



Figure S1: A dendrogram generated for genotypic data from 15 polymorphic microsatellite markers (SSRs), illustrating the genetic distance among the donor plants of *Helianthus verticillatus*. The matrix of genetic distances was calculated in R version 3.6.1 using RStudio version 1.2.5019, and the package *poppr* version 2.8.3 [68] with Bruvo's genetic distance [69] that regards the repeated motif lengths. Bootstrap support values for each split were calculated over 10,000 permutations of the dataset; only values ≥ 30 are displayed