Leveraging a broad gradient of plant-plant interactions to efficiently breed for agroecological mixtures.

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Résumé

Under the constraints of climate change, energy sobriety, and pesticide reduction, a major lever of the agroecological transition consists of diversifying farmers' practices to reduce the risk of crop failure. With crops exposed to increased abiotic and biotic stresses, farmers may opt for intercropping (mixtures of crop species) to benefit from their advantageous yield stability, disease control, and, notably, for cereal-legume mixtures, lower dependence on nitrogen fertilizers.
However, breeding programs work on pure stands only, i.e., fields sown with a single variety, despite evidence of phenotypic plasticity and a moderate correlation between yield in pure vs. mixed stands. This argues for the development of specific varieties adapted for intercropping, but the combinatorial explosion is a major issue for breeders (N genotypes per species enable NxN balanced binary mixtures to be assembled).

We overcame this situation by proposing incomplete experimental designs along with a new genetic modeling of plant-plant interactions. Specifically, we leveraged the theoretical framework of Griffing (1967) that decomposes the phenotype of a focal genotype as the sum of the direct effect of this genotype (direct breeding value, DBV) and the indirect effect of its neighbor genotype (social breeding value, SBV). Furthermore, as proposed by Forst et al. (2019), we explicitly modeled the contribution of intra-genotype interactions (called here SIS for social intra-specific) that occur in both pure and mixed stands so that the classical breeding value in pure stands, cBV, equals DBV + SIS.

The corresponding statistical model consists of a linear mixed model where the genetic effects are modeled as random to handle incomplete designs, using genomic kinship. It takes

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notably into account the covariance between DBV and SBV as well as between errors in mixed stands. Based on simulations, we first checked the estimation accuracies from complete versus incomplete designs. We then explored various incomplete designs contrasted for their relative proportion of pure vs mixed stands. They were compared based on the genetic gain over a range of genetic (co)variances.

As a result, we can demonstrate under which scenario and experimental design a breeder can expect a genetic gain that balances the mean performance of the population in both pure and mixed stands.

Mots-Clés: quantitative genetics, plant, plant interactions, phenotypic plasticity, intercropping