Figure S1  Histograms of the off-diagonal realized relationship coefficients.
Figure S2  Maximizing accuracy vs. minimizing MSE for the 2+6-row barley population (see Figure 3 caption).
Starting from the parent-offspring regression (Equation 31):

\[ \beta^2 = \frac{\text{cov}(\alpha_i, y_i)}{\text{var}(y_i)} = \frac{a'(y - \mu I)}{|y - \mu I|^2} \]

we derive an expression for heritability in terms of the variance components of the mixed model

\[ y = \mu I + a + \varepsilon, \quad \text{where} \quad a \sim N(0, G), \quad G = \Lambda \sigma^2, \quad \text{and} \quad \varepsilon \sim N(0, I \sigma^2_\varepsilon). \]

The numerator \((N)\) and denominator \((D)\) in Equation 31 are univariate random variables that can be written as quadratic forms:

\[ N = a'(y - \mu I) = z'Q_N z \]

\[ D = (y - \mu I)'(y - \mu I) = z'Q_D z \]

where the stacked vector \(z\) and matrices \(Q_N, Q_D\) are

\[ z = \begin{bmatrix} a \\ y - \mu I \end{bmatrix} \sim N \left( \begin{bmatrix} 0 \\ 0 \end{bmatrix}, \begin{bmatrix} G & G \\ G & G + \sigma^2_\varepsilon I \end{bmatrix} \right) \]

\[ Q_N = \frac{1}{2} \begin{bmatrix} 0 & 1 \\ 1 & 0 \end{bmatrix} \]

\[ Q_D = \begin{bmatrix} 0 & 0 \\ 0 & 1 \end{bmatrix} \]

Since \(E[z'Qz] = \text{tr}(QV)\) for \(z \sim N(0, V)\) (Searle 1971), it follows that

\[ E[N] = E[z'Q_N z] = \frac{1}{2} \text{tr} \left( \begin{bmatrix} 0 & I \\ I & 0 \end{bmatrix} \begin{bmatrix} G & G \\ G & G + \sigma^2_\varepsilon I \end{bmatrix} \right) = \text{tr}(G) \]

\[ E[D] = E[z'Q_D z] = \text{tr} \left( \begin{bmatrix} 0 & 0 \\ 0 & 1 \end{bmatrix} \begin{bmatrix} G & G \\ G & G + \sigma^2_\varepsilon I \end{bmatrix} \right) = \text{tr}(G) + n \sigma^2_\varepsilon \]
Since the trace of $G$ equals $n(1+f)\sigma^2$, an approximate formula for heritability is

$$E[h^2] = E\left[\frac{N}{D}\right] \approx \frac{E[N]}{E[D]} = \frac{(1+f)\sigma^2}{(1+f)\sigma^2 + \sigma_i^2} \quad (S4)$$

Equation S4 is only approximate because the expectation of the ratio of two random variables does not equal the ratio of expectations. By Taylor series expansion a more accurate formula is (Rice 2006)

$$E\left[\frac{N}{D}\right] = \frac{E[N]}{E[D]} + \left(\text{var}[D]E[N] - \text{cov}[N,D]E[D]\right) + \ldots \quad (S5)$$

To investigate the magnitude of the correction term, note that for $z \sim N(0, V)$,

$$\text{var}[z'Q_hz] = 2\text{tr}((Q_h V)^2) \quad (S6)$$
$$\text{cov}[z'Q_hz, z'Q_hz] = 2\text{tr}(Q_h V Q_h V)$$

(Searle 1971). Upon substituting S2 into S6 and simplifying, the result is

$$\text{var}[D] = 2n\left[\sigma^4 n \langle A_i^2 \rangle + 2\sigma^4 \sigma_i^2 (1+f) + \sigma_i^4\right]$$
$$\text{cov}[N,D] = 2n\left[\sigma^4 n \langle A_i^2 \rangle + \sigma^4 \sigma_i^2 (1+f)\right] \quad (S7)$$

where

$$\langle A_i^2 \rangle = n^{-1} \sum_{i=1}^{n} \sum_{j=1}^{n} A_{ij}$$

(S8)

is the mean-squared element of $A$. From Equation S7 the correction is

$$\frac{\text{var}[D]E[N] - \text{cov}[N,D]E[D]}{E^3[D]} \approx \frac{2\sigma^4 \sigma_i^2 (1+f)^2 - n \langle A_i^2 \rangle}{n^2 \left[\sigma_i^2 + \sigma^2 (1+f)\right]^3} \approx \frac{-2 \langle A_i^2 \rangle \sigma^4 \sigma_i^2}{n \left[\sigma_i^2 + \sigma^2 (1+f)\right]^3} \quad (S9)$$

where the last expression holds for large populations.
Using Equation 13, the mean-squared realized relationship is

$$
\langle A_{ij}^2 \rangle = \left( 2 \langle \tilde{p}_i \tilde{q}_j \rangle \right)^2 n^2 \sum_{i=1}^{r} \sum_{j=1}^{n} \sum_{k=1}^{\bar{n}} \sum_{l=1}^{\bar{n}} \left( \tilde{X}_{ik} - 2 \tilde{p}_i \right) \left( \tilde{X}_{lj} - 2 \tilde{p}_l \right) \left( \tilde{X}_{jk} - 2 \tilde{p}_j \right) \left( \tilde{X}_{ik} - 2 \tilde{p}_k \right) \tag{S10}
$$

$$
= \left( 2 \langle \tilde{p}_i \tilde{q}_j \rangle \right)^2 \bar{m} \sum_{i=1}^{r} \sum_{j=1}^{n} r_{ik}^j \tilde{p}_i \tilde{q}_j \tilde{p}_k \tilde{q}_l
$$

where

$$
r_{ik}^j = \left( \tilde{p}_i \tilde{q}_j \tilde{p}_k \tilde{q}_l \right)^{1/2} n^{-1} \sum_{i=1}^{r} \left( \tilde{X}_{ik} - 2 \tilde{p}_i \right) \left( \tilde{X}_{jk} - 2 \tilde{p}_j \right) \tag{S11}
$$

is the correlation between loci. If the correlation length between causal loci is small compared to the size of the genome, then $\langle A_{ij}^2 \rangle$ will also be small. For example, if the causal loci are in linkage equilibrium, then $\langle A_{ij}^2 \rangle$ will also be small. For example, if the causal loci are in linkage equilibrium, then

$$
\langle A_{ij}^2 \rangle = \frac{\langle \tilde{p}_i^2 \tilde{q}_j^2 \rangle}{4 \bar{m} \langle \tilde{p}_i \tilde{q}_j \rangle^2} \tag{S12}
$$

More generally we can write $\langle A_{ij}^2 \rangle = c/\bar{m}$ for some finite constant $c$, which upon substitution in Equation S9 shows the correction term tends to zero under the infinitesimal model ($\bar{m} \to \infty$).

**Literature Cited**
