

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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Gaps of knowledge:

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

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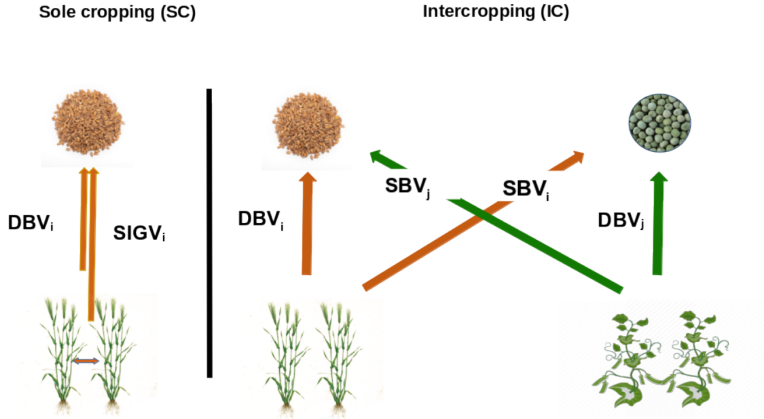
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# Genetic model



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

# Genetic model

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

$$Y_{i(j)} = \mu^{s_1, IC} + \textcolor{red}{DBV}_i + SBV_j^{IC} + (DBV \times SBV)_{ij}^{IC}$$

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

Sole crop of  $i$  and sole crop of  $j$ :

►  $Y_i = \mu^{s_1, SC} + \textcolor{red}{DBV}_i + SIGV_i$

►  $Y_j = \mu^{s_2, SC} + DBV_j + SIGV_j$

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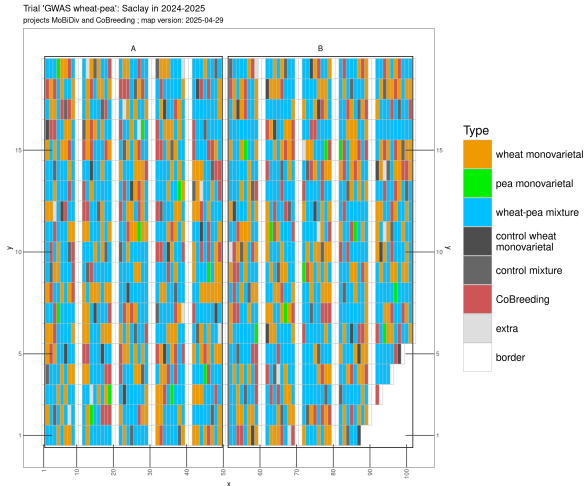
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- ▶ Software implementation: `plantmix` (R package)

# 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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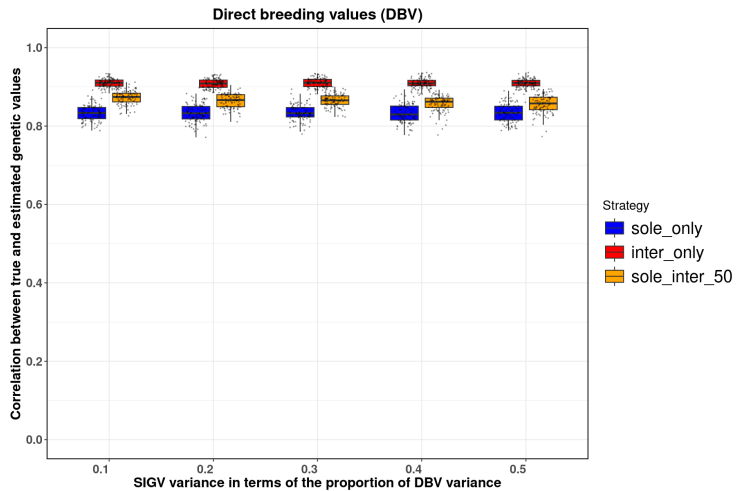
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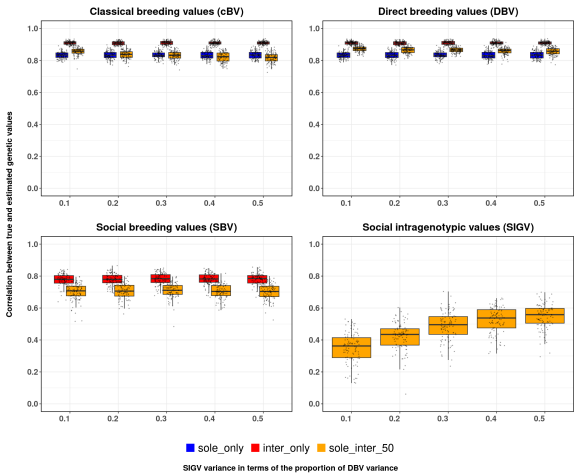
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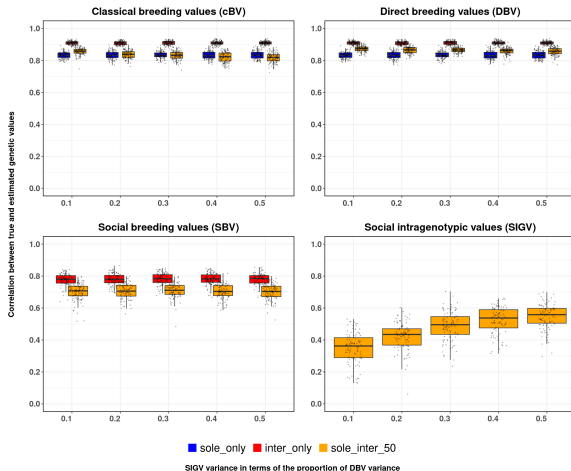
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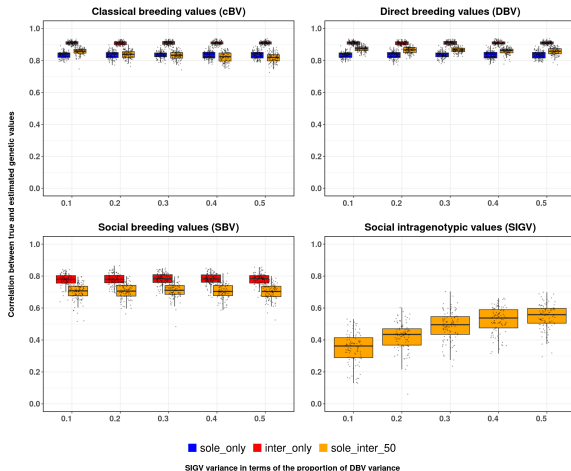


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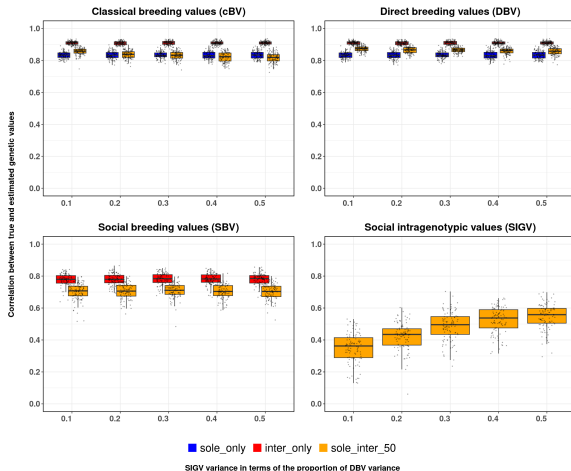
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- **Experimental design, genetic effects, and the ratio  $\sigma_{SIGV}^2/\sigma_{DBV}^2$  influence accuracy.**
- **Inter\_only provides the most accurate estimates.**
- **Sole\_inter\_50 helps decoupling SIGV and DBV, improving their estimation.**

# Variance estimates for grain yield

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

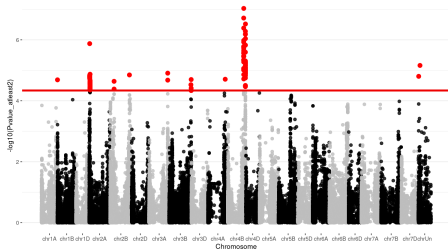


# Correlation estimates for grain yield

$\rho_{\text{DBV-SBV}}$	$\rho_{\epsilon\text{-mix}}$
0.24	-0.19
[0.01, 1]	[-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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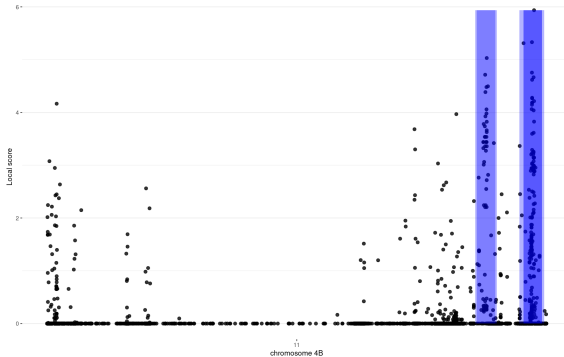
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- **Preliminary GWAS identified several regions associated with at least two types of breeding values.**
- **Analyze the other traits, notably those from drone imaging (PhD V. Freitas).**



# Acknowledgments

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  - ▶ E. Akaffou, L. Wang, M. Mesnil, D. Wang, F. Petit, R. Diallo, U. Louis, C. Coste, F. Alléhaut
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- ▶ **BIOGER:** T. Vidal, M. Delrieu
- ▶ **IGEPP:** N. Moutier, 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.