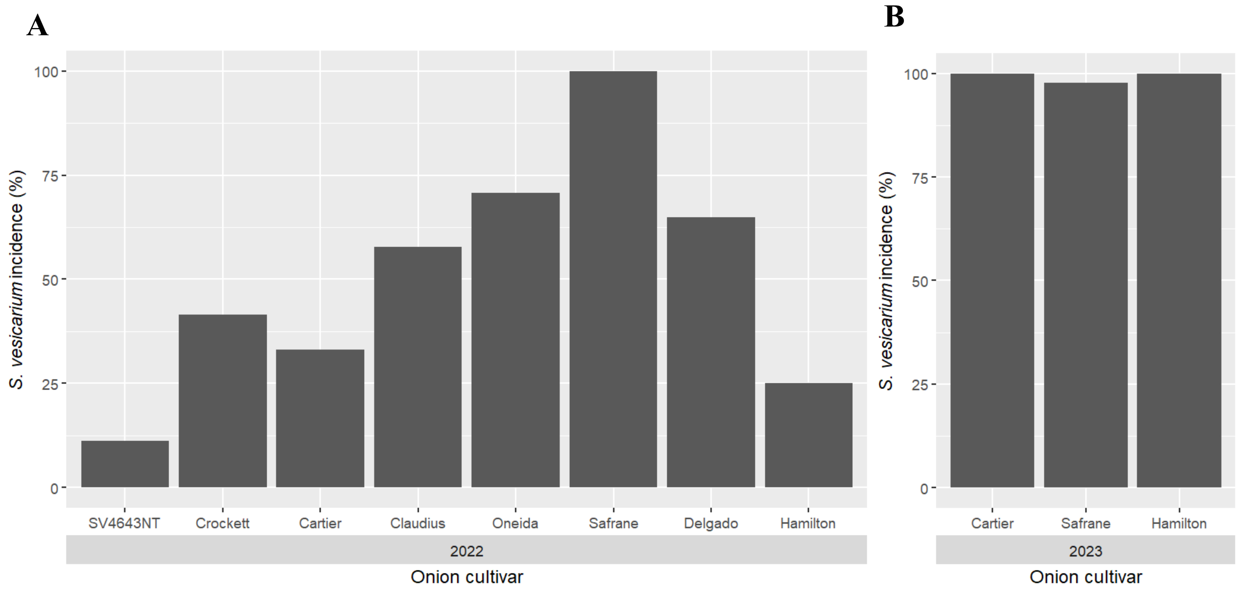
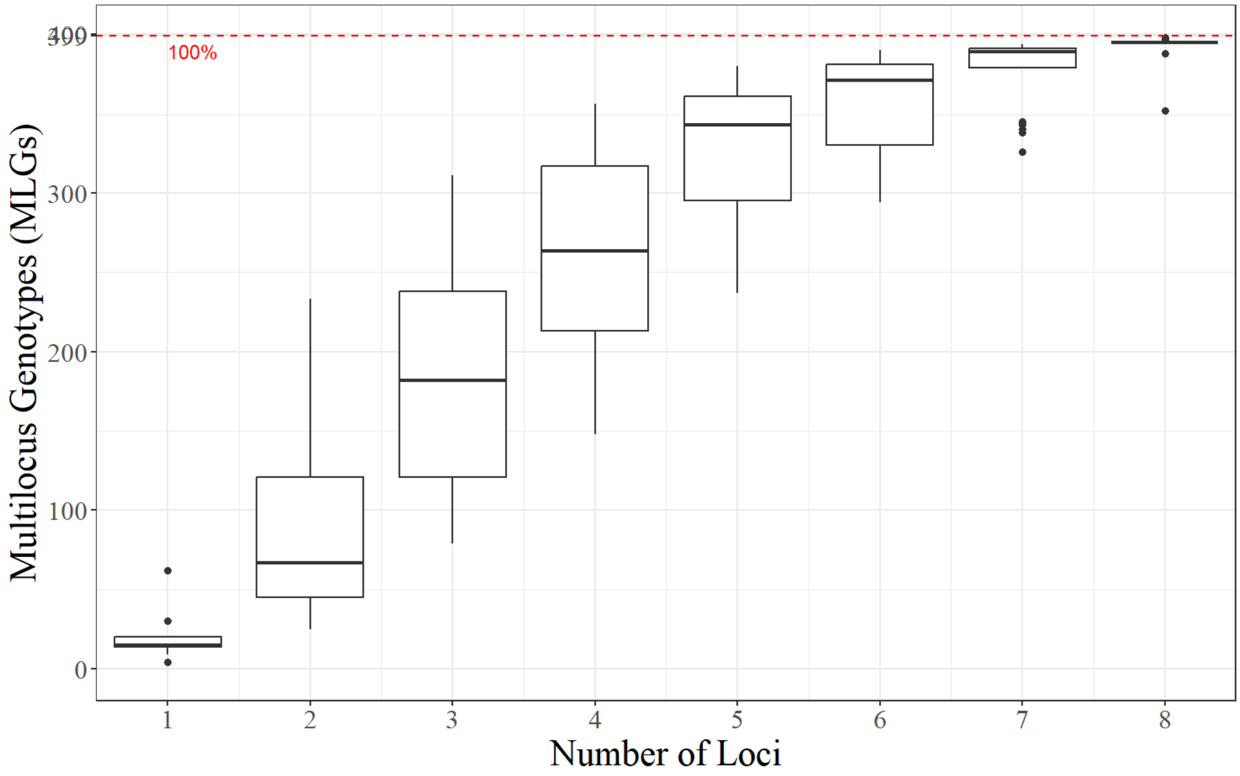
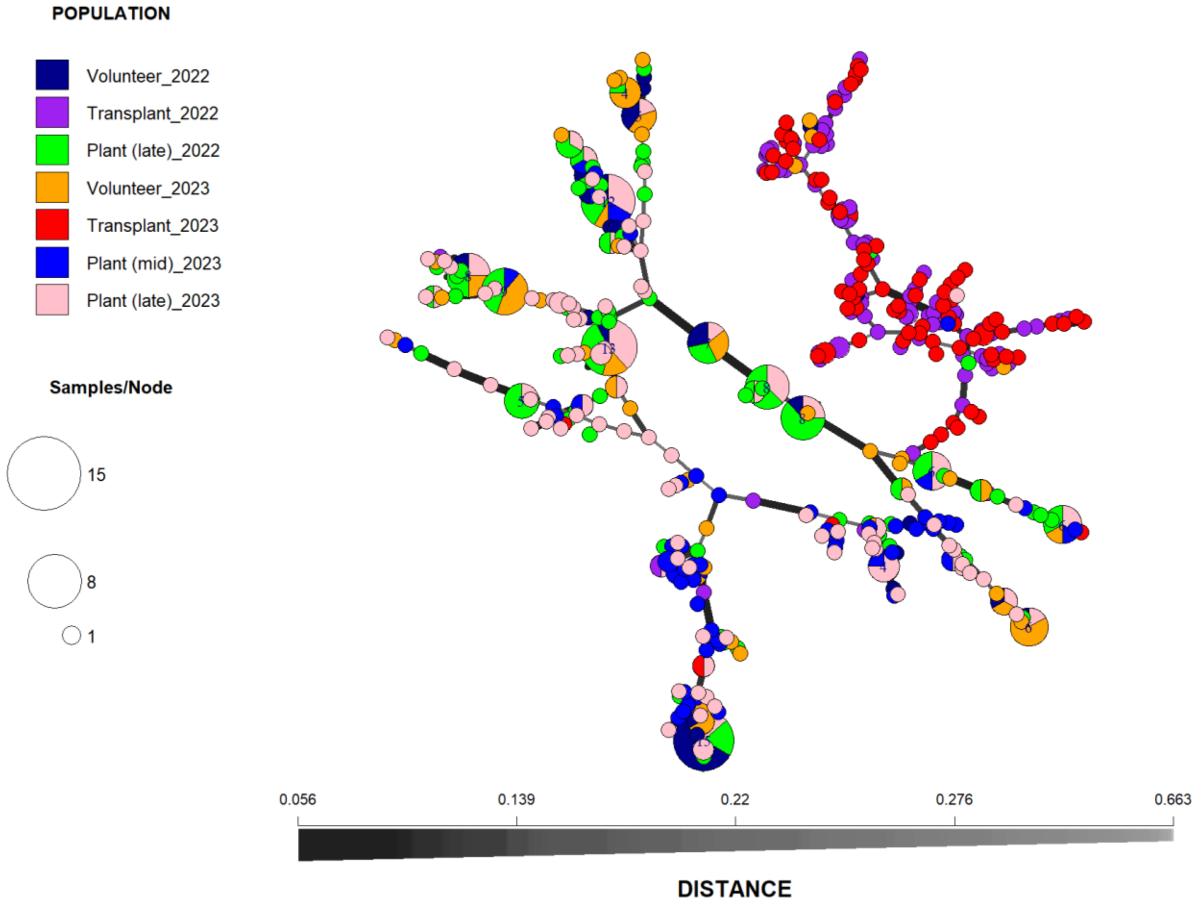
Supplementary Fig. S1. Incidence of *Stemphylium vesicarium* in onion bare root transplants from eight cultivars in **A,** 2022 and three cultivars in **B**, 2023.



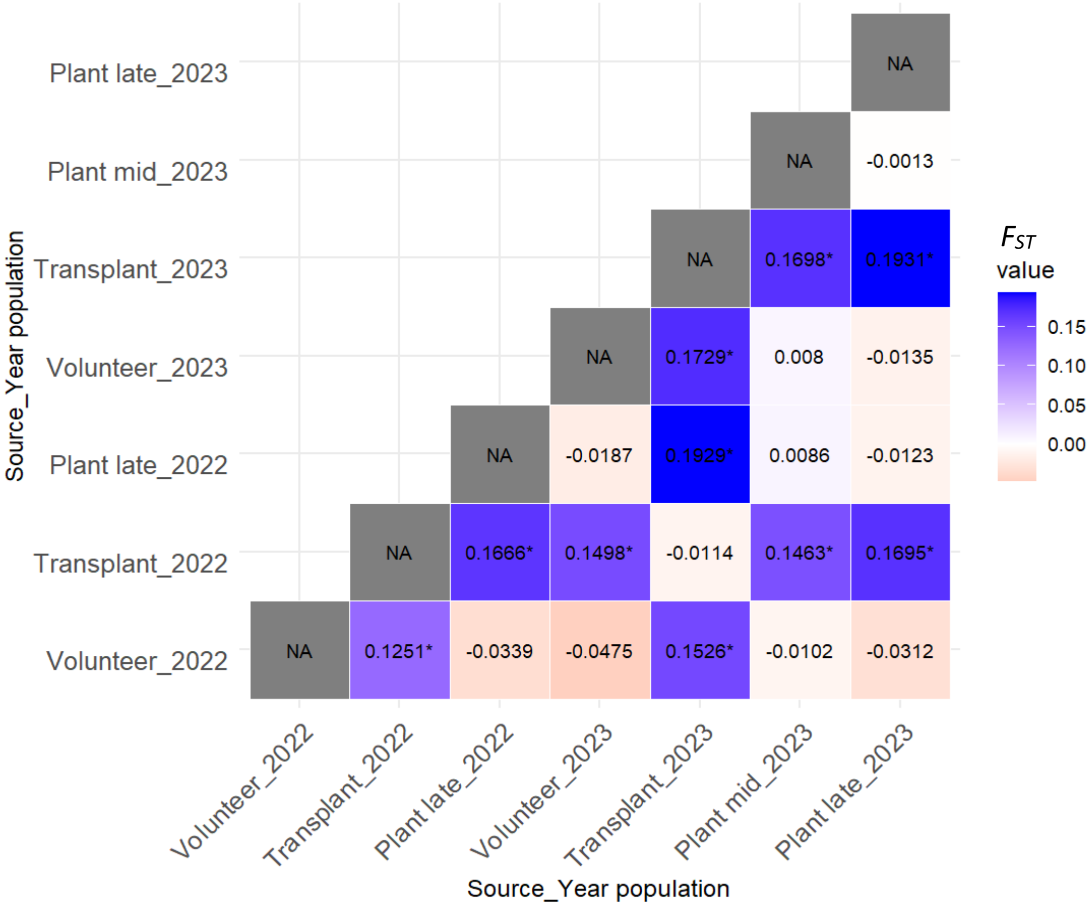
Supplementary Fig. S2. Genotype accumulation curve of nine microsatellite markers used for the population biology study of 537 *Stemphylium vesicarium* isolates collected from different onion plant materials in 2022 and 2023.



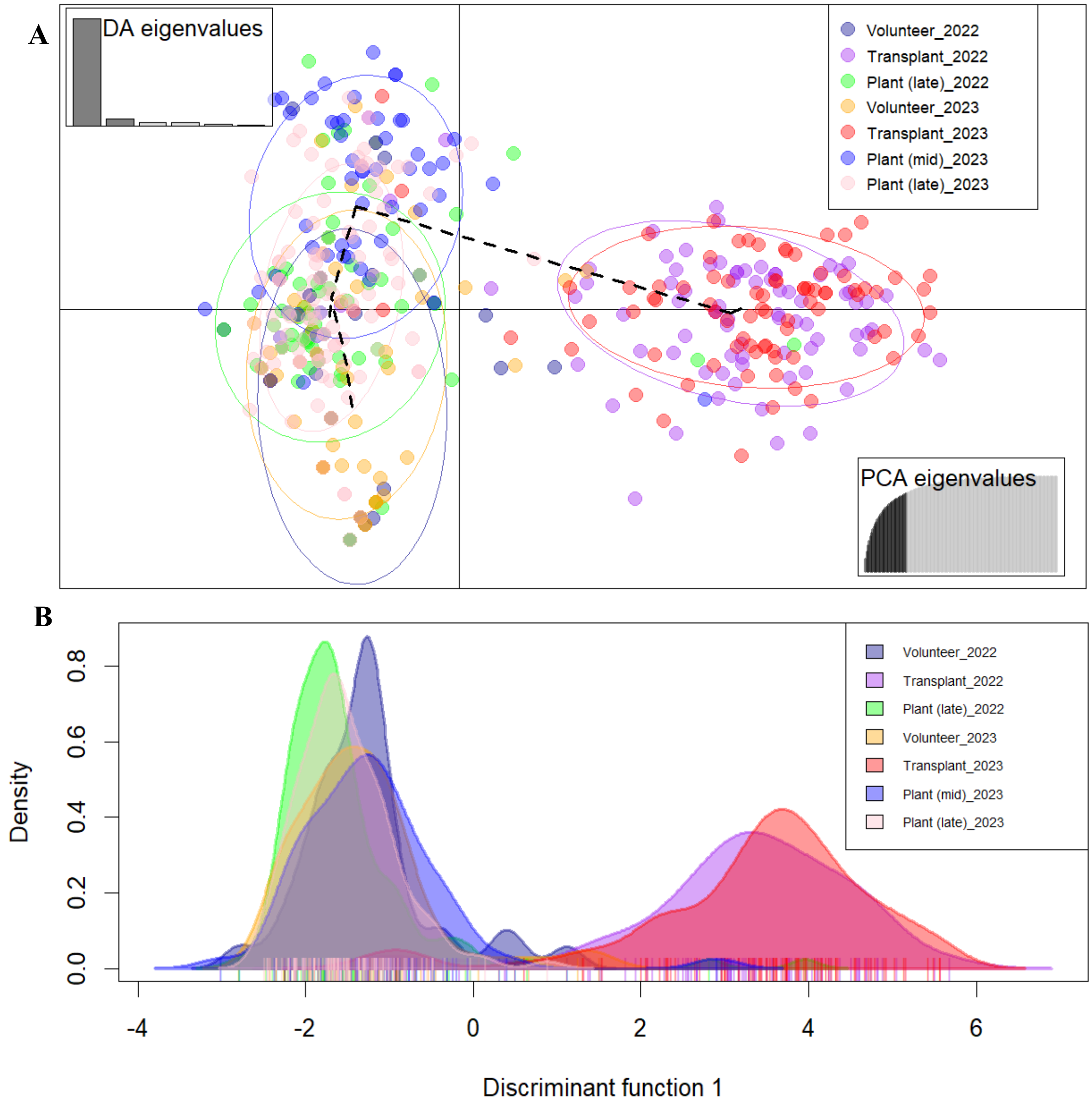
Supplementary Fig. S3. Minimum Spanning Network (MSN) for 399 *Stemphylium vesicarium* multilocus genotypes (MLGs) based on Bruvo's measure of genetic distance. The MSN was constructed according to onion plant material source (volunteers, transplants, and main crop plants collected at mid- and late season samplings) and year (2022 and 2023). Each node represents an MLG, and the node size represents the number of isolates corresponding to each MLG.



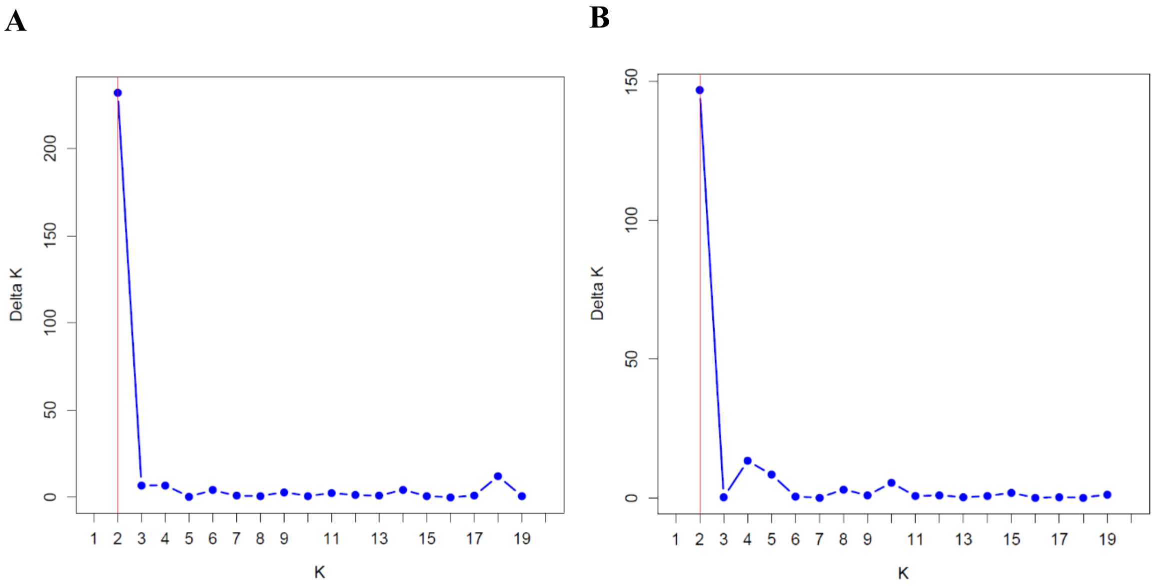
Supplementary Fig. S4. Pairwise F_{ST} heatmap with values ranging from 0 to 0.19 between source populations of *Stemphylium vesicarium* from infected transplants, volunteers, and main crop onion plants collected at mid- and late season samplings and year (2022 and 2023). F_{ST} values were estimated with clone-corrected datasets and significant differentiation between populations ($P < 0.01$) is marked with asterisks.



Supplementary Fig. S5. Discriminant Analysis of Principal Components for non-clone-corrected data of 399 *Stemphylium vesicarium* multilocus genotypes (MLGs) stratified by source (transplants, volunteers, and main crop plants at the mid- and late season samplings) and year (2022 and 2023) depicted as a **A,** scatter plot (dots represent MLGs) and **B,** density plot on the first discriminant function.



Supplementary Fig. S6. Plot of Δ*K* from the STRUCTURE analysis of 537 *Stemphylium vesicarium* isolates. Log-likelihood of Δ*K* values across a range of possible *K* values (*K* = 1 to 20, number of genetic clusters) for populations according to **A**, source; *K* = 2, and **B,** year; *K* = 2.



Supplementary Fig. S7. **A**, STRUCTURE analysis results of 537 *Stemphylium vesicarium* isolates assigned into genetic clusters according to source (transplants, volunteers, and main crop plants at the mid- and late season samplings) and year (2022 and 2023), on a non-clone-corrected dataset with *a priori* population assignment. Each bar represents a single isolate with the height showing the estimated proportion of that isolate's membership in the identified clusters. Different colors represent the predicted number of genetic clusters ($K = 2$). **B**, Plot of ΔK from the STRUCTURE analysis of 537 *Stemphylium vesicarium* isolates. Log-likelihood of ΔK values across a range of possible K values ($K = 1$ to 20, number of genetic clusters) for populations according to source and year; $K = 2$.