Genetic mapping of *gar2-1*

We crossed *gar2-1 gai* (Landsberg *erecta* background) with the Columbia laboratory strain (carrying wild-type *GAR2* and *GAI* alleles). We selected severely dwarfed plants from the F_2 of this cross. Since both *gai* and *gar2-1* are both semi-dominant alleles, we reasoned that these severely dwarfed plants were homozygous both for *gai* and for the Columbia-derived *GAR2* allele. Homozygosity for *gai* was confirmed in 384 of these dwarfed plants via a PCR assay that can distinguish between *GAI* and *gai* (data not shown). We then used DNA markers polymorphic between the Landsberg *erecta* and Columbia backgrounds to identify regions of chromosome that were consistently homozygous for Columbia DNA in the 384 dwarfed plants. An intial test of 48 of these plants with 20 markers spread throughout the genome identified a single genomic region between markers *PG11* and *RPS2* on chromosome 4 (within which the *SLY1* gene was known to reside) that fitted this criterion (Fig. S1). Higher-resolution mapping of this region using all 384 dwarfed plants identified a short region of chromosome 4 containing *SLY1*, that was consistently homozygous in all dwarfed plants. One recombinant (in 768 chromosomes) was found with *Indel f22183/-3*, no recombinants were found *Indel t22a610/-10* or *Indel t19f63/-3* (Fig. S1). Thus *GAR2* maps close to *SLY1*.

Details concerning constructs used in making transgenic plants, yeast two-hybrid experiments, and *in vitro* protein-protein interaction experiments

The *35S:RNAi-ASK1* construct was made via amplification of a 150bp fragment of the ASK1 coding region using Expand Long template PCR System (Roche) with primers:

5’-ggggacaagtttgtacaaaaaagcaggctactgcgaagaagattgtgttgaa

5’-ggggaccactttgtacaagaaagctgggtaaggatcttgctcgtgacgtt

and then cloned twice in inverse orientation using the Gateway System (Invitrogen).

The *35S:SLY1*, *35S:sly1*$^{gar2\text{-}1}$ and *35S:SLY2* constructs were made as follows. The coding *SLY1*, *sly1*$^{gar2\text{-}1}$ and *SLY2* coding regions were amplified with primers:

5’-gccctaggatgaagcgcagtactaccgactct and 5’-gcggatccatttggattctggaagaggtc;

5’-gccctaggatgtcgtcggagaaacgtgtagg and 5’-gcggatcctcagacaacgttaacgggcttccg,

then subcloned in the *Avr*II and *Bam*HI sites of a pGreen0229-based vector, to generate 35S-driven plant expression constructs.

For yeast two-hybrid constructs, primers used for fragment amplification were:

GAI/gai primers:

1, cgggatccgtatgaagagagatcatcatcatcat

2, tggcggccgctcaattggtggagagtttccaagc

SLY1/sly1$^{gar2\text{-}1}$ primers:

1, tggaattcatgaagcgcagtactaccgatcct

2, cgctcgagatttggattctggaagaggtc

3, tggaattcactcgtcactggactaacatcggct

4, tggaattccgtgctaggttcggtaaggacgag

5, cgctcgagagtacagatcagctcccaaagccg

6, cgctcgagcggattgggtttagagagaggcca

RGA primers:

1, cgggatccgtatgaagagagatcatcatcaattccaaggtcg

2, tggcggccgctattattcgacgaagacgaagaatcaatcgccgg