Supplemental Material for

Genome-Wide Prediction of the Performance of Three-Way Hybrids in Barley

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Supplemental Information

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Supplemental Information

Generalization of the GSA-RRBLUP model

Suppose that three-way hybrids can be symbolized as parent1 × (parent2 × parent3). In the previous sections, we discussed GSA-RRBLUP applied in the special situation where exclusively information on single-cross hybrids parent1 × parent2 is known. In general, the performances of three-way hybrids can also be predicted based on the information on all types of single-cross hybrids, i.e. parent1 × parent2, parent1 × parent3, and parent2 × parent3. Then, the generalized GSA-RRBLUP model is:

\[
\begin{bmatrix}
  y_1 \\
  y_2 \\
  y_3
\end{bmatrix} =
\begin{bmatrix}
  1_{n_1 \mu_1} \\
  1_{n_2 \mu_2} \\
  1_{n_3 \mu_3}
\end{bmatrix} +
\frac{1}{2}\begin{bmatrix}
  Z_{A1} & Z_{A2} & 0_{n_1 \times m} \\
  Z_{A2} & Z_{A3} & 0_{n_2 \times m} \\
  Z_{A3} & Z_{A1} & 0_{n_3 \times m}
\end{bmatrix} \begin{bmatrix}
  a_{P1S} \\
  a_{P2S} \\
  a_{P3S}
\end{bmatrix} +
\begin{bmatrix}
  Z_{DP1P2} \\
  Z_{DP1P3} \\
  Z_{DP2P3}
\end{bmatrix} d_0 +
\begin{bmatrix}
  Z_{DP1P2} & 0_{n_1 \times m} & 0_{n_1 \times m} \\
  0_{n_2 \times m} & Z_{DP1P3} & 0_{n_2 \times m} \\
  0_{n_3 \times m} & 0_{n_3 \times m} & Z_{DP2P3}
\end{bmatrix} \begin{bmatrix}
  d_{P1P2S} \\
  d_{P1P3S} \\
  d_{P2P3S}
\end{bmatrix} + \varepsilon,
\]

where \( y_1, y_2 \) and \( y_3 \) are \( n_1 \)-, \( n_2 \)-, and \( n_3 \)-dimensional vectors of phenotypic records of the three types of single-cross hybrids, respectively. \( n_1, n_2 \) and \( n_3 \) are the number of genotypes of the three type of single-cross hybrids, \( \mu_1, \mu_2 \) and \( \mu_3 \) refer to the means of the three types of single-cross hybrids, \( Z_{A1}, Z_{A2}, \) and \( Z_{A3} \) are \( n_1 \times m, n_2 \times m, \) and \( n_3 \times m \) design matrices for the additive effects of the three types of single-cross hybrids. \( Z_{AP1,1} \) and \( Z_{AP2,1} \) are \( n_1 \times m \) design matrices for the additive effects of the parents corresponding to single-cross hybrids parent1 × parent2. \( Z_{AP1,2} \) and \( Z_{AP3,2} \) are \( n_2 \times m \) design matrices for the additive effects of the parents corresponding to single-cross hybrids parent1 × parent3. \( Z_{AP2,3} \) and \( Z_{AP3,3} \) are \( n_3 \times m \) design matrices for the additive effects of the parents corresponding to single-cross hybrids parent2 × parent3. \( Z_{DP1P2}, Z_{DP1P3} \) and \( Z_{DP2P3} \) are design matrices for the dominance effects of the three
types of single-cross hybrids. \( d_0 = (d_{0,1}, d_{0,2}, ..., d_{0,m})^T \) is a vector of general effects of dominance effects. \( d_{P_1P_2S} = (d_{P_1P_2S,1}, d_{P_1P_2S,2}, ..., d_{P_1P_2S,m})^T \), \( d_{P_1P_3S} = (d_{P_1P_3S,1}, d_{P_1P_3S,2}, ..., d_{P_1P_3S,m})^T \), and \( d_{P_2P_3S} = (d_{P_2P_3S,1}, d_{P_2P_3S,2}, ..., d_{P_2P_3S,m})^T \) are specific dominance effects of the three types of single-cross hybrids, respectively. Other terms are the same as defined above. \( d_0 \sim N\left(0_m, I_m \sigma^2_{d_0}\right) \), \( d_{P_1P_2S} \sim N\left(0_m, I_m \sigma^2_{d_{P_1P_2S}}\right) \), \( d_{P_1P_3S} \sim N\left(0_m, I_m \sigma^2_{d_{P_1P_3S}}\right) \), \( d_{P_2P_3S} \sim N\left(0_m, I_m \sigma^2_{d_{P_2P_3S}}\right) \). \( a_0 \), \( a_{P_1S} \), \( a_{P_2S} \), \( a_{P_3S} \), \( d_0 \), \( d_{P_1P_2S} \), \( d_{P_1P_3S} \), \( d_{P_2P_3S} \) and \( \varepsilon \) are mutually independent.

Then the prediction model for three-way hybrids of parent1 × (parent2 × parent3) becomes:

\[
y' = 1_n \hat{\mu} + Z_A \hat{\alpha}_0 + \frac{1}{2} Z_{A_{P_1}} \hat{\alpha}_{P_1S} + \frac{1}{4} Z_{A_{P_2}} \hat{\alpha}_{P_2S} + \frac{1}{4} Z_{A_{P_3}} \hat{\alpha}_{P_3S} + Z_D \hat{d}_0 + \\
\frac{1}{2} Z_{D_{P_1}} \hat{d}_{P_1P_2S} + \frac{1}{2} Z_{D_{P_3}} \hat{d}_{P_1P_3S}.
\]

Equation [S1] implicitly assumes that single-cross hybrids based on three genetically distinct subpopulations/heterotic groups can be generated in all possible combinations. This is for instance possible if three heterotic groups are characterized by absence of restorer genes and if parental lines can be converted into male lines by introgression of a major restorer gene. Often, however, single-cross hybrids cannot be generated on a large scale in all directions and therefore, phenotypic data of single-cross hybrids parent1 × parent2 and parent1 × parent3 are only available. Then Eq. [S1] simplifies to:
\[
\begin{bmatrix}
y_1 \\
y_2
\end{bmatrix} = \begin{bmatrix} 1_{n_1}\mu_1 \\ 1_{n_2}\mu_2 \end{bmatrix} + \begin{bmatrix} Z_{A,1} \\ Z_{A,2} \end{bmatrix} a_0 + \frac{1}{2} \begin{bmatrix} Z_{AP_1,1} \\ Z_{AP_1,2} \end{bmatrix} a_{P_1}\Sigma + \frac{1}{2} \begin{bmatrix} Z_{AP_2,1} \\ Z_{AP_2,2} \end{bmatrix} a_{P_2}\Sigma + \begin{bmatrix} 0_{n_1\times m} \\ 0_{n_2\times m} \\ Z_{AP_3,2} \end{bmatrix} \begin{bmatrix} a_{P_2}\Sigma \\ a_{P_3}\Sigma \end{bmatrix} +
\begin{bmatrix}
z_{DP_1P_2} \\
z_{DP_1P_3}
\end{bmatrix} d_0 + \begin{bmatrix} Z_{DP_1P_2} \\ 0_{n_2\times m} \end{bmatrix} \begin{bmatrix} 0_{n_1\times m} \\ Z_{DP_1P_3} \end{bmatrix} \begin{bmatrix} d_{P_1P_2}\Sigma \\ d_{P_1P_3}\Sigma \end{bmatrix} + \epsilon.
\]

Supplemental Figure S1. Mating design of 363 single-cross (Female 1 × Male; blue points) and 361 three-way hybrids ((Female 1 × Female 2) × Male; red points) in barley.