

Some contents are common across the six datasets:

Matriline: All of the plants descended from the Binghamton NY population (BINY; 42.184089E, 75.835319W) and have a code with a capital letter A-E and a number up to 475. This refers to the original mothers in the seed collection, where 5 transects (A-E), one meter apart, were run across an alfalfa field and seeds were collected from one maternal plant every meter. The transects varied in length – the last plant collected in each was A368, B385, C355, D475, and E100. The numbers refer to the same grid position in each transect, i.e., B1 is one meter from A1, B2, and C1. Seeds were collected from a total of 1575 maternal plants, although some have no seeds left.

Floral traits: the core set are Petal Length (PetLen), Petal Width (PetWid), Corolla Tube Length (Tube), Short Filament Length (ShrtFil), Long Filament Length (LongFil), and Pistil Length. In the early generations of artificial selection these traits were measured using calipers on dissected flower as described in Conner and Via (¹). In later studies, these are measured from floral photographs, and also include the length of the anther on one short and one long stamen (ShrtAnther and LongAnther). Often the ovules were counted (Ovule#). We often calculated Anther Exsertion as Long Filament minus Corolla Tube. All values are mm.

Treatment: High or H -- selection for increased exsertion; Low or L -- selection for decreased exsertion; Cntrl -- randomly mated controls

Replicate line: 1 (= Reed = R) or 2 (= KBS = K) respectively for the two replicates nested within each Treatment.

Photo: Some files have the code from the camera denoting the image the measurement was made from, available from the first author.

ArtificialSelectionExsertion.csv:

Offspr: the replicate offspring grown from each matriline; in later generations usually 1-10.

ID: a unique integer identifier added in later generations to track the pedigree.

MomID, DadID: the ID of the parents of that plant. In the first generation with IDs, these are lower case letters, because the parents of these individuals were not recorded.

RelFit: Relative fitness = RawFit/Mean Fitness for that line and generation.

RawFit: Number of offspring grown and measured in the next generation from that plant. Within each matriline, typically only one will have nonzero fitness, except when different plants within a matriline were used as males vs. females due to incompatibility.

Gen: generation of selection

CorrelatedResponses.csv and 2001FieldFlowerMeas.csv:

Matriline, AvPetLen, AvgTube, AvShrtFil, AvgLongFil, Pistil, Ovules: See above, except the four traits with 'Av' were the average of two measurements of different structures within the same flower, i.e., two different petals, filaments, etc. The third flower was measured in most cases, but sometimes a later flower close to the third was used.

Treatment: Direction of artificial selection

Replicate Line: the two replicates within each treatment

Block: Plants were grown at KBS or Reed; some traits differed between sites.

CRoffspring#: up to four plants were grown at each location from each matriline

Days to flower: number of days from planting to first open flower.

Nectar vol: volume of nectar in microliters from the 5th and 6th flowers on the central inflorescence.

Nectar conc%: % sugar concentration from refractometry using the same nectar sample

FlowerNo: The total number of flowers was counted on some plants at Reed at harvest, just over two months after planting

Biomass: aboveground dry biomass in grams was measured at Reed at harvest

Total pollen: Number of pollen grains produced were counted using a Coulter Counter on all six anthers from one flower at KBS, and 3 long and 1 short stamen anther at Reed

LongPollen: the count for the four long stamen anthers at KBS

ShrtPollen: the count for the short stamen anthers at KBS

QTL ParentalMeasurements.csv and QTL F1 measurements.csv:

All columns as described above except Offspr denotes the six offspring grown from each maternal plant. There are two additional Cross Types in the F₁ dataset, the High X High and Low X Low; seeds from these are available, but have not been used to make F₂ plants to date.

F₂ measurements.csv:

Cross: The four possible crosses between the two replicate high and low exsertion lines -- RH = Rep 1 (Reed) High, RL = Rep 1 Low, KH = Rep 2 (KBS) High, KL = Rep 2 Low.

Family: There are five outbred full sib families within each cross; these correspond to the parental 'octets'.

Mom: Crosses to make each full-sib family were done reciprocally, so there is Mom A or B depending on the direction of the cross.

F2: Replicate offspring from each cross. Note that this is redundant with Mom A or B, because all F2s within each family were given a unique number – A is mom for 1-25, 51-75 etc, and B is mom to 26-50, 76-100 etc.

Block: 1-10 for the 10 temporal blocks.

Flwr date: the date that the first flower opened on that plant.