

Population structure and phenotypic variation of *Sclerotinia sclerotiorum* from dry bean in the United States

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ABSTRACT

The ascomycete pathogen *Sclerotinia sclerotiorum* is a necrotrophic pathogen on over 400 known host plants, and is the causal agent of white mold on dry bean. Currently, there are no known cultivars of dry bean with complete resistance to white mold. For more than 20 years, bean breeders have been using white mold screening nurseries with natural populations of *S. sclerotiorum* to screen new cultivars for resistance. 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. We genotyped 366 isolates of *S. sclerotiorum* from producer fields and white mold screening nurseries surveyed over 10 years in 2003–2012 representing 11 states, Mexico, France, and Australia at 11 microsatellite loci resulting in 165 MLHs. Populations were loosely structured over space and time based on analysis of molecular variance and discriminant analysis of principal components, but not by cultivar, aggressiveness, or field source. Of all the regions tested, only Mexico (n=18) shared no MLHs with any other region. Using a bipartite network-based approach, we found no evidence that the MCGs accurately represent MLHs. Our study suggests that breeders should continue to test dry bean lines in several white mold screening nurseries across the US to account for both the phenotypic and genotypic variation that exists across regions.

INTRODUCTION

Sclerotinia sclerotiorum (Lib.) de Bary is an ascomycete plant pathogen with a worldwide distribution. This is a necrotrophic pathogen that is primarily homothallic (self-fertilization) and has the ability to survive for more than five years in soil using melanized survival structures called sclerotia (Bolton et al., 2006; Sexton et al., 2006). It causes disease on more than 400 plant species belonging to 75 families (Boland & Hall, 1994) including crops of major economic importance such as sunflower (*Helianthus spp.*), soybean (*Glycine max* L.), canola (*Brassica napa* L., *Brassica campestris* L.), and dry bean (*Phaseolus vulgaris* L.) (Bolton et al., 2006). On dry bean, *S. sclerotiorum* is the causal agent of white mold, a devastating disease that can be a yield-limiting in temperate climates (Steadman, 1983).

Currently, there are no known resistant cultivars of dry bean commercially available (Otto-Hanson et al., 2011). Organized breeding efforts have used a common-garden approach with white mold screening nurseries in dry bean production areas across the United States with additional sites in Mexico, France, and Australia (Steadman et al., 2003, 2004, 2005, 2006; Otto-Hanson & Steadman, 2007, 2008; McCoy & Steadman, 2009). These white mold screening nurseries use no chemical or cultural treatments against *S. sclerotiorum* and employ standardized protocols for screening new cultivars for resistance to white mold. It has previously been shown that aggressiveness (the severity of disease symptoms on the host) is significantly different across white mold screening nursery sites in separate geographic regions (Otto-Hanson et al., 2011). The genetic structure and mode of reproduction in these populations, however, is

46 currently unknown.

47 Understanding genetic relationships and reproduction behavior of *S. sclerotiorum* populations is
48 beneficial for breeders seeking to develop new resistant cultivars for worldwide deployment (Milgroom,
49 1996; McDonald & Linde, 2002). In particular, genetically diverse populations with high rates of sexual
50 reproduction are more likely to overcome host resistance. Most populations of *S. sclerotiorum* are
51 predominantly clonal with low genetic diversity and have a large degree of population fragmentation
52 (Kohli et al., 1995; Cubeta et al., 1997; Kohli & Kohn, 1998; Carbone & Kohn, 2001; Ekins et al., 2011;
53 Attanayake et al., 2012). Some studies, however have found populations that show signatures of sexual
54 reproduction (Atallah et al., 2004; Sexton & Howlett, 2004; Attanayake et al., 2013; Aldrich-Wolfe et al.,
55 2015).

56 Nearly all population genetic studies of *S. sclerotiorum* employ a macroscopic assay to determine
57 mycelial compatibility, the ability for fungal hyphae from different colonies to appear to grow together
58 without forming a barrier of dead cells between them (known as a barrage line) (Leslie, 1993; Sirjusingh
59 & Kohn, 2001). Mycelial compatibility has been used as a proxy for vegetative compatibility, a fungal
60 trait controlled by several independent genes controlling the ability for two hyphae to fuse and grow as
61 a single unit (Leslie, 1993; Schafer & Kohn, 2006). Because of the genetic connection to vegetative
62 compatibility, two isolates that are mycelially compatible were considered clones (Leslie, 1993); but
63 correlation with genetic markers, such as microsatellites, have shown mixed results (Ford et al., 1995;
64 Micali & Smith, 2003; Jo et al., 2008; Attanayake et al., 2012; Papaioannou & Typas, 2014; Lehner et al.,
65 2017).

66 In this study, we analyze and characterize the genetic and phenotypic diversity of 366 *S. sclerotiorum*
67 isolates collected over 10 years between 2003 and 2012 from dry bean cultivars among different geographic
68 locations in the United States, France, Mexico, and Australia. We wanted to know if the *S. sclerotiorum*
69 populations from white mold screening nurseries were representative of the fields within the same region.
70 As these nurseries were not treated with any chemical or cultural control of white mold, we hypothesized
71 that these nurseries would represent the natural population of *S. sclerotiorum*. Furthermore, we wanted
72 to investigate the potential effect of cultivar on genetic diversity by assessing three dry bean cultivars
73 with different levels of resistance, Beryl (great northern bean, susceptible), Bunsu (navy bean, low
74 susceptibility), and G122 (cranberry bean, partial resistance) (Otto-Hanson et al., 2011). We additionally
75 wanted to determine categorical or phenotypic variables that best predicted genetic structure and if
76 there was correlation between multilocus haplotype and mycelial compatibility group. Knowing what
77 variables predict genetic structure can help direct breeding efforts. By investigating these aims, we hope
78 to effectively describe the population structure of *S. sclerotiorum* in the USA and make available our
79 database of isolates for use in future dry bean breeding efforts.

80 MATERIALS AND METHODS

81 Isolate collection

82 Several of the isolates used for this study were collected as reported in previous studies using the
83 same methods (Otto-Hanson et al., 2011). Broadly, isolates were collected from two sources: white mold
84 screening nurseries (wmn) or producer fields. White mold screening nurseries were 5m x 10m in size and
85 maintained without application of fungicides to observe natural incidence of white mold. The nursery
86 plots were incorporated with a basal dressing of N:P:K = 1:3:2 and side dressing of 0:3:2 during the
87 growing season (Steadman et al., 2003).

88 Sampling was carried out by collecting sclerotia from diseased tissue in zig-zag transects across field
89 plots. Because sampling depended on disease incidence, the number of samples isolated varied from
90 year to year. Although the nursery locations were the same over sampling years, sampling plots within a
91 location varied for sampling years.

92 Sclerotia of *S. sclerotiorum* were collected over several years from grower fields and/or wmn in
93 11 states of the United States of America, Mexico, France, and Australia (Table S1). After collection,
94 sclerotia were stored in Petri plates lined with filter paper, then stored at 20 °F or -4 °C. Sclerotia were
95 surface-sterilized with 50% Clorox bleach (at least 6% NaOCL, The Clorox Company, Oakland, CA)
96 solution for 3 min, and double rinsed with ddH₂O 3 min. The sterilized sclerotia were then placed on
97 water agar plates (16g of Bacto agar per liter of ddH₂O, BD Diagnostic Systems, Sparks, MD), with four
98 to five sclerotia of each isolate separated on each plate and stored on the counter top at room temperature
99 for 5 to 6 days. An 8-mm plug from a 5- or 6-day-old culture was transferred from the advancing margin

of the mycelia onto a plate of Difco potato dextrose agar (PDA at 39 g/liter of ddH₂O) (Otto-Hanson et al., 2011). In combination with the 156 isolates described previously, we collected 210 isolates for a total of 366 isolates (Otto-Hanson et al., 2011).

103 **Mycelial Compatibility**

104 MCG was determined as described previously through co-culturing pairs of 2-day-old isolates 2.5
105 cm apart on Diana Sermons (DS) Medium (Cubeta et al., 2001). Incompatibility of different MCGs
106 resulted in formation of a barrage line accompanied by formation of sclerotia on either side of the barrage
107 line, indicating the limits of the isolates' growth (Kohn et al., 1990; Leslie, 1993; Otto-Hanson et al.,
108 2011). Isolates were compared in a pairwise manner for each site and then representatives among sites
109 were compared to determine mycelial compatibility groups by scoring compatible and incompatible
110 interactions (Otto-Hanson et al., 2011). No MCGs were compatible with any other MCG.

111 **Aggressiveness**

112 Aggressiveness of each isolate was assessed using a straw test as described in Otto-Hanson et al.
113 (2011) that rated necrotic lesion size (Petzoldt & Dickson, 1996; Teran et al., 2006). Briefly, the straw
114 test uses 21-day-old G122 plants as the host in a greenhouse setting. Clear drinking straws cut to 2.5 cm
115 and sealed were used to place two mycelial plugs of inoculum on the host plant after removing all plant
116 growth >2.5 cm above the fourth node. Measurements of the necrotic lesion were taken 8 days later using
117 the Modified Petzoldt and Dickson scale of 1–9, where 1 is no disease and 9 is plant death (Petzoldt &
118 Dickson, 1996; Teran et al., 2006).

119 **Microsatellite genotyping**

120 Prior to DNA extraction, isolates were grown on PDA and plugs were subsequently transferred to
121 Potato Dextrose Broth (PDB) where they were grown until there was significant mycelial growth, but
122 before the mycelial mat became solidified (4–5 days). Mycelia for each plate was collected in a buchner
123 funnel, agar plugs removed, lyophilized and pulverized manually in Whirl-pak® HDPE sampling bags
124 (Sigma-Aldrich, St. Louis, MO). Lyophilized mycelia was then stored in microcentrifuge tubes at -20 °C
125 until needed for DNA extraction. DNA from 25mg of pulverized mycelia was purified using a phenol-
126 chloroform extraction method followed by alcohol precipitation and evaporation, suspending the DNA in
127 200µl TE (Sambrook et al., 1989). Suspended DNA was stored at 4 °C until genotyping.

128 We genotyped each *S. sclerotiorum* isolate using 16 microsatellite primer pairs developed previously
129 (Sirjusingh & Kohn, 2001). PCR was carried out as described previously, using primers labeled with
130 FAM fluorophore. Resulting amplicons were first resolved in a 1.5% agarose gel stained with ethidium
131 bromide to ensure product was within the expected size range prior to capillary electrophoresis. Capillary
132 electrophoresis (fragment analysis) of amplicons, with size standard GeneScan™ 500 LIZ®, was
133 performed using an ABI 3730 genetic analyzer (Life Technologies Corporation, Carlsbad, CA) at the
134 Michigan State University Genomic Sequencing Center (East Lansing, MI). Alleles were scored using
135 PeakScanner version 1.0 (Life Technologies Corporation, Carlsbad, CA) and recorded manually in a
136 spreadsheet.

137 **Data processing and Analysis**

138 All data processing and analyses were performed in R version 3.4.1 (R Core Team, 2017)
139 and are openly available and reproducible at [https://github.com/everhartlab/
140 sclerotinia-366/](https://github.com/everhartlab/sclerotinia-366/). Of the 16 microsatellite loci genotyped, five included compound re-
141 peats, which made it challenging to accurately/confidently bin alleles into fragment sizes expected
142 for each locus based on the described repeat motif. Loci with compound repeats were removed for
143 the reported statistics. To ensure the integrity of the results we additionally processed these loci and
144 included them in concurrent analyses. We assessed the power of our 11 markers by generating a genotype
145 accumulation curve in the R package *poppr* version 2.5.0, looking for evidence of saturation, which
146 would indicate that loci were sufficiently sampled to adequately represent the full set of haplotypes
147 (Arnaud-Hanod et al., 2007; Kamvar et al., 2015). To avoid including isolates potentially collected from
148 the same plant (which increases the probability of collecting sclerotia from the same point of infection
149 more than once), data were clone-corrected on a hierarchy of Region/Source/Host/Year—meaning that
150 duplicated genotypes were reduced to a single observation when they were collected in the same year
151 from the same host cultivar located in the same source field (wmn or producer)—for subsequent analysis.

We assessed haplotype diversity by calculating Stoddart and Taylor's index (G) (Stoddart & Taylor, 1988), Shannon's index (H) (Shannon, 1948), Simpson's index (λ) (Simpson, 1949), evenness (E_5), and the expected number of multilocus haplotypes ($eMLH$) (Hurlbert, 1971; Heck et al., 1975; Pielou, 1975; Grünwald et al., 2003). To assess the potential for random mating, we tested for linkage disequilibrium with the index of association, I_A and its standardized version, \bar{r}_d using 999 permutations (Brown et al., 1980; Smith et al., 1993; Agapow & Burt, 2001). Both haplotype diversity and linkage disequilibrium were calculated in *poppr* (Kamvar et al., 2014).

Assessing Importance of Variables

Distance-based Redundancy Analysis

A distance-based redundancy analysis (dbRDA) (Legendre & Anderson, 1999) was performed with the function `capscale()` in the *vegan* package version 2.4.4 (Oksanen et al., 2017). This method uses constrained ordinations on a distance matrix representing the response variable to delineate relative contribution of any number of independent explanatory variables. We used this method to delineate the phenotypic (Aggressiveness, Mycelial Compatibility Group (MCG)), geographic (Region, Host, Location), and temporal (Year) components in predicting genetic composition of the populations. The distance matrix we used as the response variable was generated using Bruvo's genetic distance from clone-corrected data (procedure described above) as implemented in *poppr*, which employed a stepwise mutation model for microsatellite data (Bruvo et al., 2004; Kamvar et al., 2014). Because aggressiveness measures differed between isolates that were reduced to a single observation during clone-correction, aggressiveness was first averaged across clone-corrected isolates. To identify explanatory variable(s) correlated with genetic variation, a forward-backward selection process was applied with the *vegan* function `ordistep()`. An analysis of variance (ANOVA) was then performed to test for significance of the reduced model and marginal effects using 999 permutations. The `varpart()` function of *vegan* was used to determine variation partitioning of explanatory variables.

Aggressiveness Assessment

We used ANOVA to assess if aggressiveness was significantly different with respect to Region, MCG, or multilocus haplotype (MLH). To minimize complications due to small sample sizes, we chose the top 10 MCGs, representing 56.5% of the isolates collected, the 10 most abundant MLHs representing 26.7% of the isolates, and populations with more than five isolates. If ANOVA results were significantly different at $\alpha = 0.05$, pairwise differences were assessed using Tukey's HSD test ($\alpha = 0.05$) using the `HSD.test()` function in the package *agricolae* version 1.2.8 (Mendiburu & Simon, 2015).

Correlating Multilocus Haplotypes with Mycelial Compatibility Groups

We wanted to assess if there was correlation between MLHs and MCGs. This was performed using a network-based approach where both MLHs and MCGs were considered nodes and the number of isolates in which they were found together was the strength of the connection between an MLH and an MCG node. The network-based approach allowed us to assess the associations between MLHs and MCGs. To construct the network, a contingency table was created with MLHs and MCGs and converted to a directed and weighted edgelist where each edge represented a connection from an MCG to an MLH, weighted by the number of samples shared in the connection. This was then converted to a bipartite graph where top nodes represented MLHs and bottom nodes represented MCGs. To identify clusters of MLHs and MCGs within the network, we used the cluster walktrap community detection algorithm as implemented in the `cluster_walktrap()` function in *igraph* version 1.1.2 (Csardi & Nepusz, 2006; Pons & Latapy, 2006). This algorithm attempts to define clusters of nodes by starting at a random nodes and performing short, random "walks" along the edges between nodes, assuming that these walks would stay within clusters. For this analysis, we set the number of steps within a walk to four and allowed the algorithm to use the edge weights in determining the path. All of the resulting communities that had fewer than 10 members were then consolidated into one. Community definitions were used to assess the average genetic distance (as defined by Bruvo's distance) within members of the community (Bruvo et al., 2004).

Genetic Diversity

Population Differentiation

We used analysis of molecular variance (AMOVA) with Bruvo's genetic distance in *poppr* to test for differentiation between populations in wmn and producer fields from the same region and collected in

the same year (Excoffier et al., 1992; Bruvo et al., 2004; Kamvar et al., 2014). To identify Regions with greater differentiation, we used discriminant analysis of principal components (DAPC) as implemented in *adegenet* version 2.1.0, assessing the per-sample posterior group assignment probability (Jombart, 2008). This method decomposes the genetic data into principal components, and then uses a subset of these as the inputs for discriminant analysis, which attempts to minimize within-group variation and maximize among-group variation (Jombart et al., 2010). To avoid over-fitting data, the optimal number of principal components was selected by using the *adegenet* function `xvalDapc()`. This function implements a cross-validation procedure to iterate over an increasing number of principal components on a subset (90%) of the data, trying to find the minimum number of principal components that maximizes the rate of successful group reassignment. To assess if cultivar had an influence on genetic diversity between wmn, we first subset the clone-corrected data to contain only samples from wmn and from the cultivars Beryl, Bunsu, and G122 and tested differentiation using AMOVA and DAPC as described above. We additionally assessed population stability over time by calculating DAPC over the combined groups of Region and Year as described above.

Analysis of Shared Multilocus Haplotypes

We wanted to evaluate patterns of connectivity between shared multilocus haplotypes across geographic regions. We first tabulated the multilocus haplotypes shared between at least two populations (defined as states or countries) with the *poppr* function `mlg.crosspop()` (Kamvar et al., 2014). From these data, we constructed a graph with populations as nodes and shared haplotypes as edges (connections) between nodes using the R packages *igraph* (Csardi & Nepusz, 2006), *dplyr* version 0.7.3 (Wickham et al., 2017), and *purrr* version 0.2.3 (Henry & Wickham, 2017). Each node was weighted by the fraction of shared MLHs. Each edge represented a single MLH, but because a single MLH could be present in more than one population, that MLH would have a number of edges equivalent to the total number of possible connections, calculated as $(n*(n-1))/2$ edges where n represents the number of populations crossed. Edges were weighted by $1 - P_{sex}$, where P_{sex} is the probability of encountering the same haplotype via two independent meiotic events (Parks & Werth, 1993; Arnaud-Hanod et al., 2007). This weighting scheme would thus strengthen the connection of edges that represented genotypes with a low probability of being produced via sexual reproduction. We then identified communities (among the Regions) in the graph using the `cluster_optimal()` function from *igraph* (Csardi & Nepusz, 2006). The graph was plotted using the R packages *ggplot2* version 2.2.1 (Wickham, 2009) and *ggraph* 1.0.0 (Pedersen, 2017). To ensure that we captured the same community signal, we additionally performed this analysis including the five polymorphic markers described above.

RESULTS

A total of 366 isolates were collected from 2003 to 2012 (except 2006 and 2011) from diseased dry bean plants in Australia, Mexico, France, and 11 states in the USA (Table S1). We observed a total of 165 MLHs (215 with 16 loci). Over 50% of the isolates came from four states, MI (62), ND (60), WA (59), NE (47). Four regions had fewer than 10 isolates, Australia (6), WI (2), NY (1), ID (1). We observed 87 MCGs, the most abundant of which ('MCG 5') was represented by 73 isolates over 37 MLHs (Fig 1A,C).

The number of observed alleles per locus ranged from two to 10 with an average of 6.27 (Table 1). Locus 20-3, which contained only 2 alleles, showed low values of both h (0.0533) and evenness (0.42), indicating that there was one dominant allele present. Analysis of the haplotype accumulation curve showed no clear plateau for 11 or 16 loci (Supplemental Information), indicating that we would likely obtain more multilocus haplotypes if we were to genotype more loci.

After clone-correction on the hierarchy of Region/Source/Host/Year, we were left with 318 isolates representing 165 MLHs (Table 2). The results show that most populations exhibited relatively high amounts of genotypic diversity, with the exception of MI and NE, which exhibited lower-than average E_5 values. Mexico had the lowest average value of gene diversity, h and the lowest $eMLH$, suggesting low overall genetic diversity. Nearly all populations showed evidence for linkage (Table 2), which serves as evidence for clonal reproduction or other forms of non-random mating. The only exceptions are CA and Australia. Both of these populations showed only moderate significance ($P < 0.05$) with \bar{r}_d values of 0.03 and 0.12, respectively.

Table 1. Allelic diversity on full data set at loci used in this study. h = Nei's Gene Diversity (Nei, 1978). Average h = 0.583, average Evenness = 0.693, average no. alleles = 6.27

| Locus | Range | Repeat Motif | No. alleles | h | Evenness |
|-------|---------|--------------|-------------|------|----------|
| 5-2 | 318–324 | di- | 4 | 0.45 | 0.62 |
| 6-2 | 483–495 | hexa- | 3 | 0.64 | 0.95 |
| 7-2 | 158–174 | di- | 7 | 0.73 | 0.76 |
| 8-3 | 244–270 | di- | 7 | 0.74 | 0.79 |
| 9-2 | 360–382 | di- | 9 | 0.35 | 0.41 |
| 12-2 | 214–222 | di- | 5 | 0.58 | 0.78 |
| 17-3 | 342–363 | tri- | 7 | 0.55 | 0.53 |
| 20-3 | 280–282 | di- | 2 | 0.05 | 0.42 |
| 55-4 | 153–216 | tetra- | 10 | 0.72 | 0.66 |
| 110-4 | 370–386 | tetra- | 5 | 0.76 | 0.91 |
| 114-4 | 339–416 | tetra- | 10 | 0.83 | 0.80 |

Table 2. Genotypic diversity and Linkage Disequilibrium summary for geographic populations arranged by abundance after clone-correction by a hierarchy of Region/Source/Host/Year. Pop = Population, N = number of individuals (number of MLH in parentheses), eMLH = expected number of MLHs based on rarefaction at 10 individuals (standard error in parentheses), H = Shannon-Weiner Index, G = Stoddardt and Taylor's Index, λ = Simpson's Index, h = Nei's 1978 gene diversity, E_5 = Evenness, \bar{r}_d = standardized index of association. An asterix indicates a significant value of \bar{r}_d after 999 permutations, $P \leq 0.001$.

| Pop | N | eMLH | H | G | λ | E_5 | h | \bar{r}_d |
|-----------|---------|-------------|-----|------|-----------|-------|------|-------------|
| WA | 58 (56) | 9.95 (0.23) | 4.0 | 54.3 | 0.98 | 0.98 | 0.60 | 0.07* |
| MI | 58 (43) | 9.3 (0.79) | 3.6 | 29.0 | 0.97 | 0.78 | 0.54 | 0.14* |
| ND | 41 (35) | 9.44 (0.73) | 3.5 | 25.9 | 0.96 | 0.82 | 0.54 | 0.1* |
| NE | 37 (28) | 8.93 (0.94) | 3.2 | 17.8 | 0.94 | 0.75 | 0.55 | 0.25* |
| CO | 34 (28) | 9.46 (0.67) | 3.3 | 24.1 | 0.96 | 0.92 | 0.56 | 0.27* |
| France | 21 (14) | 8.5 (0.85) | 2.6 | 12.6 | 0.92 | 0.95 | 0.48 | 0.11* |
| CA | 18 (15) | 9.12 (0.72) | 2.7 | 13.5 | 0.93 | 0.94 | 0.51 | 0.03 |
| OR | 17 (13) | 8.52 (0.85) | 2.5 | 10.7 | 0.91 | 0.89 | 0.47 | 0.1* |
| Mexico | 15 (9) | 7.1 (0.85) | 2.1 | 7.3 | 0.86 | 0.89 | 0.28 | 0.37* |
| MN | 9 (7) | 7 (0) | 1.9 | 6.2 | 0.84 | 0.93 | 0.47 | 0.19* |
| Australia | 6 (6) | 6 (0) | 1.8 | 6.0 | 0.83 | 1.00 | 0.48 | 0.12 |
| WI | 2 (2) | 2 (0) | 0.7 | 2.0 | 0.50 | 1.00 | 0.27 | - |
| NY | 1 (1) | 1 (0) | 0.0 | 1.0 | 0.00 | NaN | NaN | - |
| ID | 1 (1) | 1 (0) | 0.0 | 1.0 | 0.00 | NaN | NaN | - |

Variable Assessment

Variable Contributions

The forward-backward selection process of the dbRDA models on clone-corrected data revealed Year, Region, Host, and MCG to be the optimal variables for the reduced model, accounting for 45% of the total variation. ANOVA showed that the reduced model was significant with an adjusted R^2 of 0.0675 ($P = 0.001$). Assessment of the marginal effects showed that all variables significantly explained genetic variation ($P = 0.001$, $P = 0.007$ for Region). We found that there was multicollinearity when MCG was combined with any other variable, so repeated the analysis, dropping MCG from the list of potential predictors. From these results, Year, Region, Host, and Aggressiveness were found to be optimal, accounting for 17.6% of the total variation. ANOVA revealed significant effects with an adjusted R^2 of 0.0325 ($P = 0.001$). While the marginal effect assessment revealed that Year, Region, and Host significantly explained variation at $P = 0.001$, and Aggressiveness significantly explained variation at $P = 0.039$. Much of the variation appeared to be driven by isolates from Mexico and 2005 (Fig. 2). Variance

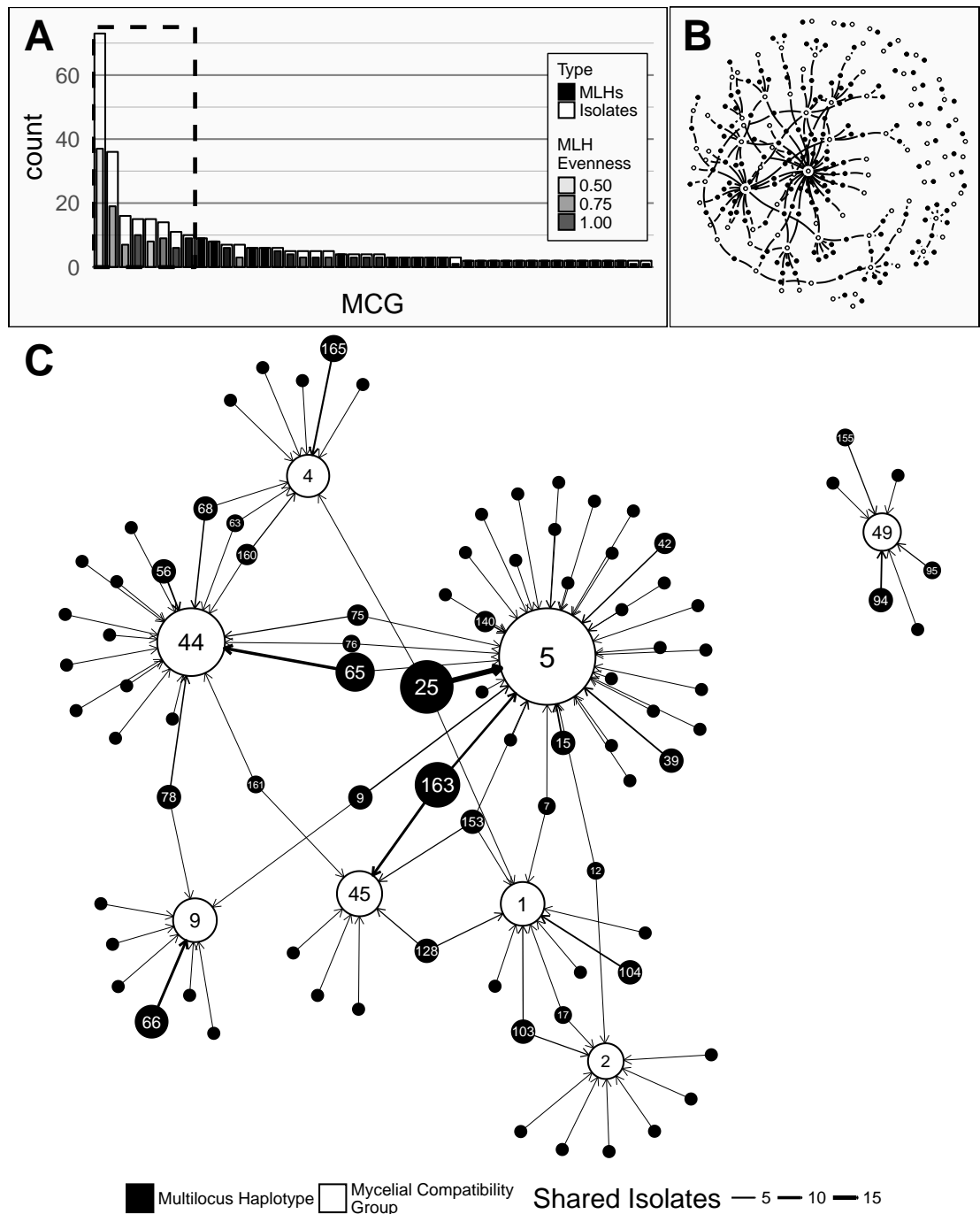


Figure 1. Associations between Mycelial Compatibility Groups and Multilocus Haplotypes. **A)** Barplot of Mycelial Compatibility Group (MCG) abundance in descending order. Singletons (46) were truncated, leaving 41 MCGs. White bars represent sample counts and grey bars represent counts of unique multilocus haplotypes (MLH). The transparency of the bars represent the evenness of the distribution of the MLHs within a given MCG. A dashed box surrounds the eight most common MCGs representing > 51% of the data. **B)** Full graph-representation of the relationship between MCGs (open circles) and MLHs (filled circles). Details in Fig. S1. **C)** A subset of **B** representing the 8 most common MCGs and their associated MLHs (dashed box in **A**). Filled nodes (circles) represent MLHs and open nodes represent MCGs. Node area scaled to the number of samples represented (range: 1–73). Numbers inside nodes are the MLH/MCG label (if $n > 1$). Edges (arrows) point from MLH to MCG where the weight (thickness) of the edge represents the number of shared isolates (range: 1–19). Edges extending from MLHs displayed to other MCGs are not shown.

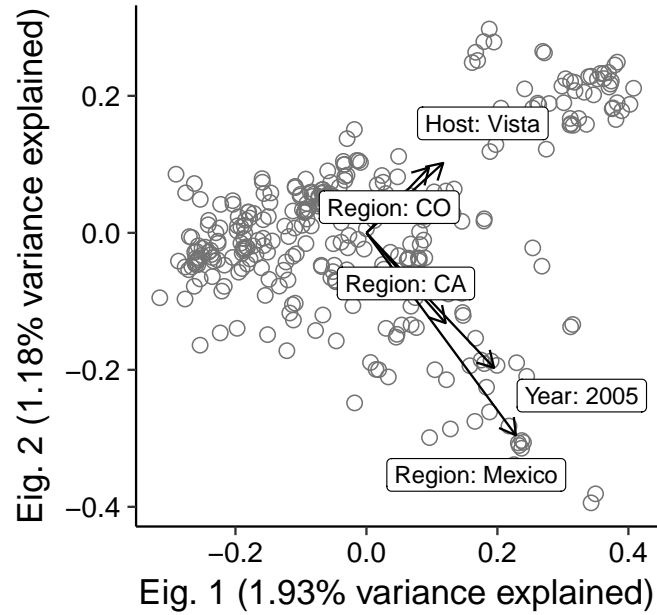


Figure 2. Biplot showing five most influential explanatory variables (arrows) overlaid on the first two eigenvectors of distance based redundancy analysis of *Sclerotinia sclerotiorum* isolates. The length of the arrows are directly proportional to the strength of the correlation between explanatory and molecular variables. Open circles represent the 318 clone-corrected haplotypes in ordination space.

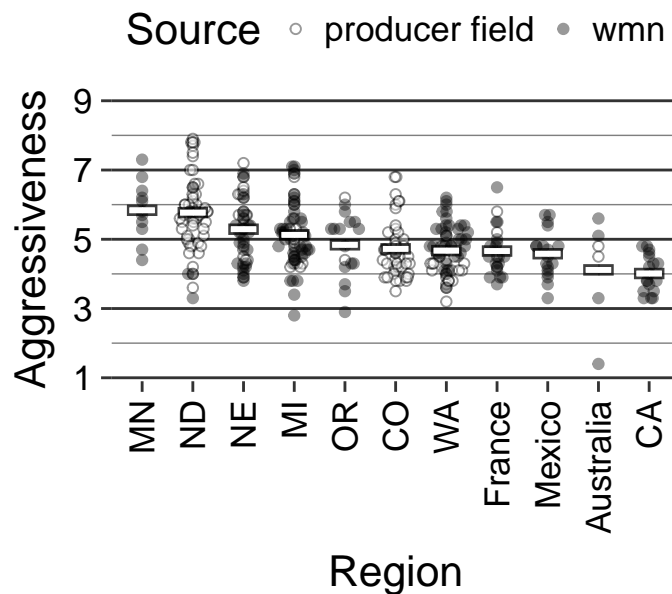


Figure 3. Strip Plot of aggressiveness by population arranged in descending order of mean aggressiveness for all populations with $N > 5$. White bars represent mean value. Circles represent individual isolates where filled circles are isolates from white mold screening nurseries (wmn) and open circles are isolates from producer fields.

partitioning of the independent variables without MCG indicated aggressiveness to be the least influential factor with 0.1% contributing to explaining the variation of molecular data, whereas the combination of variables accounted for 3.3%.

Aggressiveness

Aggressiveness of the isolates ranged from 1.4 to 7.9 with a mean of 5.02 and median of 4.85. The group mean averages were 4.88, 5.13, and 5.19 for Region, MCG, and MLH, respectively. Our assessment of aggressiveness in association with Region showed a significant effect ($P < 1.00e^{-4}$), with means that ranged from 5.8 (MN) to 4.0 (CA) (Fig. 3, Table S2). MCGs also showed a significant effect ($P < 1.00e^{-4}$), with means that ranged from 6.0 ('MCG 44') to 4.6 ('MCG 49'; Table S3). We additionally found a significant effect for MLHs ($P = 7.44e^{-4}$) for MLHs, with means that ranged from 6.0 ('MLH 78') to 4.3 ('MLH 140') (Table S4).

Correlation of Multilocus Haplotypes and Mycelial Compatibility Groups

In our analysis, we found 165 MLHs with 70 singletons and 87 MCGs with 43 singletons (Fig. 1A,B) where the eight most abundant MCGs represented $> 51\%$ of the data over 11 Regions, and all years except for 2012. Our network-based approach to correlating MLHs with MCGs revealed a large and complex network (Fig. 1, Table 3). Community analysis showed 51 communities, 15 of which consisted of a single MLH unconnected with any other community indicating that just 9.09% of the 165 MLHs are unable to cross with any other MLH in this data set (Fig. S1). The three communities with the most members contained eight of the 10 most abundant MCGs. Comparing these communities with Bruvo's genetic distance showed an average distance of 0.451 among communities and an average distance of 0.437 within communities, which were not significantly different. When we assessed the number of times two different MLHs that are in the same MCG, considering these as potential heterothallic pairings that could result in sexual recombination, we found an average of 14.3 potential heterothallic pairings per MLH. Representing just four isolates, 'MLH 75' had 57 neighbors that shared the same mycelial compatibility group (Fig 1, S1). Overall, there was no clear pattern to the association between MLH and MCGs.

Table 3. The five most abundant Multilocus Haplotypes (MLH) with the probability of second encounter (P_{sex}), Mycelial Compatibility Groups (MCG), and Regions with sample sizes in parentheses.

| MLH | P_{sex} | MCG | Region |
|-----|-----------|-----|-------------------------|
| 25 | 0.016824 | 5 | ND (15), CO (2), MI (2) |
| | | 13 | ND (3) |
| | | 60 | ND (2), WA (1) |
| | | 1 | NE (1) |
| | | 4 | MI (1) |
| 163 | 0.049932 | 45 | CO (5), ND (2), NE (1) |
| | | 5 | MI (7) |
| 65 | 0.000071 | 44 | NE (10) |
| | | 5 | MI (1) |
| 140 | 0.000155 | 8 | CO (5) |
| | | 5 | MI (3) |
| | | 20 | MI (2) |
| 66 | 0.000016 | 9 | NE (4), CO (2), MI (2) |

Structure of Shared Multilocus Haplotypes

The most abundant MLH was represented by 27 isolates (Table 3) from five Regions (NE, MI, WA, CO, and ND). Within Regions, haplotypes were relatively evenly distributed with moderate to high diversity (Table 2). Of the 165 MLHs, 76 (46%) were found in at least two Regions, except those found in WI (2), ID (1), and Mexico (18) (Fig. 4).

We had performed an analysis on a network where the connections represented shared MLHs across populations, weighted by $1 - P_{sex}$ (Fig. 4, Table 3). Community analysis of the MLHs shared between populations revealed 4 communities with a modularity of 0.17: A coastal community (CA, OR, WA, and NY), a midwest community (CO, NE, ND, MI), and an international community (MN, France, Australia).

302 Although analysis with 16 loci resulted in the removal of the NY node because it no longer shared a
 303 haplotype with OR, the same overall community structure was present with a modularity of 0.2 (Fig. S2).
 304 Relative to the US, the international community appears to be driven by MLH 4, which is shared between
 305 all three populations and has a P_{sex} value of $2.87e^{-5}$, in contrast to the abundant MLH 25, which has a P_{sex}
 306 value of 0.0168.

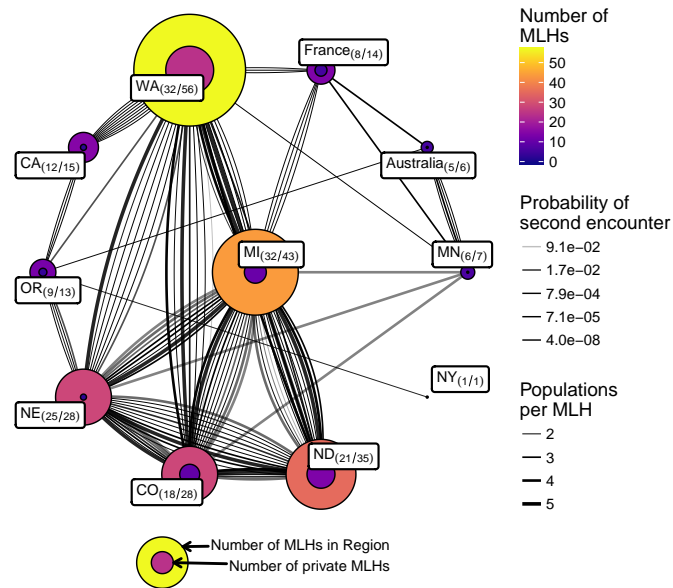


Figure 4. Network of populations (nodes/circles) and their shared multilocus haplotypes (MLH) (edges/lines) genotyped over 11 loci. Each node is labeled with **name (number of MLHs shared/number of MLHs total)**. The shade and area of the nodes are proportional to the number of unique MLHs within the node and the inner nodes are proportional to the number of private MLHs to the region (bottom legend). Each edge represents a single MLH where its thickness represents the number of populations that share the MLH and the shade represents the value of P_{sex} , or the probability of encountering that MLH from two independent meiotic events.

307 Population Differentiation

308 Analysis of Molecular Variance

309 The analysis of molecular variance (AMOVA) for clone-corrected samples over the hierarchy of
 310 Region, Source, and Year showed significant variation between Regions and Years, but no significant
 311 variation between wmn and producer fields (Table 4). In contrast, when we compared the three cultivars,
 312 Beryl, Bunsu, and G122, we found no significant differentiation (Supplementary Information).

Table 4. Comparison of populations in the white mold screening nurseries (wmn) and producer fields using an analysis of molecular variance on Bruvo's genetic distance showing no apparent differentiation between wmn and other sources. The hierarchy was constructed as Source/Region where source is defined as belonging to a wmn or producer field. Bold Φ values indicate significant difference ($P < 0.05$). S.S. = Sum of Squares, d.f. = degrees of freedom.

| Hierarchy | d.f. | S.S. | % variation | Φ statistic | P |
|------------------------------|------|-------|-------------|------------------|-------|
| Between Region | 13 | 10.19 | 8.45 | 0.0845 | 0.029 |
| Between Source within Region | 8 | 2.74 | -2.29 | -0.0250 | 0.486 |
| Between Year within Source | 22 | 9.37 | 16.28 | 0.173 | 0.001 |
| Within Year | 274 | 47.30 | 77.56 | 0.224 | 0.001 |

Discriminant Analysis of Principal Components

Discriminant Analysis of Principal Components (DAPC) was performed grouping by Region with the first 21 principal components, representing 88.1% of the total variance. The first discriminant axis (representing 36.1% of the discriminatory power) separated the centroid for the Mexico isolates from the rest of the data, indicating strong differentiation (Fig. 5b). The second discriminant axis, representing 25.3% of the discriminatory power, separated the centroid for the CA isolates. The mean population assignment probabilities for all populations with $n > 10$ showed that only isolates from Mexico, CA, and France had $> 50\%$ probabilities of being reassigned to their source populations (Fig. 5a).

DAPC grouping by cultivar used the first 20 principal components, representing 89% of the total variance. The first two discriminant axes (representing 38.5% of the discriminatory power) failed to separate any of the cultivars where the mean posterior assignment probabilities were 34% (G122), 35.9% (Beryl), and 30.1% (Bunsi). DAPC grouping by Region and Year used the first 15 principal components, representing 80.3% of the total variance. The North Central USA populations (NE, MI, CO, ND) did not appear to have any variation across time in contrast to WA, which showed a shift in population structure in the last year of sampling, 2008 (Fig. 6). Further analysis of this population revealed that all 12 isolates in WA circa 2008 originated in a wmn; nine haplotypes were shared with CA, and three were shared with France (Fig. 4, S2).

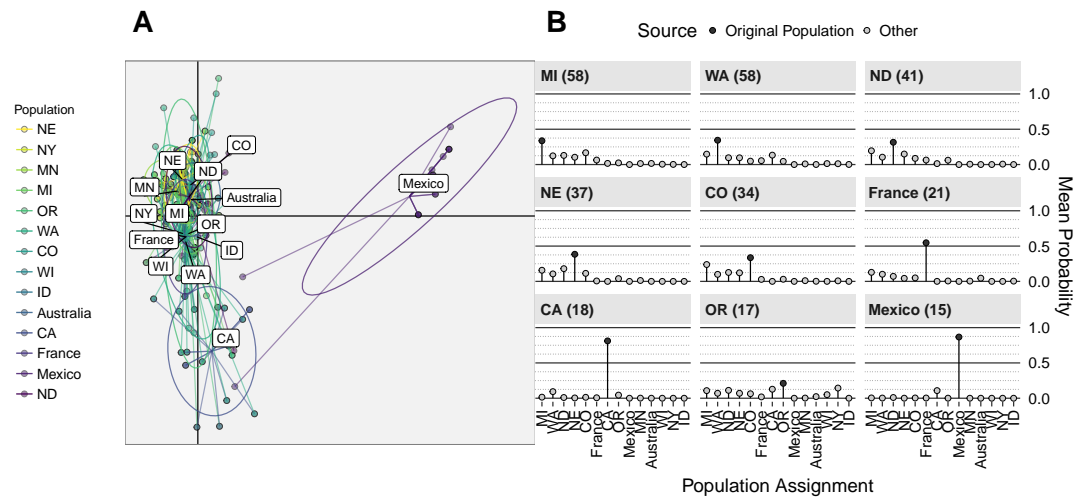


Figure 5. Discriminant Analysis of Principal Components on regions showing that Mexico is differentiated from other populations. **A)** Scatter plot of first two components from DAPC. Points represent observed individuals connected to the population centroids with ellipses representing a 66% confidence interval for a normal distribution. The center of each component is represented as black grid lines. **B)** Mean population assignment probability from the DAPC for all populations with $N > 10$ (facets). Populations represented along the horizontal axis and probability of assignment on the vertical. Numbers next to source populations indicate population size. All values sum to one.

DISCUSSION

In this study, we characterized the diversity of *Sclerotinia sclerotiorum* from dry bean fields across the United States. Our results suggest that, broadly, populations from white mold screening nurseries reflect the populations of the surrounding regions, indicating that resistance screening may be successful within regions. We found significant population differentiation by geographic region and year, mainly differentiated into three broad North American groups based on shared haplotypes and posterior groupings, a Coastal Region, Midwestern Region, and Mexico. To date, with 366 isolates, this is the largest single population genetic study of *S. sclerotiorum* assessing population structure within managed and unmanaged agricultural environments. These findings indicate that the white mold screening nurseries can be effective at screening for potential resistant lines within growing regions.

We found that the best predictors of genetic structure are Region and Year, supporting the hypothesis

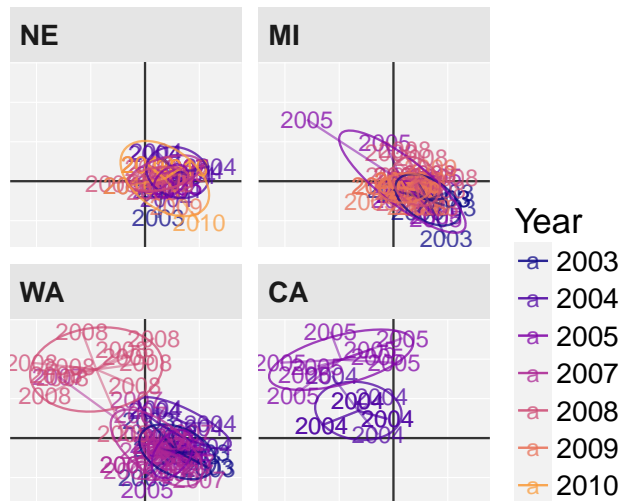


Figure 6. Scatter plot of Discriminant Analysis of Principal Components on Regions and Years showing non-differentiated temporal variation NE and MI and temporal variation in WA and CA. Points (text labels) represent observed individuals connected to the population centroids with ellipses representing a 66% confidence interval for a normal distribution. The center of each component is represented as black grid lines. A more detailed view is shown in Fig. S3.

that *S. sclerotiorum* populations are spatially structured (Carbone & Kohn, 2001). Borrowing a technique often used in the ecological literature, we used dbRDA to elucidate the effect of all variables (MCG, Region, Source, Year, Host, and Aggressiveness) (Legendre & Anderson, 1999). From the initial results, it appeared that the most important factors for predicting genetic structure were MCG, region, and year. When we inspected the biplot of the initial results, we saw that the most important predictors were ‘MCG 44’, ‘MCG 5’, and ‘MCG 9’. We believe that this was driven by the fact that these particular MCGs have uneven MLH distributions, meaning that they are heavily associated with one particular MLH (Fig. 1). We note these results with caution because of the apparent multicollinearity between MCG and Region, which is a violation of the analysis (Legendre & Anderson, 1999). While the results indicated that Mexico and the year 2005 were the two most important variables, it’s worth noting that all Mexico isolates were collected in 2005 (Fig. 2). The results also show that the Vista cultivar explains some of the variance, but this represents six isolates in MI, and thus we cannot draw broad conclusions from this axis. Aggressiveness and source field had little to no effect on prediction of genetic diversity. These results are in agreement with studies that examined differentiation based on Host (Aldrich-Wolfe et al., 2015) and Aggressiveness (Atallah et al., 2004; Attanayake et al., 2012, 2013) reporting little or no correlation of genetic diversity to these variables. This indicates that a) breeders should keep in mind regional differences when assessing resistance and b) it is possible that we have not yet measured biologically relevant variables that can predict genetic differentiation, which could include variables such as soil community composition.

While aggressiveness was not shown to predict genetic structure, it is an important factor in breeding efforts, and we observed significant differences in aggressiveness based on Region (Fig. 3, Table S2). These results show a similar pattern to what was found previously in Otto-Hanson et al. (2011) with the exception of North Dakota, which increased in mean aggressiveness from 5 to 5.77. This increase was due in part to new data from producer field isolates collected after the previous study. These straw tests were performed by a different person for these later isolates, which could suggest a more lenient or strict scoring system. However, when we examined the within-region differences, we found no significant effect by individual. Many of the ND isolates fell within the 6–7 range, which denotes a physical boundary (disease symptoms around the second node) between intermediate and susceptible (Otto-Hanson et al., 2011). Thus, we observed a shift in aggressiveness without a significant shift in genotypic structure, which may indicate that aggressiveness may be controlled by environmental factors as opposed to genetic profile.

372 The primary interest of this study was to assess if isolates sampled from white mold screening
373 nurseries represent isolates from producer fields within the region (Steadman et al., 2003; Otto-Hanson
374 et al., 2011). According to our AMOVA results, we have evidence for differentiation at the Region and
375 Year, but little to no differentiation between wmn isolates and production field isolates (Table 4). This
376 lack of differentiation, however, may reflect the breeder practice of inoculating screening plots with
377 sclerotia collected from sources within the region. When we analyze the AMOVA results in light of the
378 DAPC results (Fig. 5), it becomes clear that the regional patterns of differentiation are largely driven by
379 isolates from Mexico and CA. Isolates from these Regions had a higher posterior probability (> 0.75) of
380 being reassigned to their own populations than any other (Fig. 5A). All other populations in comparison
381 (except France) has reassignment probabilities of < 0.5 , which is reflected in the failure of the first two
382 discriminant functions to separate these populations (Fig. 5B).

383 Despite the evidence that Mexico and CA contributed to much of the population differentiation,
384 Regions like WA still had a large amount of internal variation. The two distinct clusters for the WA Region
385 showed that the 2008 population appeared differentiated and, under further investigation, we found that
386 all the haplotypes from this year were shared between CA and France (Fig. 4, 6, S3). All of the isolates
387 from WA in 2003–2005, and 2008 came from the same wmn; within the wmn, those in 2003–2005 came
388 a Northeastern field location cropped with dry bean since 2002, and those in 2008 from a Southeastern
389 field that was previously cropped with brassica, sundgrass, peas, beans, and potatoes (Miklas, Phil Pers.
390 comm.). Both of these fields were inoculated with sclerotia in 2002, the Northeastern field with sclerotia
391 provided by a commercial bean producer and the Southeastern field with sclerotia from peas (although
392 this was thought to be unsuccessful). Despite this information, it is still unclear what has contributed to
393 the differentiation of the 2008 population from WA. While the evidence may suggest host as being a factor,
394 previous studies have shown no significant differentiation across host species (Aldrich-Wolfe et al., 2015).

395 With the exception of the WA Region, populations that were sampled across several years appeared to
396 be relatively stable over time with overlapping distributions in the DAPC (i.e. NE and MI, Fig. 6). DAPC
397 is based on the principal components of Euclidean distance between genotypes (Jombart et al., 2010).
398 Unlike Bruvo's distance, Euclidean distance does not take into account the magnitude of the difference
399 between alleles, which could inflate the distance measure in the presence of private alleles (Bruvo et
400 al., 2004). We found no evidence of private alleles in the Mexico and CA isolates, suggesting that this
401 pattern separating these populations from the others was not an artifact. We believe that the differences
402 we observe from Mexico may reflect differences in climate.

403 Many of the isolates in our study were from temperate climates and the only isolates representing a
404 sub-tropical climate were from Mexico. It has been proposed within the *S. sclerotiorum* literature that
405 isolates from sub-tropical and tropical climates are differentiated or more variable than populations from
406 temperate climates [Carbone & Kohn (2001); Attanayake et al. (2013); Lehner & Mizubuti (2017);]. This
407 has been attributed to the notion that the fungus has the chance to undergo more reproductive cycles in
408 the warmer climate (Carbone & Kohn, 2001; Attanayake et al., 2013). The strongest evidence to date
409 supporting this hypothesis is from Attanayake et al. (2013), showing that populations in sub-tropical
410 regions of China have been found to be more variable, sexually reproducing, and unrelated to populations
411 in temperate regions of the USA. This result however, may be driven more by geography and agricultural
412 practice as opposed to climate.

413 The results from our shared haplotype analysis show several populations with at least one haplotype
414 between them, except for Mexico and two states that had fewer than three samples each (Fig. 4). Our
415 network-based approach by treating the haplotypes as edges and weighting each edge with the inverse
416 of P_{sex} treated the edges as springs connecting the populations with the strength proportional to the
417 probability of obtaining the same haplotype as a clone. This allowed us to use a graph walking algorithm
418 to see how close the populations were simply based off of the proportion of clones they shared. The
419 most abundant haplotype was shared across four populations, but its high value of P_{sex} meant that it did
420 not contribute significantly to the overall structure. The graph walking algorithm was able to divide the
421 network into three groups, but had a modularity of 0.17, which indicates that the groups are only weakly
422 differentiated.

423 The widespread nature of multilocus haplotypes in both wmn and production fields with relatively
424 small values of P_{sex} may indicate the spread of inoculum between regions. While seedborne transmission
425 is thought to be of insignificant epidemiological importance (Strausbaugh & Forster, 2003), it has since
426 been shown that *S. sclerotiorum* infections can be transmitted through seed (Botelho et al., 2013). Thus,

we hypothesize that shared haplotypes between populations may arise due to transmission events of seed or sclerotia. This could explain the fact that we see shared genotypes with low P_{sex} values shared between France, Australia, and the US. While we speculate that these transmission events are rare due to the genetic structuring by Region, these results suggest that seedborne infections may indeed reflect a source of inoculum. This may, in turn increase the risk of introducing new sources of genetic variation through potential outcrossing events.

When we tested for sexual reproduction, we were unable to find evidence for it in any region except for CA and Australia. While the Australia population had a non-significant value of \bar{r}_d —which would suggest that we cannot reject the null hypothesis of random mating—the sample size was insufficient from which to draw conclusions (Milgroom, 1996; Agapow & Burt, 2001). The low value of \bar{r}_d in the CA population may represent sexual reproduction, but we can see in Figure 6 that there is differentiation by year. Thus, this could also be an artifact of sampling two different populations, which is known to reduce the value of \bar{r}_d (Prugnolle & de Meeûs, 2010).

The previous study of the white mold screening nursery populations used MCGs to assess genotypic diversity (Otto-Hanson et al., 2011). Historically, MCGs have been used as a proxy for clonal lineages, and thus, of interest in this study was testing the association between multilocus haplotypes (MLHs) and mycelial compatibility groups (MCGs) (Kohn et al., 1990; Leslie, 1993; Kohn, 1995; Carbone et al., 1999; Schafer & Kohn, 2006; Otto-Hanson et al., 2011). Our results, however, do not support this assumption. It can be seen in Fig. 1A that the most abundant MCG contains several MLHs, but the diversity of those MLHs are low as indicated by the evenness (transparency), which indicates that there is one dominant MLH ('MLH 25'). What is not shown in Fig. 1A is the MLHs that are shared between MCGs. This is illustrated in both Table 3 and Fig. 1B,C. It could be argued, however that 'MLH 25', with its high value of P_{sex} represents different true MLHs across the five MCGs it occupies, but this does not account for the overall structure of Fig. S1 where, for example, 'MLH 75' ($P_{sex} = 1.81e^{-4}$) is compatible with 57 other haplotypes through three MCG when the population structure of *S. sclerotiorum* is known to be clonal.

Over the past few years, researchers have noticed inconsistencies among the relationship between MCGs and MLHs (Carbone et al., 1999; Attanayake et al., 2012; Aldrich-Wolfe et al., 2015; Lehner et al., 2015). Either several MCGs belong to one MLH, which could be explained by insufficient sampling of loci; several MLHs belong to one MCG, which could be explained by clonal expansion; or a mixture of both. Some studies have shown a correlation between MCG and MLH (Carbone et al., 1999; Aldrich-Wolfe et al., 2015; Lehner et al., 2015), whereas other studies have shown no apparent correlation, even on small spatial scales (Atallah et al., 2004; Attanayake et al., 2012, 2013).

One long-held assumption was that MCGs (as determined via barrage reaction) represent vegetative compatibility groups (VCGs) (Kohn et al., 1990; Schafer & Kohn, 2006; Lehner et al., 2015), which are known to have a genetic component (Saupe, 2000; Hall et al., 2010; Strom & Bushley, 2016). While our protocol for assessing MCGs utilized a different substrate for the MCG reactions, the patterns we observe are not dissimilar from what have previously been reported in the literature. It has been demonstrated in several Ascomycetes—including *Neurospora crassa* (Micali & Smith, 2003), *Sclerotinia homoeocarpa* (Jo et al., 2008), *Verticillium dahliae* (Papaioannou & Typas, 2014), and *S. sclerotiorum* (Ford et al., 1995)—that barrage reactions are independent from stable anastomosis. Thus, the inconsistencies in this study and other studies indicate that researchers studying *S. sclerotiorum* should not rely on MCG data derived from barrage reactions as an indicator for genetic diversity.

Limitations

One of the main limitations of this study is the focus on *P. vulgaris* as a host. It has been shown that *S. sclerotiorum* in the midwestern United States does not have a particular preference for host (Aldrich-Wolfe et al., 2015). If the distribution of *S. sclerotiorum* is even across agricultural hosts in the USA, then our sample may yet be representative of the genetic pool present in other crops and weedy species.

Another limitation was the microsatellite markers used for this particular study (Sirjusingh & Kohn, 2001). The haplotype accumulation curve showed no indication of a plateau, indicating that if we had sampled more loci, we would have resolved more multilocus haplotypes. While 16 loci showed us similar results and began to show a plateau for the haplotype accumulation curve, we were unable to use these results due to our uncertainty in the allele calls for these five extra loci. With the availability of an optically-mapped genome (Derbyshire et al., 2017), future studies describing the genetic diversity of *S. sclerotiorum* should employ techniques such as Genotyping-By-Sequencing (Davey et al., 2011),

481 Sequence Capture (Grover et al., 2012), or Whole Genome Sequencing.

482 **Conclusions**

483 This study represents the largest genetic analysis of *S. sclerotiorum* from the USA to date, giving us a
484 unique insight to continent-wide population structure and relationships between phenotypic and genotypic
485 variables. Populations in wmn appear to show no significant differentiation when compared to their
486 production field counterparts, suggesting that the wmn populations of *S. sclerotiorum* may be considered
487 representative of the surrounding regions. While we found no direct relationship between haplotype and
488 severity, it is evident that there is a gradient of severity by region, further supporting the need for screening
489 in multiple locations. Based on our analysis of the relationships between MCG and MLH, we found
490 no clear evidence that the two are directly related, suggesting that MCG do not necessarily represent
491 vegetative compatibility groups and thus should not be used as a proxy for identifying clones.

492 **Data Availability**

493 All scripts, data, and resources used to generate the results presented in this publication (including
494 Supplementary Information) are fully reproducible and available at The Open Science Framework
495 <https://osf.io/ejb5y>.

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504 **Conflicts of Interest**

505 The authors declare no conflict of interest.

506 **Author Contributions**

- 507 • **Zhian N. Kamvar** analyzed the data, contributed analysis tools, wrote the paper, prepared figures
508 and tables, reviewed drafts of the paper.
- 509 • **Bimal Sajeewa Amaradasa** ...
- 510 • **Rachana Jhala** ...
- 511 • **Serena McCoy** ...
- 512 • **James Steadman** ...
- 513 • **Sydney E. Everhart** ...

Table S1. Description of *Sclerotinia sclerotiorum* isolates used in this study. N = Number of Isolates. Key abbreviations: wmn = white mold screening nursery, producer = producer field, unk = unknown cultivar.

| Country | State | Field Code | Year | Host | N |
|-----------|-------|------------|------------------------------|--|----|
| USA | CA | wmn | 2004, 2005 | Beryl, Buns, G122 | 18 |
| USA | CO | producer | 2007, 2010 | Pinto, Yellow | 41 |
| | | wmn | 2003 | GH | 1 |
| USA | ID | producer | 2003 | GH | 1 |
| USA | MI | wmn | 2003, 2004, 2005, 2008, 2009 | 11A, 37, 38, B07104, Beryl, Buns, Cornell, G122, Orion, PO7863, WM31 | 43 |
| | | producer | 2003, 2008, 2009 | BL, Black, Fuji, GH, Merlot, SR06233, unk, Vista, Zorro | 19 |
| USA | MN | wmn | 2003, 2004 | Beryl, Buns, G122 | 11 |
| USA | ND | producer | 2007, 2010 | unk | 53 |
| | | wmn | 2005 | Beryl, Buns, G122 | 7 |
| USA | NE | wmn | 2004, 2005, 2008, 2010 | Beryl, Buns, G122, PO7683, unk | 27 |
| | | producer | 2003, 2007, 2009, 2010 | Beryl, Emerson, GH, Orion, Pinto, Weihing | 20 |
| USA | NY | producer | 2003 | GH | 1 |
| USA | OR | wmn | 2003, 2004 | Beryl, Buns, G122 | 15 |
| | | producer | 2003 | G122, GH | 2 |
| USA | WA | wmn | 2003, 2004, 2005, 2008 | 11A, 37, 38, Beryl, Buns, Cornell, G122, Orion, PO7104, PO7863, WM31 | 36 |
| | | producer | 2003, 2007 | GH, Merlot, Pinto, Redkid | 23 |
| USA | WI | producer | 2003 | GH | 2 |
| Mexico | - | wmn | 2005 | Beryl, Buns, G122 | 18 |
| France | - | wmn | 2004, 2005 | Beryl, Buns, G122 | 18 |
| | | producer | 2012 | unk | 4 |
| Australia | - | wmn | 2004 | Beryl, Buns, G122 | 4 |
| | | producer | 2004 | Beryl | 2 |

Table S2. Mean aggressiveness ratings for Regions with more than five samples; groupings according to 95% family-wise confidence interval.

| Region | Mean Aggressiveness | Group |
|-----------|---------------------|-------|
| MN | 5.84 | a |
| ND | 5.77 | a |
| NE | 5.29 | ab |
| MI | 5.13 | abc |
| OR | 4.84 | abcd |
| CO | 4.72 | bcd |
| WA | 4.67 | cd |
| France | 4.66 | cd |
| Mexico | 4.58 | cd |
| Australia | 4.12 | cd |
| CA | 4.01 | d |

Table S3. Mean aggressiveness ratings for the 10 most abundant MCG; groupings according to 95% family-wise confidence interval.

| MCG | Mean Aggressiveness | Group |
|-----|---------------------|-------|
| 44 | 6.03 | a |
| 3 | 5.50 | ab |
| 5 | 5.40 | b |
| 2 | 5.25 | b |
| 9 | 5.11 | b |
| 1 | 4.95 | b |
| 45 | 4.88 | b |
| 4 | 4.87 | b |
| 53 | 4.69 | b |
| 49 | 4.60 | b |

Table S4. Mean aggressiveness ratings for the 10 MLH most abundant; groupings according to 95% family-wise confidence interval.

| MLH | Mean Aggressiveness | Group |
|-----|---------------------|-------|
| 78 | 6.07 | a |
| 65 | 5.94 | a |
| 9 | 5.67 | ab |
| 25 | 5.41 | ab |
| 66 | 5.30 | ab |
| 104 | 5.22 | ab |
| 160 | 4.80 | ab |
| 163 | 4.80 | ab |
| 165 | 4.34 | b |
| 140 | 4.31 | b |

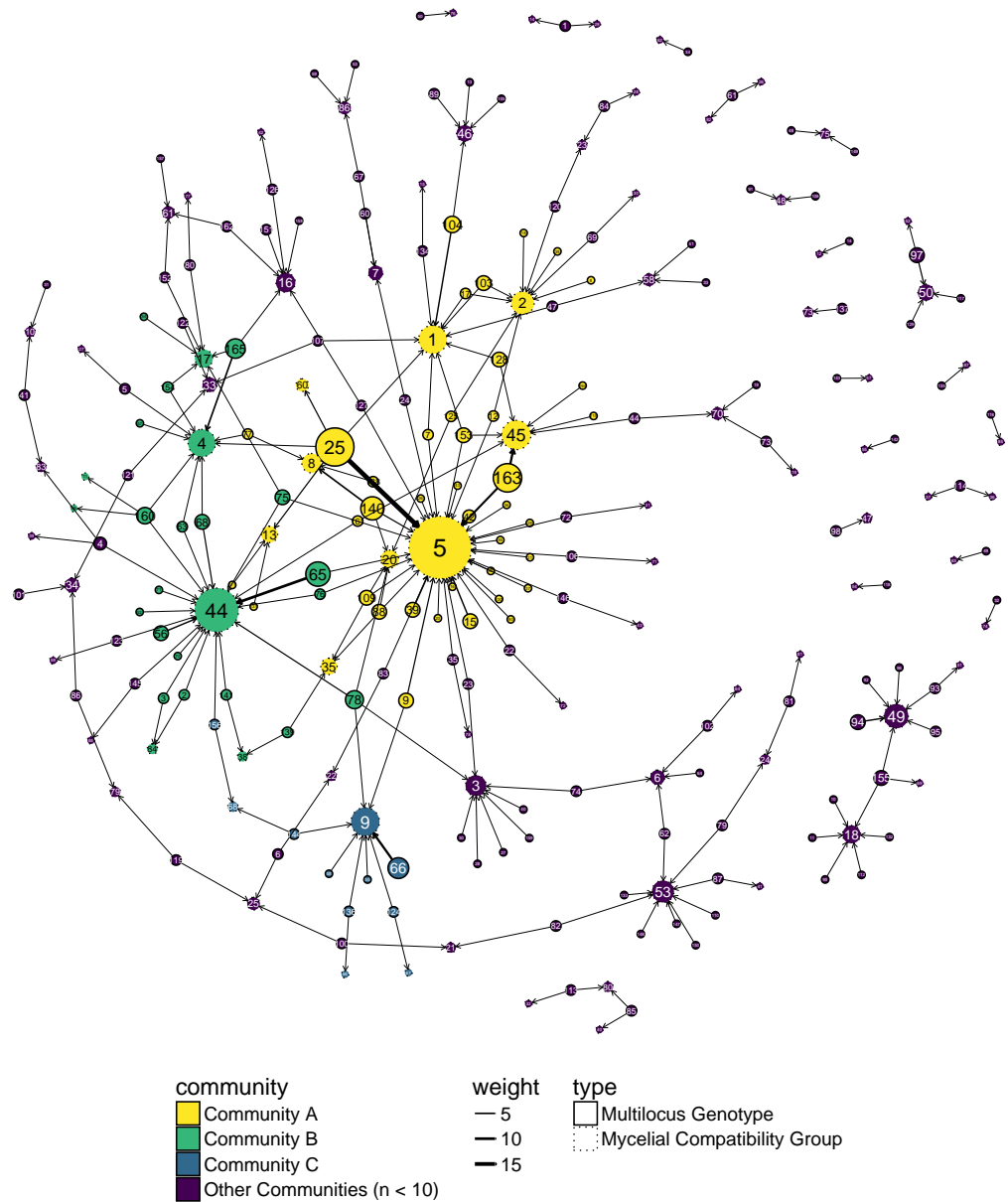


Figure S1. Graph showing complex associations between Mycelial Compatibility Groups (MCG) (dotted nodes) and Multilocus Haplotypes (MLH) (full nodes) where the number in each node represents the MLH/MCG assignment. Node size reflect the number of samples represented by each node (circle). Edges (arrows) point from MLH to MCG where the weight (thickness) of the edge represents the number of samples shared. Node color represents the community assignment based on the walktrap algorithm with a maximum of four steps (Pons & Latapy, 2006).

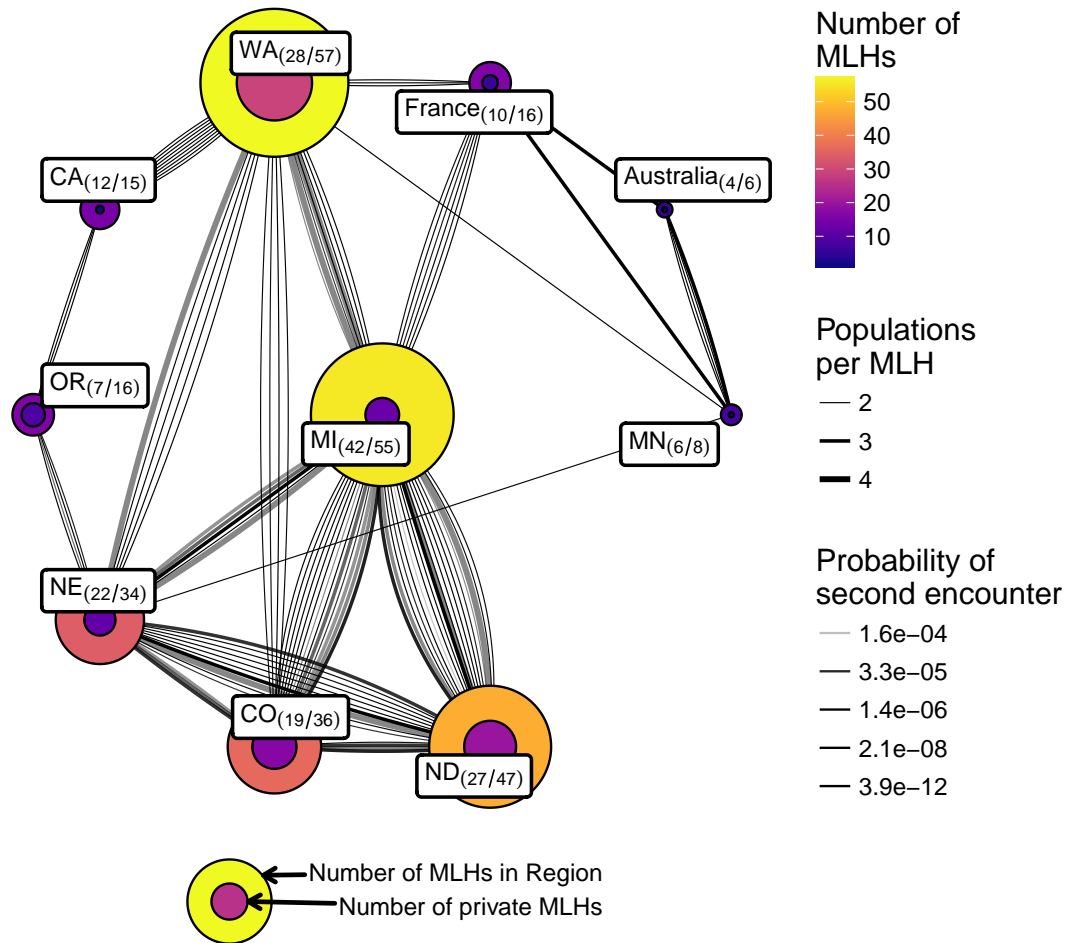


Figure S2. Network of populations (nodes/circles) and their shared multilocus haplotypes (MLH) (edges/lines) haplotyped over 16 loci. Each node is labeled with **name (number of MLHs shared/number of MLHs total)**. The shade and area of the nodes are proportional to the number of unique MLHs within the node and the inner nodes are proportional to the number of private MLHs to the region (bottom legend). Each edge represents a single MLH where its thickness represents the number of populations that share the MLH and the shade represents the value of P_{sex} , or the probability of encountering that MLH from two independent meiotic events.

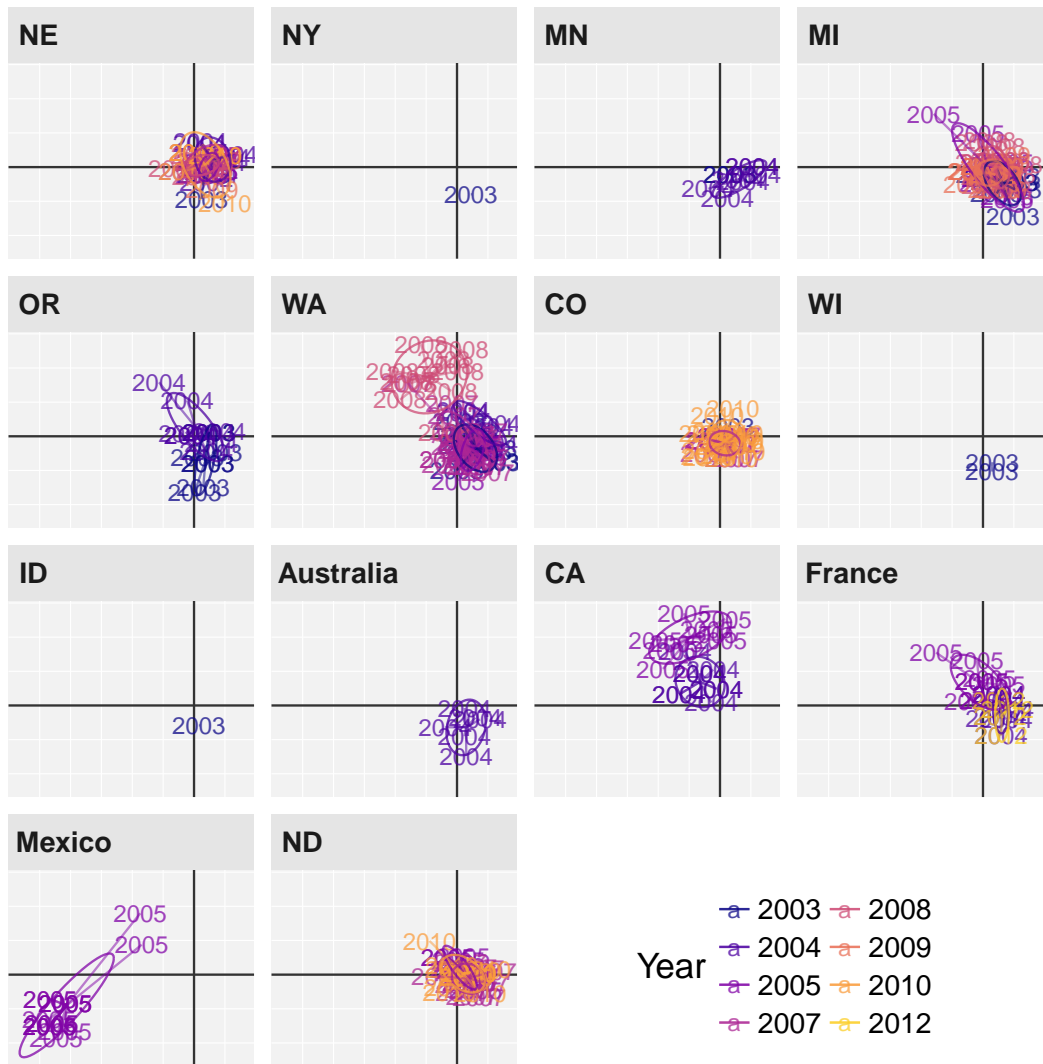


Figure S3. Scatter plot of Discriminant Analysis of Principal Components on Regions and Years showing temporal variation across all Regions. Points (text labels) represent observed individuals connected to the population centroids with ellipses representing a 66% confidence interval for a normal distribution. The center of each component is represented as black grid lines.

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