Appendix A

Bertheloot et al. (8) used experimental data to describe phenotypic variation for time to bud outgrowth within a shoot branching network as a system of differential equations. The shoot branching network takes levels of auxin and sucrose as inputs, calculates cytokinins, strigolactones and a signal integrator as intermediate outputs, and the time to bud outgrowth (days) as the final output. The levels of the intermediate outputs are described by differential equations, which each contained three terms: (i) a synthesis term, (ii) an interaction term and (iii) a degradation term. Bertheloot et al. (8) applied a grid search approach, using observed times to bud outgrowth and levels of cytokinins, to parameterize the coefficients of the differential equations.

To quantify the response to selection for time to bud outgrowth in a breeding population, phenotypic variation within the shoot branching network was connected to allelic variation across a simulated genome. The simulated genomes of individuals consisted of a single chromosome, with 40 quantitative trait nucleotides (QTN). Each endogenous signal received additive genetic effects ($\boldsymbol{a}$) from 10 non-pleiotropic QTN. The magnitudes of additive genetic effects were sampled from a normal distribution, but the sum of their effects was constrained so that the additive genetic values of individuals were within the range observed in experimental data (Table S4, Bertheloot et al. (8)). Additive genetic values ($\boldsymbol{a}$) for each endogenous signal were computed by summing the 10 QTN effects ($\boldsymbol{u_i}$) according to the QTN genotypes of each individual:

$$\boldsymbol{a_{AUX}} = \sum_{\boldsymbol{i=1}}^{\boldsymbol{10}} \boldsymbol{u_{AUX_i}} \;;\; \boldsymbol{a_{SUC}} = \sum_{\boldsymbol{i=1}}^{\boldsymbol{10}} \boldsymbol{u_{SUC_i}} \;;\; \boldsymbol{a_{CK}} = \sum_{\boldsymbol{i=1}}^{\boldsymbol{10}} \boldsymbol{u_{CK_i}} \;;\; \boldsymbol{a_{SL}} = \sum_{\boldsymbol{i=1}}^{\boldsymbol{10}} \boldsymbol{u_{SL_i}} \qquad (\mathbf{1})$$

The additive genetic values ($\boldsymbol{a}$) of individuals replaced the synthesis terms in the differential equations, but all other steps remained unchanged from Bertheloot et al. (8). We provide the following, adapted equations replacing synthesis terms with additive genetic values purely for

thoroughness and reproducibility. The interaction terms ($\boldsymbol{\gamma}$) and observed levels of endogenous signals ($\boldsymbol{g}$) were calculated based on the additive genetic values ($\boldsymbol{a}$) of individuals as follows:

$$\gamma_{CK_{AUX}} = \frac{1}{1 + 0.96 \cdot a_{AUX}} \quad (2)$$

$$\gamma_{CK_{SUC}} = 0.25 \cdot \frac{a_{SUC}^2}{0.19 + a_{SUC}^2} \quad (3)$$

$$\gamma_{SL_{AUX}} = 24.89 \cdot \frac{a_{AUX}^2}{294.58 + a_{AUX}^2} \quad (4)$$

$$g_{AUX} = a_{AUX} \quad (5)$$

$$g_{SUC} = a_{SUC} \quad (6)$$

$$g_{CK} = \frac{a_{CK} \cdot \gamma_{CK_{AUX}} + \gamma_{CK_{SUC}}}{0.99} \quad (7)$$

$$g_{SL} = \frac{a_{SL} + \gamma_{SL_{AUX}}}{0.86} \quad (8)$$

The observed values of the endogenous signals were passed through a signal integrator, I, calculated as follows:

$$\gamma_{I_{CK}} = \frac{1}{1 + 1000.g_{CK}} \quad (9)$$

$$\gamma_{I_{SL:SUC}} = 5.64 \cdot \frac{g_{SL}^2}{1 + [(0.00418 + 7.10 \cdot g_{SUC}^2) \cdot g_{SL}^2]} \quad (10)$$

$$g_I = 0.33 + \gamma_{I_{SL:SUC}} + \gamma_{I_{CK}} \quad (11)$$

The level of the signal integrator (g_I) was then used to calculate time to bud outgrowth (g_{BO}), as well as the calculation of a threshold bud outgrowth trait:

$$g_{BO} = -2.2 + 3.5 \cdot g_I \quad (12)$$

$$\begin{aligned} \boldsymbol{Bud\ Ougrowth,} \quad & \boldsymbol{g_{BO} \leq 8.3} \\ \boldsymbol{No\ Bud\ Outgrowth,} \quad & \boldsymbol{g_{BO} > 8.3} \end{aligned}$$

For the *in-silico* selection experiments, we created an initial reference population of genotypes (RPG) from a single biparental cross, consisting of 1,000 F2 individuals. The genomes of individuals consisted of a single chromosome, with 40 additive quantitative trait nucleotides (QTN). Each physiological trait received additive genetic effects from 10 non-pleiotropic QTN. Phenotypes for time to bud outgrowth ($\boldsymbol{y_{BO}}$) were generated by adding random error ($\boldsymbol{e \sim N[0, v_e]}$) to the true genetic value of time to bud outgrowth, $\boldsymbol{g_{BO}}$. The value of $\boldsymbol{v_e}$ was calculated such that the broad-sense heritability, $\boldsymbol{H^2}$, of time to bud outgrowth was equal to 0.8 in the initial RPG. $\boldsymbol{v_e}$ was held constant over selection cycles to allow the $\boldsymbol{H^2}$ to change with reductions in genetic variance due to selection. The population underwent 100 cycles of truncation selection for either higher or lower time to bud outgrowth. At each cycle, the 'best' 100 individuals were selected as parents (selection proportion = 0.1) and crossed at random to create 1,000 offspring. Independent population replicates were generated by repeating the whole *in-silico* selection experiment process one hundred times.