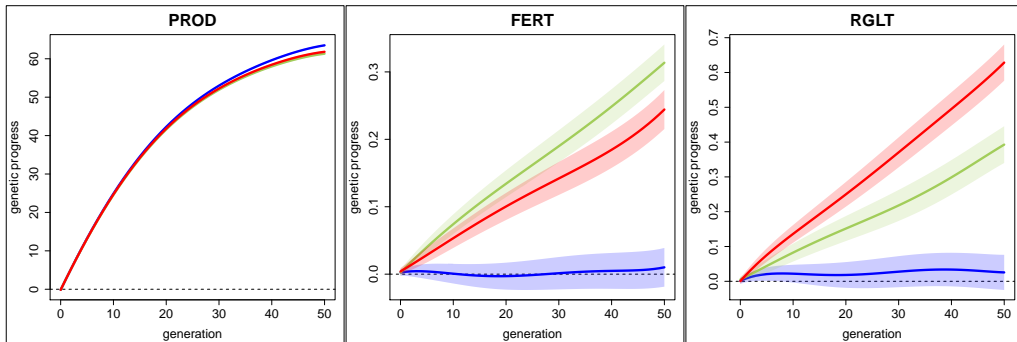
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► Trends of genetic progress:



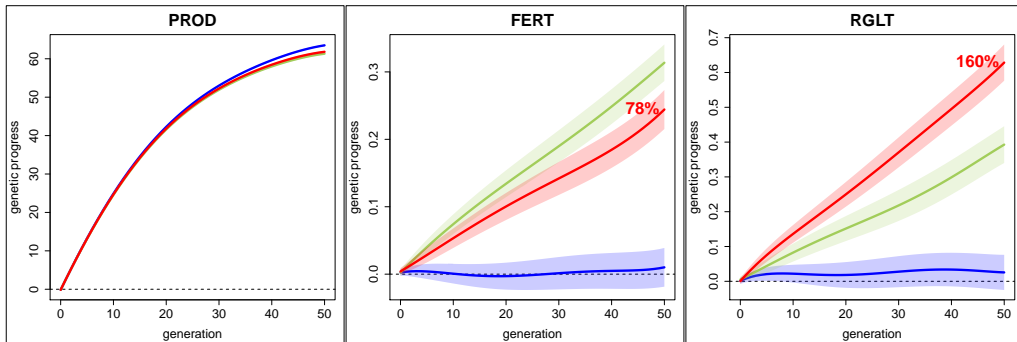
Scenarios: %PROD – %FERT – %RGLT in breeding goal

— 100 – 0 – 0

— 80 – 20 – 0

— 80 – 10 – 10

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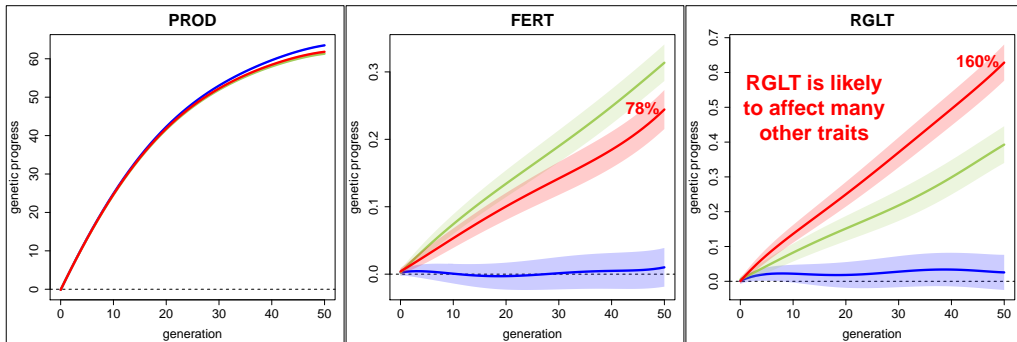
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THANK YOU!

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