

Re-evaluation of NCGR Davis *Ficus carica* and *palmata* SSR profiles

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Abstract

This analysis is the result of a mathematician's query into the ancestral relationships between his fig trees. To this end, previously published analyses of fig specimens housed at NCGR Davis were consulted. This led to more questions because some of the reported relations appeared contradictory to observed phenotypes in his collection and orchards elsewhere in the U.S. Eventually a full-scale research effort was launched to determine the nature of the genetic data, the measures used to ascertain relationships, and the methods employed to resolve genetic clades among the fig specimens. Several missteps of the prior authors were uncovered including the use of a non-metric similarity measure and applying graph partitioning software to inapplicable data. The genetic profiles were re-evaluated with geometric and pattern-matching distance metrics and the latter was found to best match what is manually observed in the profiles. The computed distances were compared with historical records and morphologic observations to produce a graph of ancestries and relations for 89 of the 175 viable NCGR profiles. The previous research found that the genetic profiles did not correlate with phenotype characteristics of the specimens which was also verified in the present study – thus pointing to the necessity of a multiple specimen SNP analysis to obtain a more discerning set of genetic markers.