

Analysis of *Geosmithia morbida* isolates using nine microsatellite loci shows absence of genetic structure by state of origin or host of origin

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ABSTRACT: We analyzed about 100 isolates of *Geosmithia morbida*, the fungus associated with Thousand Cankers Disease of walnut, using nine microsatellite loci. The microsatellites were first identified using pyrosequence data and screened for polymorphism. The nine loci chosen for analysis were sufficiently polymorphic to permit standard population genetic analysis using the software GENALEX. When isolates were divided into populations by host from which they had been isolated (*Juglans californica*, *J. hindsii*, *J. major*, *J. nigra*, *J. regia*) we observed that only about 1% of the variation at the nine microsatellite loci was partitioned within populations, indicating the fungus does not have host-specific haplotypes and there is no discernible pattern indicating that certain hosts predominated in terms of fungal variability. Similarly, when the isolates were separated into populations based on their state of origin (AZ, CA, OR, CO, NM, TN), we found that a small (2%) and statistically insignificant amount of variation was attributable to differences among populations (state of origin). This result indicates that the fungus does not have a pattern of differentiation among locations, that all the variation for the species tends to be found in every location where the fungus is present, and that no population (state) appeared to be a center of diversity.