**Soybean genetic resources**

We obtained seeds for 12 soybean genotypes selected from the soyNAM Project. These include a diverse sample of six landrace genotypes and six modern genotypes of *Glycine max* (Table1). All genotypes were planted in greenhouse trays in a completely randomized block design under controlled conditions at UC Davis. Plants were grown under 16 hours of light per day, day/night temperatures at 25°C/18°C in 4” pots filled with standard potting soil (Sunshine mix #1, Sun Gro Horticulture). Plants were watered regularly and staked upright. Starting at 14 days post germination, the plants were watered every two days with added nutrient solution (0.5% N-P-K fertilizer in a 2-1- 2 ratio; Grow More 4-18-38). Plants were ready for the detached leaf virulence assays 4 weeks after sowing, where full grown leaves were used.

**Detached leaf assay**

To measure lesion formation, we infected 12 diverse soybean varieties with 96 Botrytis isolates. We used a randomized block design with three independent biological replicates of each plant genotype by Botrytis isolate per experiment. The whole experiment was repeated twice with independent randomization between experiments leading to six measurements per soybean genotype x *B. cinerea* isolate for a total of ~6,900 lesion measurements. We randomly sampled 4 adult leaves per plant and each leaflet was used for inoculation of 2 B. cinerea isolate. For the statistical model, we kept track of the plant source for each leaflet. Leaflets were placed on 1% phytoagar flats with humidity domes on top.

Spores were collected from mature (2 weeks old) Botrytis cultures, and diluted to 10 spores/ µl in 50% filter-sterilized grape juice. 4 µl droplets of spore suspensions were inoculated onto detached leaflets at room temperature with 24h light. Control leaves were mock-inoculated with 4 µl of grape juice without spores. All leaflets infections were photographed at 24, 48, and 72 hours post inoculation for downstream image analysis.

**Automated Image Analysis**

We measured lesion areas using the EBImage and CRImage packages (Pau et al., 2010; Failmezger et al., 2010) in the R statistical environment (R Development Core Team, 2009). Leaflets were identified as objects with green hue, and lesions were identified as low-saturation objects within the leaflet. Images masks were generated for both the leaflet and lesion and manually refined by a technician to ensure proper object calling. The area of the leaflets and lesions were then automatically measured as pixels per lesion and converted to absolute area using a 1 cm control object within each image.