# Population structure and phenotypic variation of *Sclerotinia sclerotiorum* from dry bean in the USA

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## Motivation

The ascomycete pathogen and causal agent of white mold on dry bean, *Sclerotinia sclerotiorum*, is a necrotrophic pathogen on over 400 known host plants. Currently, there are no known cultivars of dry bean with complete resistance to white mold. For over 20 years, bean breeders have used white mold screening nurseries (WMSN) with natural populations of *S. sclerotiorum* to screen new cultivars for resistance [1]. It is thus important to know if the genetic diversity in populations of *S. sclerotiorum* within these nurseries a) reflect the genetic diversity of the populations in the surrounding region and b) are stable over time. Furthermore, previous studies have investigated the correlation between mycelial compatibility groups (MCG) and multilocus haplotypes (MLH), but none have formally tested these patterns.

## Objectives

- Assess genetic and genotypic diversity
- Determine if cultivar, region, year, or aggressiveness is predictive of population structure
- Assess correlation between MCG and MLH

## Methods

We genotyped 366 isolates of S. sclerotiorum from producer fields and WMSN surveyed over 10 years in 2003–2012 representing 11 states in the United States of America, Australia, France, and Mexico at 11 microsatellite loci (Fig. 1). All analyses were performed in R version 3.2.3 with the packages *poppr*, *adegenet*, *vegan*, and *igraph* [2-5]. Everything is reproducible at **https://github.com/everhartlab/sclerotinia-366**

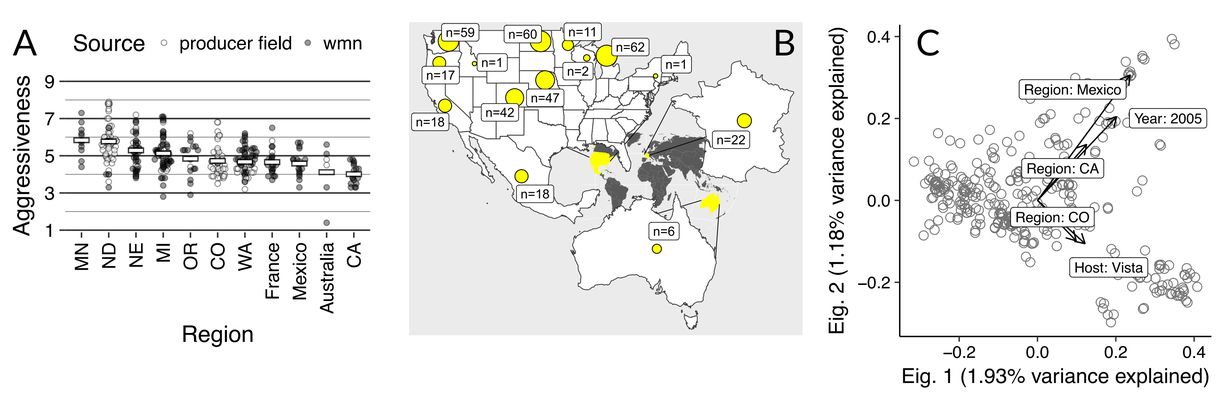


**Fig. 1** A) Aggressiveness is significantly different by region ($p < 0.05$). B) Map of sample origins. C) Distance-Based Redundancy Analysis with Bruvo's distance showing weak association of region, year, and host to genetic structure.

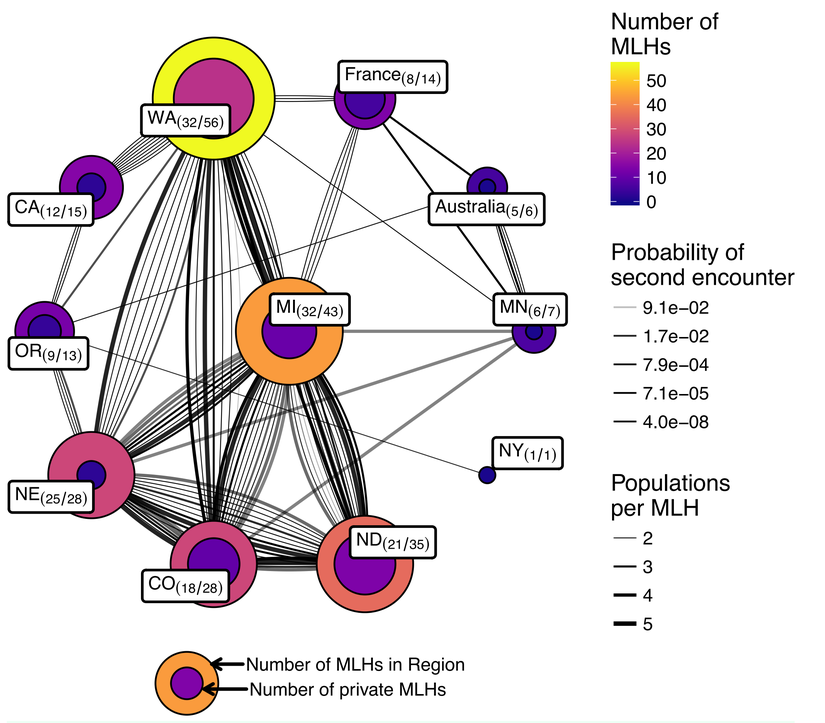


**Fig 2** Distribution of multilocus lineages across regions showing spread of genotypes is common. Numbers represent shared MLH/total MLH. Each line represents a MLH shared between populations (circles). The shading represents the probability two of the same MLH are independently derived. Thicker lines indicate MLHs shared across multiple popualtions.

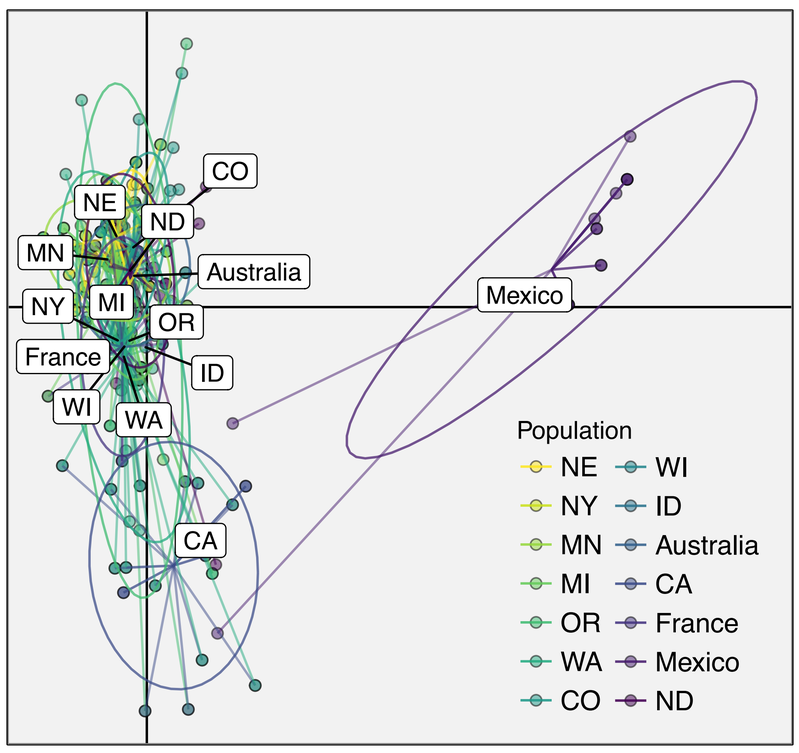


**Fig 3** Little genetic differentiation is observed between populations. Discriminant Analysis of Principal Components analysis showing Mexican and Californian populations being separated on the first and second discriminant axes, respectively. This analysis attempts to maximize variation between populations while minimizing variation within.

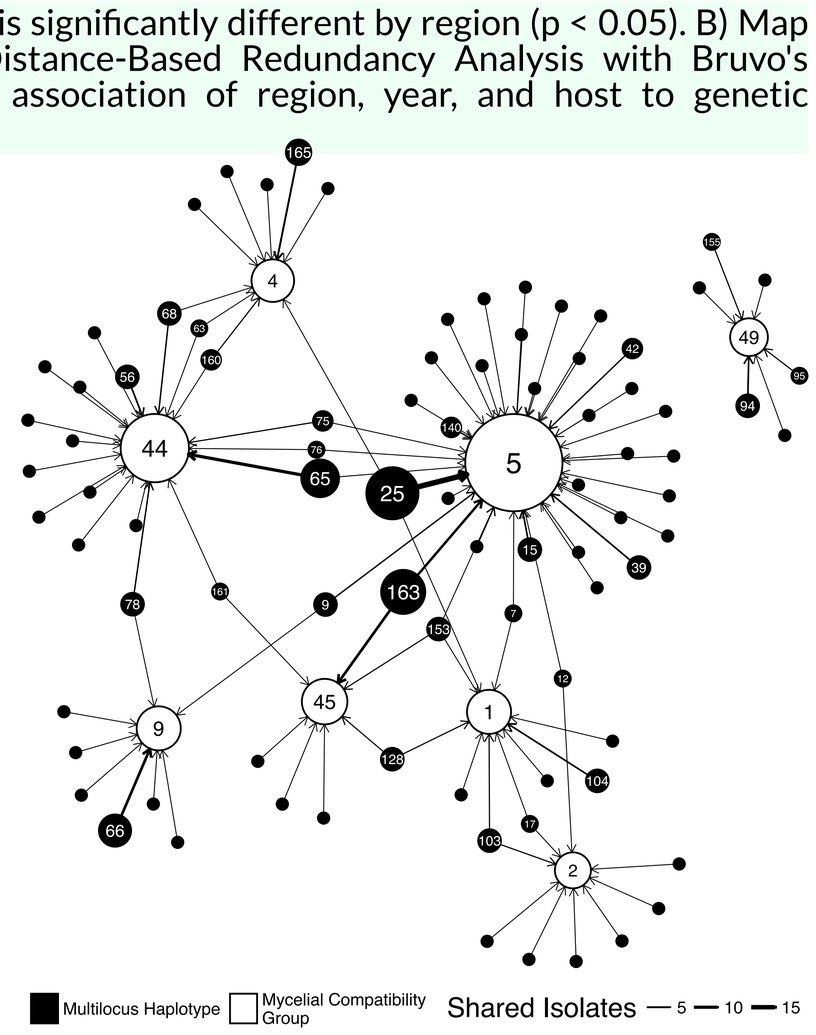


**Fig 4** The complex relationship between MLH (filled circles) and MCG (open circles) as shown by the eight most abundant MCG. Numbers indicate MLH/MCG designation. Size of circles and arrows is proportional to the number of isolates observed. If MCGs represented clonal lineages, we would expect only one arrow extending from each MLH.

## Conclusions

Our study suggests that breeders should continue to test dry bean lines in several WMSN across the USA to account for both the phenotypic and genotypic variation that exist across regions.

## Works Cited

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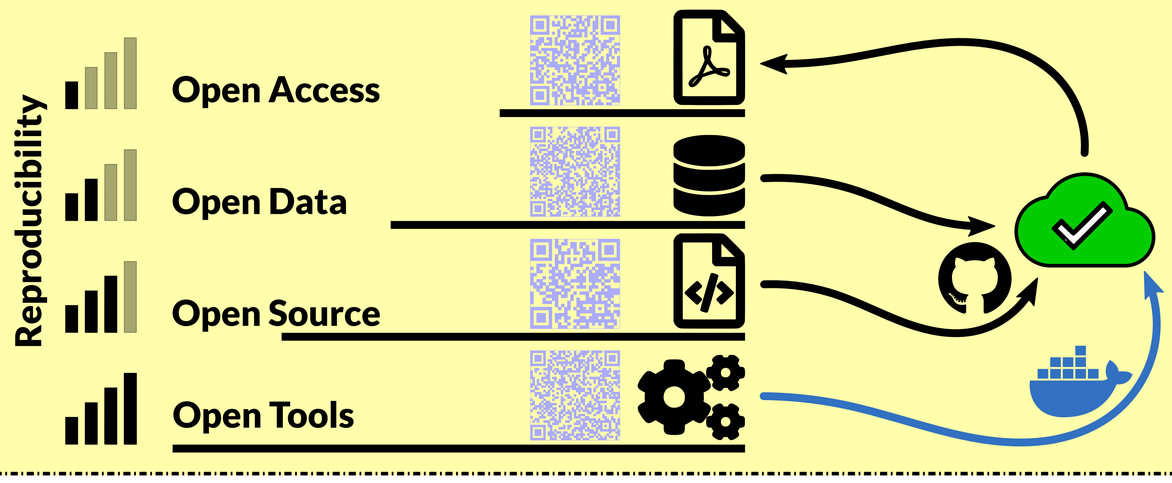


## Practicing Open Science

Open and reproduciblie research exists on a gradient from the lone published article at one end to the entire computing environment included on the other.

Our publication (DOI: 10.7717/peerj.4152) is paired with a research compendium that contains the raw data and source code used for all the analyses hosted on github (https://github.com/everhartlab/sclerotinia-366) and archived at the Open Science Framework (https://osf.io/k8wtm/).

To ensure full reproducibility, all analysis are routinely re-built from the scripts and raw data in a docker container using the free cloud computing services Circle-CI and DockerHub (https://hub.docker.com/everhartlab).