

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

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Abstract

To date all public records of *F. carica* SSR profiles are from NCGR Davis. Prior studies of this data have not been received well because several of the stated relationships do not match what is observed in the field. Upon examination of the prior authors methods it is found that the Nei similarity measures are not valid distance metrics for the profiles thus invalidating their analysis of genetic distance. Further, the data are tensor in nature and it is shown here that "flattening the data" for use in a vector method will change the problem under study. Consequently the present analysis focuses on geometric, statistical, and biostatistical tensor-based methods – finding that only the latter produces results matching what is manually observed among the profiles. Combining this with historical breeding records and morphologic observations reveals that a modest portion of the profiled accessions are mislabeled – and also reveals the existence of previously undocumented close relations. Another area of concern in the prior studies is the statistical partitioning of the complete graph of distances to define clades. In the present analysis it is shown that genetic clades cannot be defined in this profile collection due to lack of cohesion in nearest neighbor components. It is also shown that it is presently intractable to significantly rectify gaps in the sample population by profile enrichment because the number of individuals in an entire population within the estimated profile distribution exceeds 10^{14} . The profiles themselves are found to have very few occurrences of common values between the 15 loci and thus according to Fisher's theory of epistatic variance no correlation to phenotype attributes is expected – a result verified by the original investigators. Therefore further discovery of appropriate markers is needed to fully capture geno- and pheno-type characteristics in *F. carica* SSR profiles.