Fig. 1. Minimum Spanning Network (MSN) for 399 *Stemphylium vesicarium* multilocus genotypes (MLGs) based on Bruvo's measure of genetic distance for isolates obtained from transplants, volunteers, and main crop onion plants in New York across 2022 and 2023. Each node represents an MLG, and the node size represents the number of isolates corresponding to each MLG.
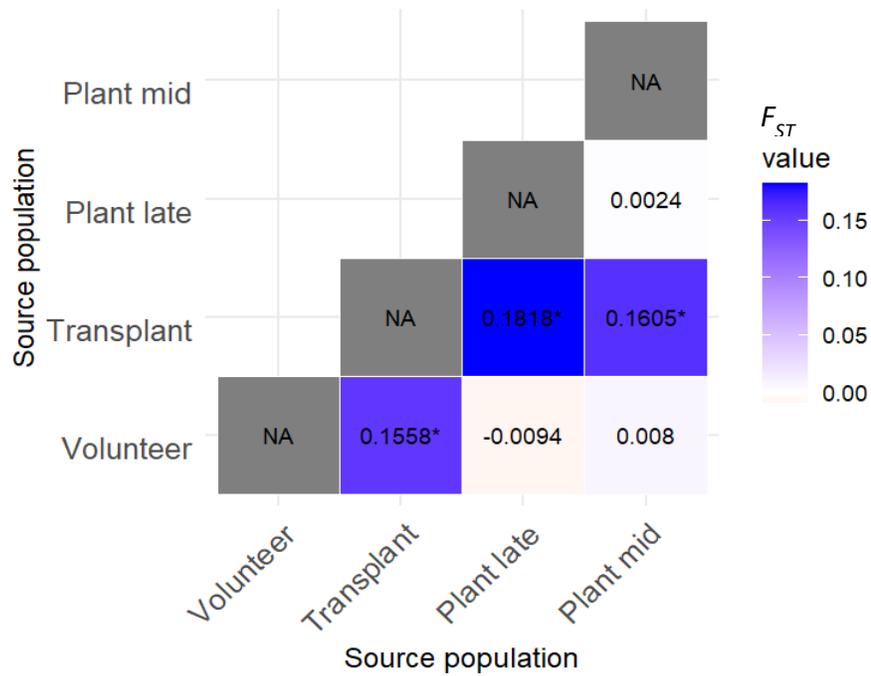
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Fig. 2. Pairwise F_{ST} heatmap with values ranging from 0 to 0.18 between *Stemphylium vesicarium* populations from transplants, volunteers, and main crop onion plants collected at mid- and late season samplings. F_{ST} values were estimated with clone-corrected datasets and significant differentiation between populations ($P < 0.01$) are marked with asterisks.
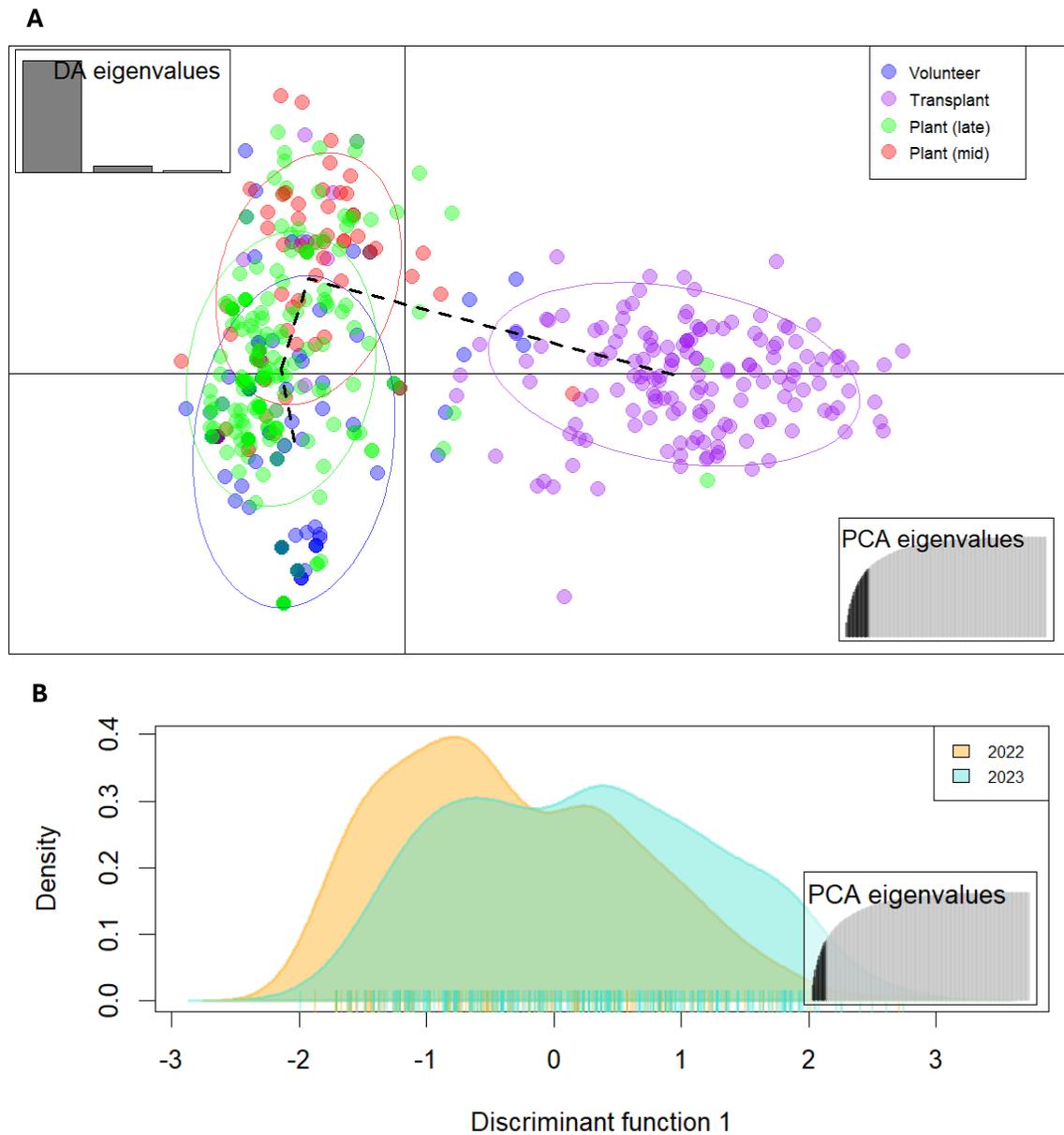
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Fig. 3. Discriminant Analysis of Principal Components for non-clone-corrected data of 399 *Stemphylium vesicarium* multilocus genotypes (MLGs) stratified by source (transplants, volunteers and main crop plants at the mid- and late season samplings) and year (2022 and 2023) depicted as a **A,** scatter plot (dots represent MLGs) and **B,** density plot on the first discriminant function.
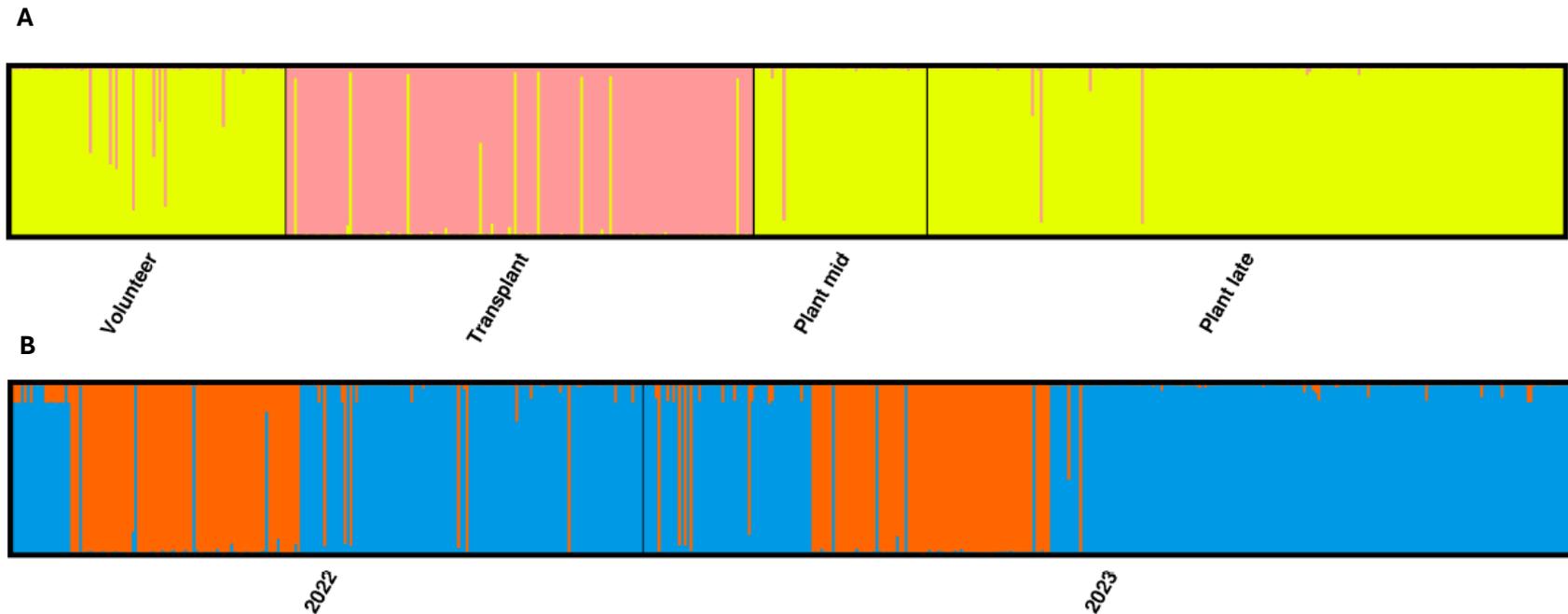
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Fig. 4. Assignment of 537 *Stemphylium vesicarium* isolates into genetic clusters according to **A,** source populations (infected transplants, volunteers, and main crop plants at mid- and late season samplings) and **B,** year populations (2022 and 2023) from onion fields in New York, using the Bayesian clustering software STRUCTURE 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 for source ($K = 2$), and year ($K = 2$) populations.

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