Exploring specific combining abilities in incomplete factorial cross designs with LABKEY™ software

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Introduction
One of the biggest challenges for plant breeders is to deal with interactions. Particularly, they aim at identifying which (female * male) combination is offering the most promising specific combining ability (SCA). After the pioneer works of Tukey (1949) and Mandel (1971), the AMMI (for “Additive main effects and multiplicative interaction”) framework became very popular during the last decade. Based on a practical example analyzed using LABKEY™, this study is intending to show how this software is providing the users with tools helping them to predict and display specific combining abilities (SCA) for non-observed hybrid combinations. These predictions are made using Principal Component Analysis (PCA) results obtained on the observed crosses, under the hypothesis that they represent a connected, unbiased subset of the complete set of possible combinations.

Material & Method
25 female lines were crossed with 8 male lines to produce 90 hybrids, i.e. with a high proportion of missing data. Each female line was crossed with a minimum of two male lines. Interactions between male and female parents (± SCA) were obtained in subtracting the estimates of additive effects of the male parent and of the female parent from the observed yield. In the LABKEY™ software, these estimates are obtained through Yates’ (Yates, 1933) method of estimation of missing data, a method which implicitly assumes a null interaction between the unobserved (female parent * male parent) combinations. These estimates are also those produced by the LSMEANS statement of the GLM procedure under SAS® with a model including only additive effects. PCA was performed on the FxM interaction estimates and we then used the SCA components on the first principal components to predict the SCA for unobserved combinations.

Results and discussion
The first two components of SCA are accounting for the major part of the (female * male) interaction (55% of the total variance): see Figure 1. Based on these first two components, there is a good adequacy (R²= 0.68) between the observed and calculated SCA for observed combinations, as shown in Figure 2. We therefore propose to use the same predictor for unobserved combinations. In this way, we obtain a table of (positive and negative) predicted interactions: see Figure 3.

Using the crosses matrix available in LABKEY™, it is possible to display all the information on the parents and on the hybrids (crosses done, predictions for the non-observed combinations) to help the breeder to choose his future crosses and to automatically generate them in LABKEY™: see Figure 4. As pointed out by Technow et al. (2014), hybrid breeders are often testing the combining ability with a limited number and range of testers, thus limiting the possibility to explore a wider range of combination for the detection of particular hybrid combination. This example shows how, with the same investment in hybrid production and experimentation, it becomes possible to explore a wider space of genetic diversity and to propose inferences for unobserved combinations.

General Framework
The AMMI approach is modeling the result of the combination of two factors (Female and Male, hereafter named I and J) as the sum of additive, main effects and of multiplicative effects of both factors, those being actually calculated through a PCA on interaction estimates:

\[ Y_{ij} = m + a_i + b_j + ab_{ij} = m + a_i + b_j + \sum_k^{k} U_k c_{iik} d_{jk} + e_{ij} \]

Where m is the grand mean, \( a_i \) and \( b_j \) are the main, additive effects of the factors I and J, and \( ab \) represents their interaction; \( c_{iik} \) and \( d_{jk} \) are the coordinates of the component k of the interaction, and \( U_k \) is the k-th component eigenvalue.

Conclusion
LABKEY™ is currently developing tools to help breeders in their aim to deal with various types of interaction. This study shows an example dealing with Female x Male interactions and mainly using two LABKEY™ tools, the PCA and the crosses matrix, configured to compute and display SCA predictions for a subset of non-observed hybrids.

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