

PLANTCOM meeting, Dijon

Quantitative genetics of plant–plant interactions: case of crop mixtures

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Outline

Context and motivation

Case of crop mixtures

Material and methods

Results

Conclusions and perspectives

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- ▶ *joint* analysis of monovarietal and mixed stands to *gradually* introduce mixing ability in breeding programs

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Gaps of knowledge:

- ▶ Which experimental designs?
- ▶ Which magnitude of genetic (co)variances?
- ▶ Which genetic architectures?

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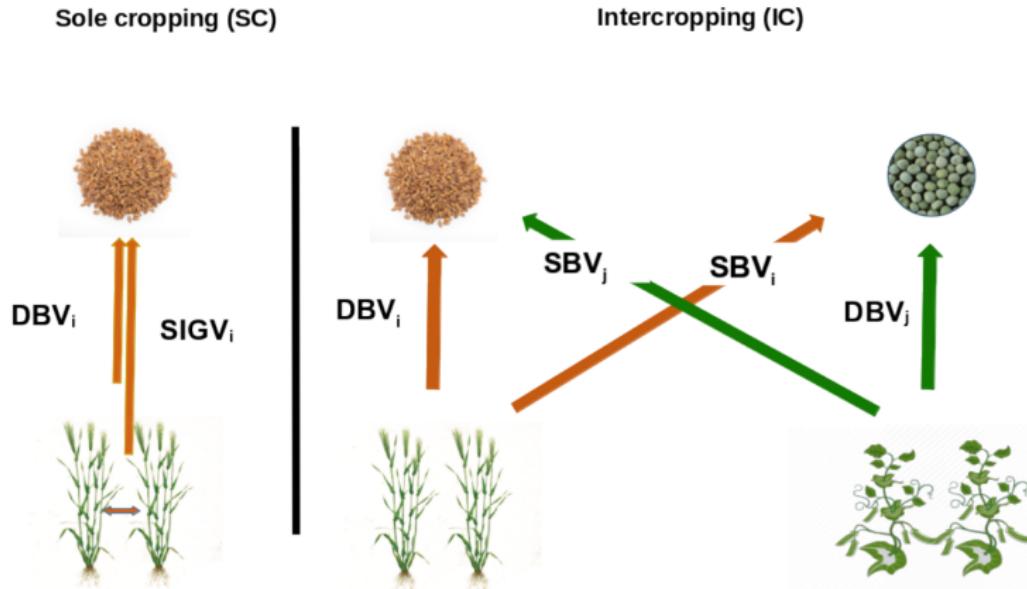
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Genetic model



Social intra-genotypic value: $SIGV := SBV^{SC} + (DBV \times SBV)^{SC}$

Genetic model

Intercrop of i (species s_1) and j (species s_2):

$$Y_{i(j)} = \mu^{s_1, IC} + DBV_i + SBV_j^{IC} + (DBV \times SBV)_{ij}^{IC}$$
$$Y_{j(i)} = \mu^{s_2, IC} + DBV_j + SBV_i^{IC} + (DBV \times SBV)_{ji}^{IC}$$

Sole crop of i and sole crop of j :

- ▶ $Y_i = \mu^{s_1, SC} + DBV_i + SIGV_i$
- ▶ $Y_j = \mu^{s_2, SC} + DBV_j + SIGV_j$

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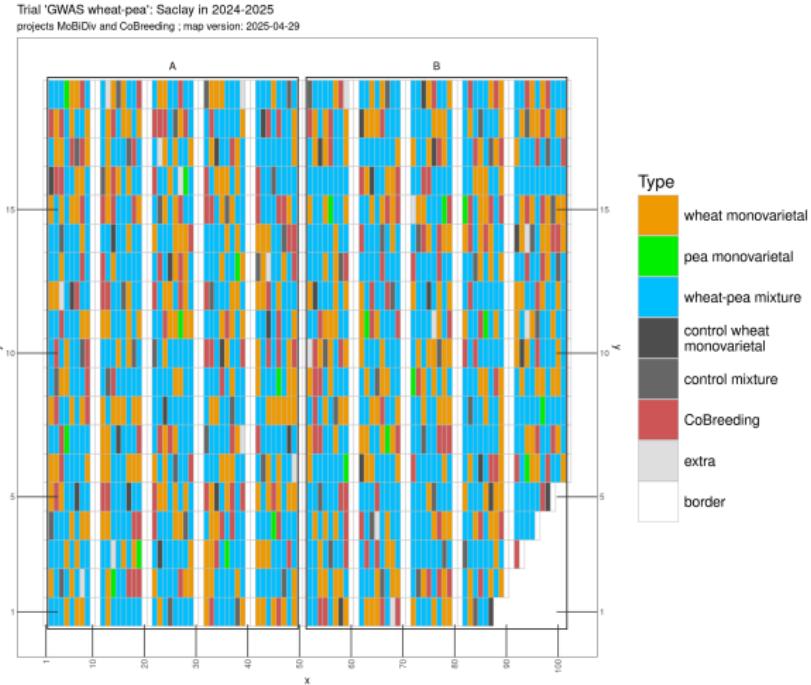
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- ▶ Software implementation: plantmix (R package)

Panel and field trial

- 200 wheat varieties
 - ▶ 395k SNPs
- 2 pea varieties (testers)
- All sole and intercrops in 2 complete blocks
- Traits per species: grain yield, TKW, final height, SLA, soil cover



Panel and field trial



Le Moulon, Saclay, 2025

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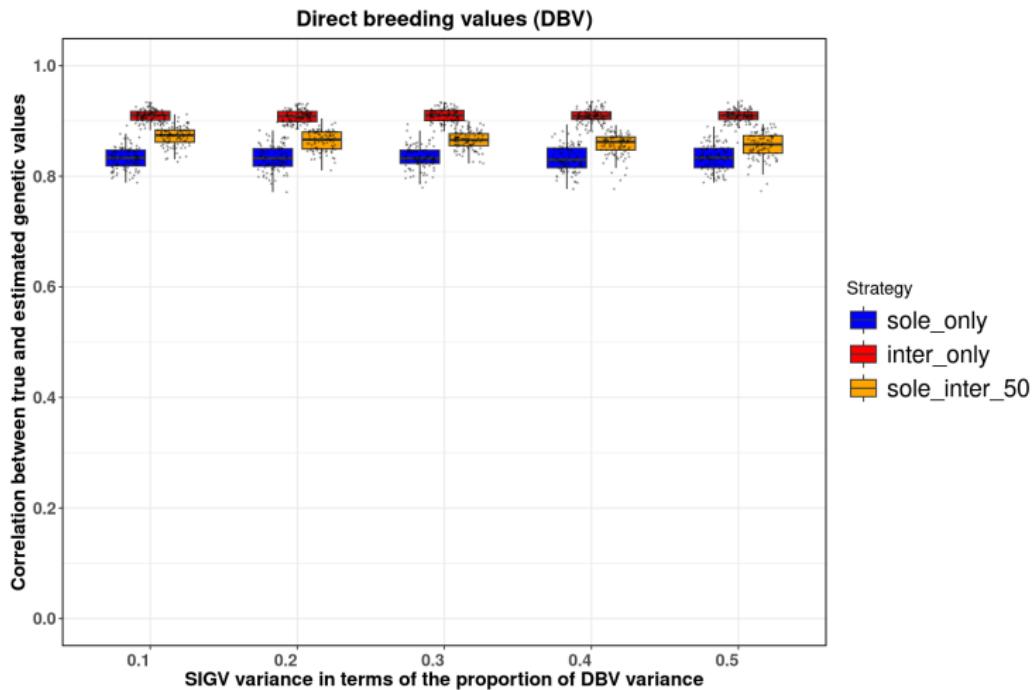
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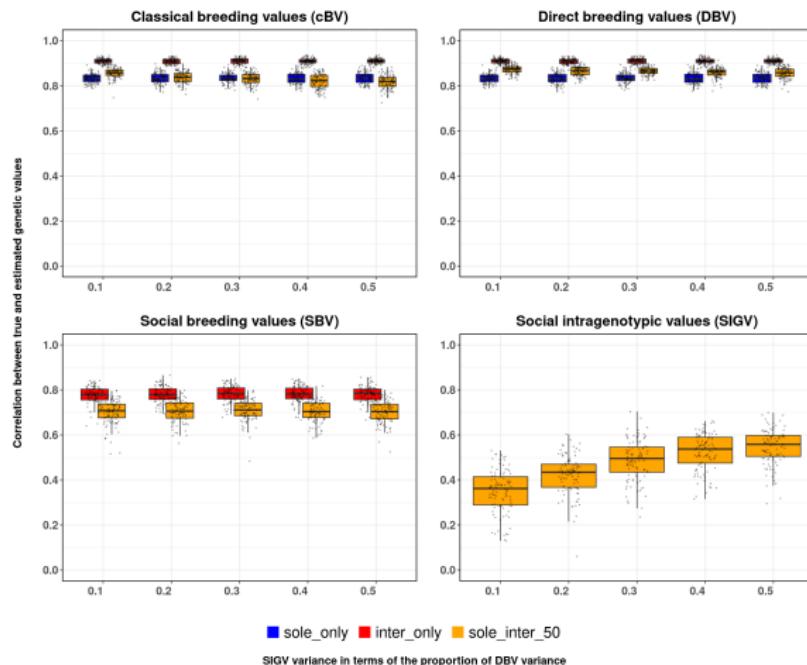
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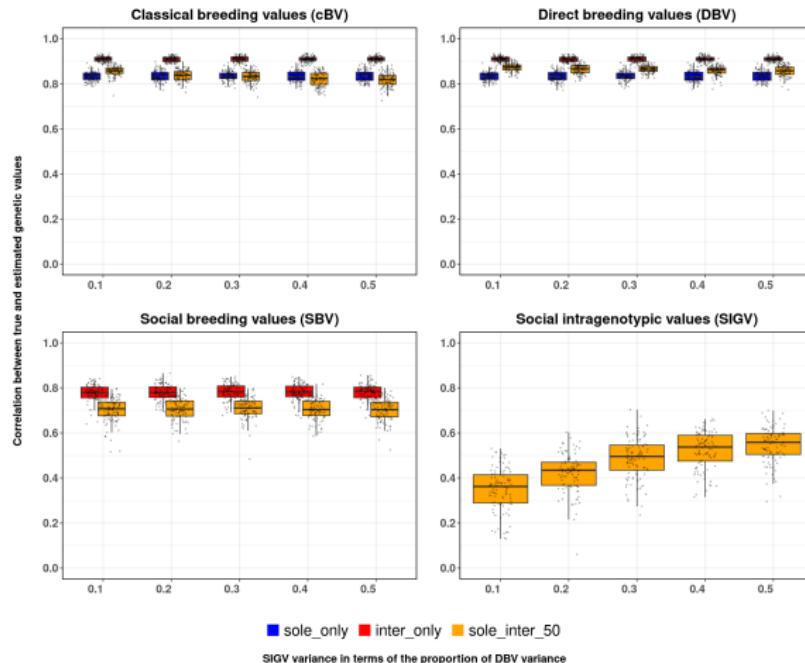
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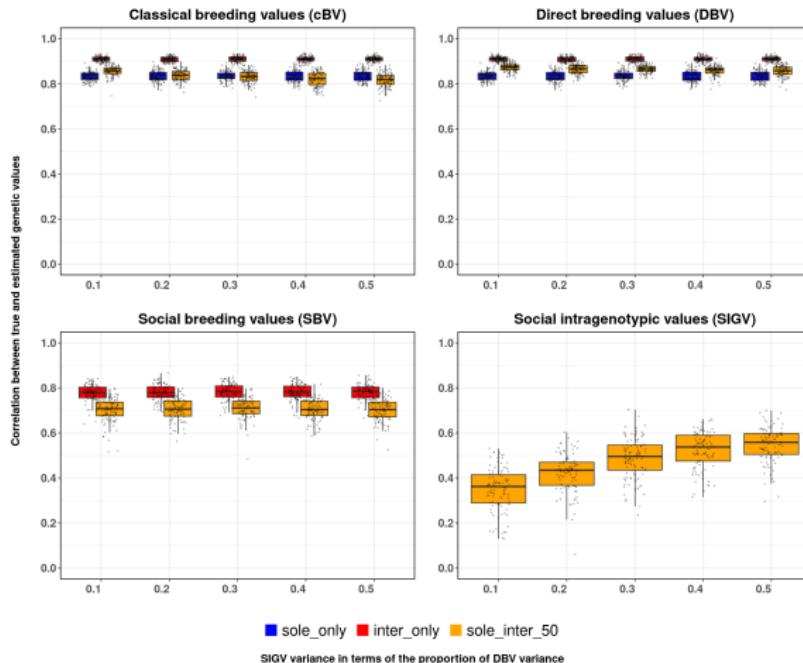


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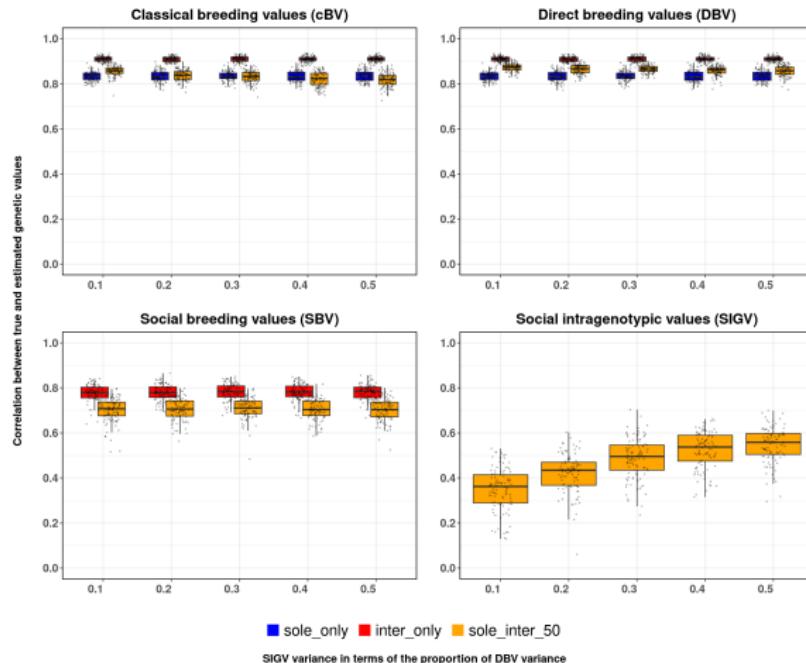
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- Inter_only provides the most accurate estimates.
- Sole inter_50 helps decoupling SIGV and DBV, improving their estimation.

Variance estimates for grain yield

σ^2_{DBV}	σ^2_{SBV}	σ^2_{SIGV}	$\sigma^2_{DBV \times SBV}$	$\sigma^2_{e-pur(w)}$	$\sum^2_{e-mix(w)}$	$\sum^2_{e-mix(p)}$
10.1 [8.01, 11.39]	1.25 [0.17, 247]	2.49 [0, 5.23]	2.19 [0.14, 5.76]	16.6 [12.00, 20.00]	12.78 [10.61, 13.98]	18.53 [15.56, 21.30]

Values are shown as the estimate (first line), followed by the 95% confidence interval in brackets (second line), calculated across 500 replicates using bootstrapping.

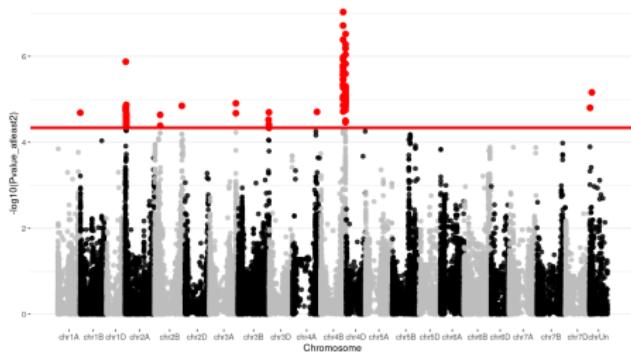
- Social genetic variances < variance of direct breeding values

Correlation estimates for grain yield

$\rho_{DBV-SBV}$	$\rho_{\epsilon\text{-mix}}$
0.24 [0.01, 1]	-0.19 [-0.29, -0.07]

- Unexpected positive correlation observed between DBV and SBV
⇒ favorable wheat-pea interactions

Meta-GWAS on grain yield [DBV, SBV, SIGV]



H0 rejected when a SNP is associated with at least two traits (FDR controlled at 5%)

► **9 pleiotropic regions detected**

- Not detected in single-trait GWAS.
- Further analyses underway for validation.

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- Preliminary GWAS identified several regions associated with at least two types of breeding values.

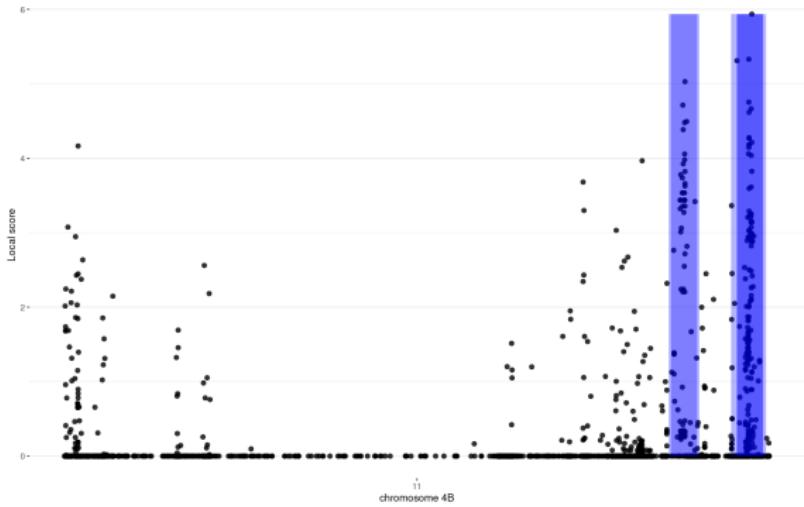
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- Preliminary GWAS identified several regions associated with at least two types of breeding values.
- Analyze the other traits, notably those from drone imaging (PhD V. Freitas).

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R. Perronne
- ▶ **AGAP:** A. Baranger

Supp 1: meta-GWAS on grain yield [DBV, SBV, SIGV]



Local scores along chromosome 4B. The boxes represent the significant zones identified. The threshold was set to $\xi = 2$, and the nominal FDR level is fixed at 0.05.