

Genetic drivers for mixture performance in pea and barley

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Extended Abstract

Mixed cropping has been proposed as one way to improve yield stability and resource efficiency of established agricultural systems. The choice of the genotype of each crop species involved in a mixture has emerged to be of key importance for the success of a mixed cropping system. However, until now, methodologies and experimental designs to tackle genetic improvement for species mixtures are yet little developed and pure stand yield is widely used as a proxy for mixture yield, yet often with limited success. To fortify future breeding strategies for mixed cropping the goal of this study was to (i) identify key genetic drivers for mixture performance such as general mixing ability (GMA), i.e. a genotype's positive or negative contribution to mixture yield, and specific mixing ability (SMA), the interaction of two genotypes of opposite species, (ii) identify functional traits that are related to these genetic drivers, (iii) compare experimental designs for their aptness and efficiency to estimate GMA and SMA and (iv) decompose GMA of each cultivar into effects that influence its own performance in a mixture (producer effect, Pr) and that influence the performance of the affiliated species (associate effect, As) in order to utilize this for optimization of mixture composition and yield.

This study comprised 26 semi-leafless and two leafy grain pea (*Pisum sativum* L.) cultivars and eight two-row barley (*Hordeum vulgare* L.) cultivars, spring-sown in a replicated 2 year, two-location experiment in Switzerland under organic management in an incomplete factorial design (IFD) including pure stands. In the IFD, every barley cultivar was only combined with eight pea cultivars while every pea cultivar was only combined with two barley cultivars in a random manner. Grain yield and putative key traits for mixing ability were measured. Based on the empirically obtained parameters (means and variances), a simulation study was done with one full factorial design (FFD) comprising eight barley and eight pea cultivars and one IFD comprising eight barley and 30 pea cultivars, using similar amounts of experimental resources with 64 and 60 plots per replicate, respectively. The IFD was identical with the design in the empirical study. With $n=1000$ simulations per design, means were computed of the estimated variances of GMA, SMA and the error and were compared with the true parameters. Estimated genetic effects of each design were compared with the true effects by their correlations. See Haug *et al.* (in prep) for further details. As discussed by Forst (2018), GMA of a simulated dataset was decomposed into Pr and As effects (Fig. 1A) and a graph of one exemplary set of simulated Pr-As values was created (Fig. 1B).

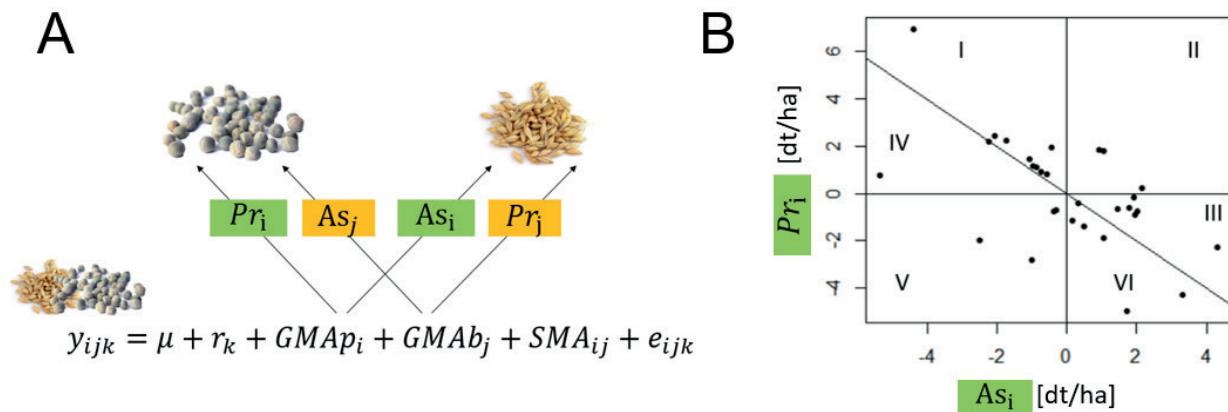


Fig. 1(A). The GMA-SMA model with with the total mixture yield, the grand mean, block-effect, and GMA effects of pea and barley, respectively, SMA effect and error term. GMA effects can be decomposed into corresponding Pr and As effects. (B) An exemplary scatterplot of Pr and As effects of 30 pea cultivars from one of 1000 simulations. The diagonal line is a function with slope -1 and intercept 0. All genotypes above the slope have positive GMA while those below have negative GMA, and genotypes on the line have zero GMA. Six sectors (I-VI) can be identified.

Pure stand yields of the 28 pea cultivars were correlated with their corresponding mixed cropping yield with a Pearson correlation coefficient of 0.41*. Excluding leafy cultivars, the correlation amounted to $r=0.60^{**}$. The GMA of both pea and barley were significant with effect sizes (Cohens f^2) of 0.72 and 0.48, respectively. However, the ranking of the genotypes partly depended on the environmental conditions, i.e., significant GMA pea \times year and GMA barley \times location interactions were observed with effect sizes of 0.62 and 0.49, respectively. SMA was not significant ($P=0.57$). Pea GMA could partly be predicted by certain traits, such as early vigour and days to flowering with GMA - trait correlations of 0.39* and -0.43*, respectively. With both the FFD and the IFD, GMA, SMA and error variances were estimated correctly. Pea GMA effects were estimated with slightly lower precision in the IFD ($\rho=0.83$ vs $\rho=0.89$ in the FFD), however, with the IFD, a fourfold higher number of genotypes could be tested.

The Pr-As scatterplot could be separated into six sectors (I-IV), divided by the graph's axes and a zero GMA-line, a function of slope -1 and intercept 0 (Fig. 1B), with all genotypes above the zero GMA-line having positive GMA values and those below showing negative GMA.

The GMA \times environment interactions might be explained by large climatic differences between 2018 (dry, hot) and 2019 (average temperatures and rainfall) as well as large differences in soil nitrogen content across the two locations. Nonetheless, genotypes with consistently high mixed cropping yield could be identified. Even though pure stand yield was a fair predictor for mixed cropping yield, selecting only by this feature bears the danger of overlooking well performing genotypes, which reveal their potential only under mixed cropping, such as otherwise lodging leafy pea cultivars. The advantage of early vigorous pea plants could be due to competitiveness towards barley in the sensitive early growth stage when both are still highly competing for soil N, while earliness potentially is a complementarity trait for temporal niche differentiation for light capture. With an IFD, a nearly fourfold higher number of genotypes can be tested with only a slight loss of precision compared with FFD. Thus, selection intensity can be increased fourfold. At the same time, GMA and SMA variances were estimated correctly by the IFD, which is crucial to determine the breeding strategy in early stages of a breeding program for mixed cropping. Categorizing genotypes by the six segments in a Pr/As scatterplot (Fig. 1B) allows genotypes to be chosen for desired mixture ratios, i.e. with high content of the focal species (I) or the companion species (III) or both (II). This concept allows further determination of the competitive (dis)advantage of a crop: by fitting a regression to the data, a slope of the regression markedly higher than -1 indicates that

the focal species is at a competitive advantage, since, in this case, total yield increases with high As effects (in sector II or III) and decreases with low As effects (sector IV and V). The findings will facilitate the design of breeding schemes for pea- barley mixtures and beyond and contribute methodologically to the emerging field of breeding for mixed cropping.

References

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