All genomic data are available from NCBI GenBank under the BioProject identifier PRJNA1027349. Computational scripts are available on the authors’ GitHub site (<https://github.com/KaneLab>).

Two additional DNA sequences used in this study that were previously uploaded to NCBI:

* SRX3073237: DNA sequences of Helianthus annuus cultivars (SRR5912307) - PPN192 a.k.a. RHA 409
* SRX3073303: DNA sequences of Helianthus annuus cultivars (SRR5912242) - PPN216 a.k.a. HA 441

Excel Tables:

2017 Carrington disease inciden table contains the raw data collected on Sclerotinia basal rot disease incidence, using the methods of Talukder et al. (2014).

Greenhouse evaluation table includes the raw data collected on Sclerotinia basal rot disease (DTD = days to death from time of inoculation), using the methods of Underwood et al. (2020).

Soil test data table includes the results of a basic soil nutrient test of three containers of soil collected from the Carrington field that was not autoclaved (I.e. native) and three containers that were repeatedly autoclaved.

References:

Talukder, Zahirul I., Brent S. Hulke, Laura F. Marek, and Thomas J. Gulya. 2014. “Sources of Resistance to Sunflower Diseases in a Global Collection of Domesticated USDA Plant Introductions.” *Crop Science* 54(2): 694–705.

Underwood, W. et al. 2021. “A Greenhouse Method to Evaluate Sunflower Quantitative Resistance to Basal Stalk Rot Caused by *Sclerotinia* Sclerotiorum.” *Plant Disease*. 105:464-472.