

Data and code from: Severity of charcoal rot disease in soybean genotypes inoculated with *Macrophomina phaseolina* isolates differs among growth environments

This README document last modified by Quentin Read on 2025-04-11

data2023-04-18.xlsx

Description of spreadsheet tabs is found in the final tab of this spreadsheet. Column names are common across tabs:

- **Genotype:** Soybean genotype identifier
- **Resistance:** Literature resistance classification of genotype: MR (moderately resistant) or S (susceptible)
- **CultureName:** Charcoal rot isolate identifier
- **Origin:** State of origin of isolate
- **RecoveredFrom:** Crop species from which the isolate was recovered
- **IsolateSource:** Plant part or substrate from which the isolate was recovered
- **PD, SD, ID:** Planting date, collection date, and inoculation date, respectively, in MMDDYY format
- **Plot:** ID number of plot
- **Stem:** ID number of stem piece (C indicates negative control)
- **Plug:** ID number of inoculation plug
- **Pot:** ID number of pot for growth chamber study
- **Rep:** ID number of replicate within pot for growth chamber study
- **Growth Stage:** growth stage code
- **DaysInStorage:** Number of days the plant material was stored before inoculation
- **DAP:** Number of days after planting that the plant material was collected
- **LesionLengthCm:** A series of columns indicating the number of days after inoculation (DAI) in the header, with the length of the lesion measured in cm
- **DeadDAI:** Number of days after inoculation when the plant died, 0 otherwise
- **AUDPC:** Area under the disease progress curve (curve formed by plotting lesion length versus days after inoculation)
- **RAUDPC:** relative area under the disease progress curve

The tabs for yield and CFU have additional columns **YldBuAc** (yield in bushels per acre) **YldKgHa** (yield in kg/ha) and **CFU/g** (colony-forming units per g)

Modified Cut-Tip Inoculation on DT974290 and LS980358 on first 32 isolates.xlsx

There are four tabs, one for each of four trials. Column names are common across tabs.

- **Isolate:** Charcoal rot isolate identifier
- **Line:** Soybean genotype identifier

- The following columns have two headers, the calendar date and an indication that those columns contain lesion length in mm
- The next columns indicate dates when nodes wilted, if applicable, and provide additional notes including indications if the plant died of CR lesion or from other causes

data_cleaning.R

This script reads the data from the Excel files, formats them to an analysis-ready format, and saves the resulting data frames to an object called `cleaned_data.RData`. The input and output files should be in a subdirectory of the current working directory called “project.”

AUDPC_fits.R

This script imports the `cleaned_data.RData` object and does all model fitting, processing of output from the fitted models, predictions, comparisons, and generation of figures and tables. Output is saved to the “project” directory, including subdirectories “audpcfits” and “figs.”

Data processing and model fitting were done using R v4.3.1 and CmdStan v2.32.2, including the packages `brms` v2.19.0, `cmdstanr` v0.5.3, `emmeans` v1.8.7, `tidybayes` v3.0.4, `fitdistrplus` v1.1-11, and `Ckmeans.1d.dp` v4.3.4.