Figure S1. Visual depiction of quantifying shoot biomass using projected shoot area. The plant is imaged from three perspectives. The two side view (SV) images are separated by 90 degrees. TV: top view; PSA: projected shoot area
Figure S2. Manhattan plots for RR approach at days 1 to 10. Each panel represents a single time point. $-\log_{10}(p)$ is shown on the $y$-axis. Statistically significant SNPs are highlighted in red ($p < 1 \times 10^{-4}$).
**Figure S3.** Manhattan plots for RR approach at days 10 to 20. Each panel represents a single time point. $-\log_{10}(p)$ is shown on the $y$-axis. Statistically significant SNPs are highlighted in red ($p < 1 \times 10^{-4}$).
**Figure S4.** QQ plots for RR approach at days 1 to 10. Each panel represents a single time point. The observed $-\log_{10}(p)$ is shown on the $y$-axis, while the expected $-\log_{10}(p)$ is shown on the $x$-axis.
Figure S5. QQ plots for RR approach at days 11 to 20. Each panel represents a single time point. The observed -log_{10}(p) is shown on the y-axis, while the expected -log_{10}(p) is shown on the x-axis.
Figure S6. Manhattan plots for TP approach at days 1 to 10. Each panel represents a single time point. $-\log_{10}(p)$ is shown on the $y$-axis. Statistically significant SNPs are highlighted in red ($p < 1 \times 10^{-4}$).
Figure S7. Manhattan plots for TP approach at days 11 to 20. Each panel represents a single time point. $-\log_{10}(p)$ is shown on the y-axis. Statistically significant SNPs are highlighted in red ($p < 1 \times 10^{-4}$).
Figure S8. QQ plots for TP approach at days 1 to 10. Each panel represents a single time point. The observed $-\log_{10}(p)$ is shown on the y-axis, while the expected $-\log_{10}(p)$ is shown on the x-axis.
Figure S9. QQ plots for TP approach at days 11 to 20. Each panel represents a single time point. The observed $-\log_{10}(p)$ is shown on the $y$-axis, while the expected $-\log_{10}(p)$ is shown on the $x$-axis.
Figure S10. Frequency of time-specific QTL. Long refers to long-duration QTL that were detected on more than 12, but less than 20 days. Mid refers to mid-duration QTL that were detected between 6 to 12-time points. Short indicates short-duration QTL, which were detected at fewer than 6-time points. Frequency was determined by dividing the number of QTL detected at time $t$ by the total number of QTL for a given class.
Appendix

Random regression gBLUP using Legendre polynomials

Polynomial functions are an attractive approach to model longitudinal data, as they require no prior knowledge of the shape of trait trajectories and can be estimated using linear modeling approaches. However, there is often a high correlation between components of the polynomial function. Orthogonal polynomials on the other hand, such as Legendre polynomials, have the same attractive characteristics of polynomial functions and also reduce the correlation between polynomial components. Legendre polynomials are defined on a standardized time interval \([-1,1]\) using

\[
m = 2 \cdot \frac{t-t_0}{t_n-t_0} - 1,
\]

where \(t_0\) is the first time point with data, and \(t_n\) is the last time point in the data set (Kirkpatrick, Lofsvold, and Bulmer 1990; Kirkpatrick, Hill, and Thompson 1994).

Consider a simple case where we wish to partition a process measured over three time points \((y)\) into fixed \((\mu)\) and random \((\alpha)\) time dependant effects. The RR model can be defined as \(y(t) = \mu(t) + \alpha(t) + \epsilon\). We can obtain a “full” fit using a second-order Legendre polynomial. The first two Legendre polynomials are \(P_0(x) = 1\) and \(P_1(x) = x\). Subsequent polynomials can be calculated using \(P_{t+1}(x) = \frac{1}{n+1}((2n+1)xP_n(x) - nP_{n-1}(x))\). Thus, for \(P_2(x)\) the Legendre polynomial is \(\frac{1}{2}(3x)P_1(x) - 1P_0(x)\). These Legendre polynomials are then normalized using \(\phi_k(t) = \sqrt{\frac{2n+1}{2}}P_k(t)\), giving \(\phi_0(t) = 0.7071\), \(\phi_1(t) = 1.2247(t)\) and \(\phi_2(t) = 2.317(t^2) - 0.7906\). Two matrices can be defined, \(\Lambda\) and \(\mathbf{M}\), that store the coefficients for the Legendre polynomials and the standardized time values, respectively.

\[
\mathbf{M} = \begin{bmatrix} 1 & -1 & 1 \\ 1 & 0 & 0 \\ 1 & 1 & 1 \end{bmatrix}
\]

\[
\Lambda = \begin{bmatrix} 0.7071 & 0 & 0 \\ 0 & 1.2247 & 0 \\ -0.7906 & 0 & 2.3717 \end{bmatrix}
\]

Multiplying the two gives \(\Phi\) where each row vector corresponds to the series of Legendre polynomials at each standardized time interval.

\[
\Phi = \begin{bmatrix} 0.7071 & -1.2247 & 1.5811 \\ 0.7071 & 0 & -0.7906 \\ 0.7071 & 1.2247 & 1.5811 \end{bmatrix}
\]

The covariance matrix for the RR coefficients is given by \(K\). The full covariance matrix \(V\) among all three time points can be obtained via \(V = \Phi K \Phi'\).

In the following study we aimed to assess the genetic and environmental covariances for shoot growth measured across a period of 20-time points. To this end, we utilized a RR model that modeled the fixed population mean \((\beta)\) growth trajectories using a second-order Legendre polynomial, and the random genetic \((u)\) and experimental effects \((s)\)
using a second-order and first-order Legendre polynomial respectively. Following the example above, these time-dependant processes can be described using a linear combination of $\Phi$. The covariances at each time point for the random genetic and experimental effects are given by $V_g = \Phi_g \Omega \Phi_g'$ and $V_s = \Phi_s \Phi_s'$, respectively. The matrices $\Omega$ and $P$ represent the covariance matrices for the RR coefficients for the genetic and experimental effects, respectively. Thus, the dimensions of $\Omega$ is $3 \times 3$ and $P$ is $2 \times 2$.

**Defining the mixed model equation**

The following random regression model was used to model trajectories for PSA across the 20-time points and obtain estimates for $\Omega$ and $P$

$$ PSA_{tij} = \mu + \sum_{k=0}^{2} \phi_{jk} \beta_k + \sum_{k=0}^{2} \phi_{jk} u_{jk} + \sum_{k=0}^{1} \phi_{itk} s_{lk} + e_{tij} $$

In matrix notation, the model can be written as

$$ y = Xb + Zu + Qs + e $$

$y$ is a vector with an order equal to the number of observations and contains the $PSA$ over the 20 days. $X$ is an covariable matrix for the fixed effects where the number of rows is equal to the number of observations ($n$) and the number of columns is equal to the order of Legendre polynomial used to model fixed effects ($k_f$). The matrices $Z$ and $Q$ are covariable matrices for the random additive genetic and random experimental effects, respectively. The number of rows for $Z$ is equal to the number of observations and the number of columns corresponds to the order of Legendre polynomial times the number of lines used to fit the additive genetic effect ($q \times k_g = 357 \times 3 = 1,071$). For $Q$ the number of columns would be 6 ($e \times k_s = 3 \times 2$) and the number of rows would be equal to the number of observations. We assume $u \sim N(0, G \otimes \Omega)$, $s \sim N(0, I \otimes P)$, and $e \sim N(0, I \otimes D)$. Here, $\Omega$ and $P$ are the covariance matrices for the RR coefficients for the additive genetic and permanent environmental effects. $D$ is a diagonal matrix that allows for heterogeneous variances over the 20-time points.

The mixed model equation (MME) is

$$ \begin{bmatrix} X'R^{-1}X & X'R^{-1}Z \\ Z'R^{-1}X & Z'R^{-1}Z + G^{-1} \otimes \Omega \\ Q'R^{-1}X & Q'R^{-1}Z \\ Q'R^{-1}Q + I \otimes P \end{bmatrix} \begin{bmatrix} b \\ \hat{u} \\ \hat{s} \\ \hat{e} \end{bmatrix} = \begin{bmatrix} X'R^{-1}y \\ Z'R^{-1}y \\ Q'R^{-1}y \end{bmatrix} $$

Solving the above MME will give three RR coefficients for each line for the random genetic effects. Using these RR coefficients, the genetic values at each time point can be obtained as described above. For line $j$, the predicted genetic values (gBLUP) at each time point is given by $gBLUP_j = \Phi \hat{u}_j$.

**Constructing the covariable matrices**

For each term, we define a matrix of Legendre polynomials evaluated at each time point. Recall that both the fixed and random additive genetic effect are modeled using a second-
order Legendre polynomial. Thus the matrix of Legendre polynomials for the fixed and random additive genetic effect for the first and last three time points is, \((\Phi_f, \Phi_g, \text{respectively})\) are

\[
\Phi_f = \Phi_g = \begin{bmatrix}
0.707 & -1.225 & 1.581 \\
0.707 & -1.096 & 1.108 \\
0.707 & -0.967 & 0.688 \\
\vdots & \vdots & \vdots \\
0.707 & 0.967 & 0.688 \\
0.707 & 1.096 & 1.108 \\
0.707 & 1.225 & 1.581
\end{bmatrix}
\]

For the experimental effect, the matrix of Legendre polynomials \((\Phi_s)\) is of order \(d \times 2\) and for the first and last three time points is

\[
\Phi_s = \begin{bmatrix}
0.707 & -1.225 \\
0.707 & -1.096 \\
0.707 & -0.967 \\
\vdots & \vdots \\
0.707 & 0.967 \\
0.707 & 1.096 \\
0.707 & 1.225
\end{bmatrix}
\]

The covariable matrix \(X\) is defined as \(X = X^0\Phi_f\) where \(X^0\) is a vector of 1 with length \(q \times e\). Similarly, we define matrices \(Z\) and \(Q\) as

\[
Z = Z^0 \otimes \Phi_g \\
Q = Q^0 \otimes \Phi_s
\]

\(Z^0\) and \(Q^0\) are incidence matrices that allocate temporal records to individuals and experiments respectively. The order of \(Z^0\) is \(q \times e \times q\) and \(Q^0\) is \(q \times e \times e\) (q is the number of individuals, e is the number of experiments).

**Calculating \(\text{Var}(\hat{\beta})\) at each time point**

The objective is to calculate SNP effects at each time point. Recall for a univariate gBLUP approach (e.g. the single time point approach), SNP effects can be obtained from breeding values through a simple linear transformation given by

\[
\text{BLUP}(\hat{\beta}) = W_{sc}'G^{-1}\hat{u}
\]

Thus,

\[
\text{Var}(\hat{\beta}) = \text{Var}(W_{sc}'G^{-1}\hat{u}) \\
= W_{sc}'G^{-1}\text{Var}(\hat{u})G^{-1}W_{sc}
\]

The prediction error variance (PEV) of \(\hat{u}\) is
\[ \text{PEV}(\tilde{u}) = C^{22} \sigma_e^2 = \text{Var}(u - \tilde{u}) = \text{Var}(u) - \text{Var}(\tilde{u}) = G \sigma_g^2 - \text{Var}(\tilde{u}) \]

By rearranging the equation above we obtain
\[ \text{Var}(\tilde{u}) = G \sigma_g^2 - C^{22} \sigma_e^2 \]

To calculate the variance of the SNP effects, we can introduce the equation above into equation for \( \text{Var}(\hat{\beta}) \) giving
\[ \text{Var}(\hat{\beta}) = W'_s c G^{-1} (G \sigma_g^2 - C^{22} \sigma_e^2) G^{-1} W_s 
= W'_s c G^{-1} W_s \sigma_g^2 - W'_s c G^{-1} C^{22} G^{-1} W_s \sigma_e^2 \]

At each time point, \( \sigma_g^2 \) is extracted from the corresponding diagonal element of the matrix of genetic covariances for each time point, given by \( \Phi_g \Omega \Phi_g' \) for the RR approach. \( C^{22} \) is obtained by inverting the coefficient matrix of the MME, and is of order \( q \times k_g \times q \times k_g \). The diagonal elements of \( C^{22} \) contain the PEV for the RR coefficients for the additive genetic effect. To obtain the variance of SNP effects at each time point, \( C^{22} \) must be transformed so that the diagonal elements correspond to the PEV for GEBVs at each time point. We will refer to this \( q \times d \times q \times d \) matrix as \( C^{22*} \). Following Mrode (2014), PEV for individual \( j \) at each time point can be obtained by taking the diagonal elements of \( \text{PEV}_j = \Phi_g C_{jj} \Phi_g' \). \( C_{jj} \) is a \( 3 \times 3 \) submatrix of RR coefficients from \( C_{22} \) for individual \( j \). To extend this approach to the full \( C_{22} \) matrix, we construct a block matrix of \( \Phi_g (\Phi_g^*) \) via \( \Phi_g^* = I \otimes \Phi_g \) and obtain \( C^{22*} \) by
\[ C^{22*} = \Phi_g^* C^{22} \Phi_g^* \]

Thus, \( C_{22} \) is \( q \times d \times q \times d \) and the diagonal elements are the PEV for GEBVs at each time point. Finally, to calculate the variance of SNP effects at each time point at each, we extract the corresponding elements of \( C^{22*} \) and introduce them into the equation for \( \text{Var}(\hat{\beta}) \). Calculation of \( p \)-values from this point is straightforward. \( C^{22} \) for each time point can be extracted from \( C^{22*} \), and calculation of \( p \)-values follows the procedures outlined in Materials and Methods.

References