

The Genetic Diversity of Wild Grapes in Mexico

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Research Article

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Abstract

This is the first report evaluating the genetic diversity of Mexican grape species utilizing DNA-based markers to understand the distribution of grape species and patterns of hybridization. The study utilized accessions maintained in three collections in Mexico, one in the USA and recently collected germplasm. Fifteen SSR markers were used to develop a fingerprint database to identify unique germplasm. Two different clustering analyses without prior population assignment, were used to identify groups that were verified by a Discriminant Analysis of Principal Components and a Principal Coordinate Analysis. Genetic diversity estimates were made across and within groups to validate the results obtained from the clustering analyses. Multiple clustering analyses and diversity parameters supported six genetic groups representing different geographic regions. The Northeastern group was the most diverse with a geographic range extending to Eastern and Central Mexico, while the Coahuila group was the least diverse. *Vitis arizonica* Engelm. and *V. cinerea* Engelm. ex Millardet were the most abundant species with many hybrid forms. We provide evidence that wild grape species in Mexico follow the physical barriers of mountain ranges like the Sierra Madre Oriental with an east-west divide and the Trans-Mexican Volcanic Belt as a corridor for gene flow among different grape species. Additional collections are required to fully understand the extent of hybridization and to clarify hybrid zones.

Full Text

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Figures

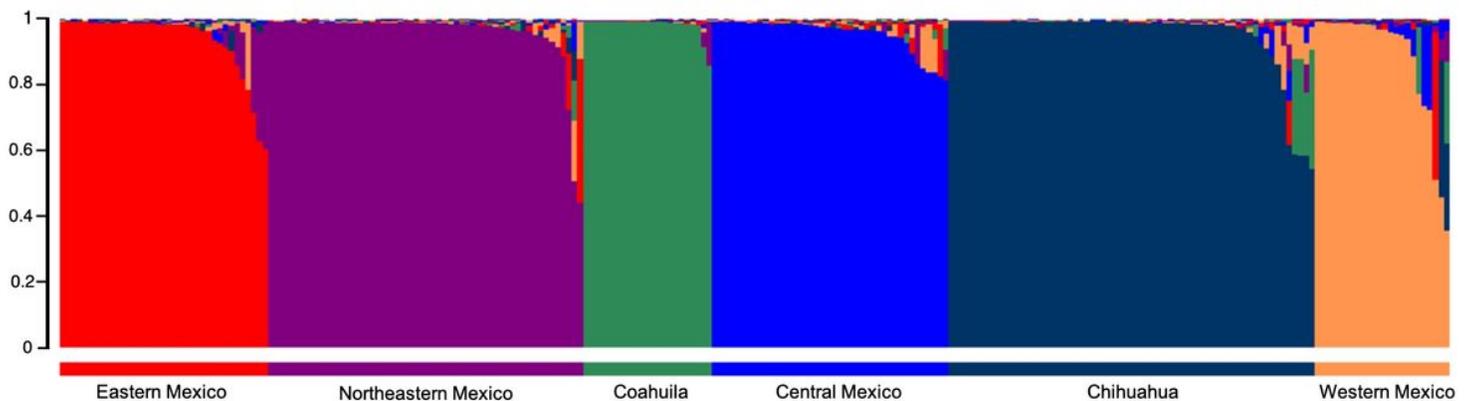


Figure 1

Graphical representation of the inferred population structure for $K=6$ using the model-based software STRUCTURE. Groups were named according to the geographic location: Eastern Mexico (red), Northeastern Mexico (purple), Coahuila (green), Central Mexico (blue), Chihuahua (navy blue), and Western Mexico (gold). Each vertical line represents one sample. Accessions were ordered from high to low Q-value in each group.

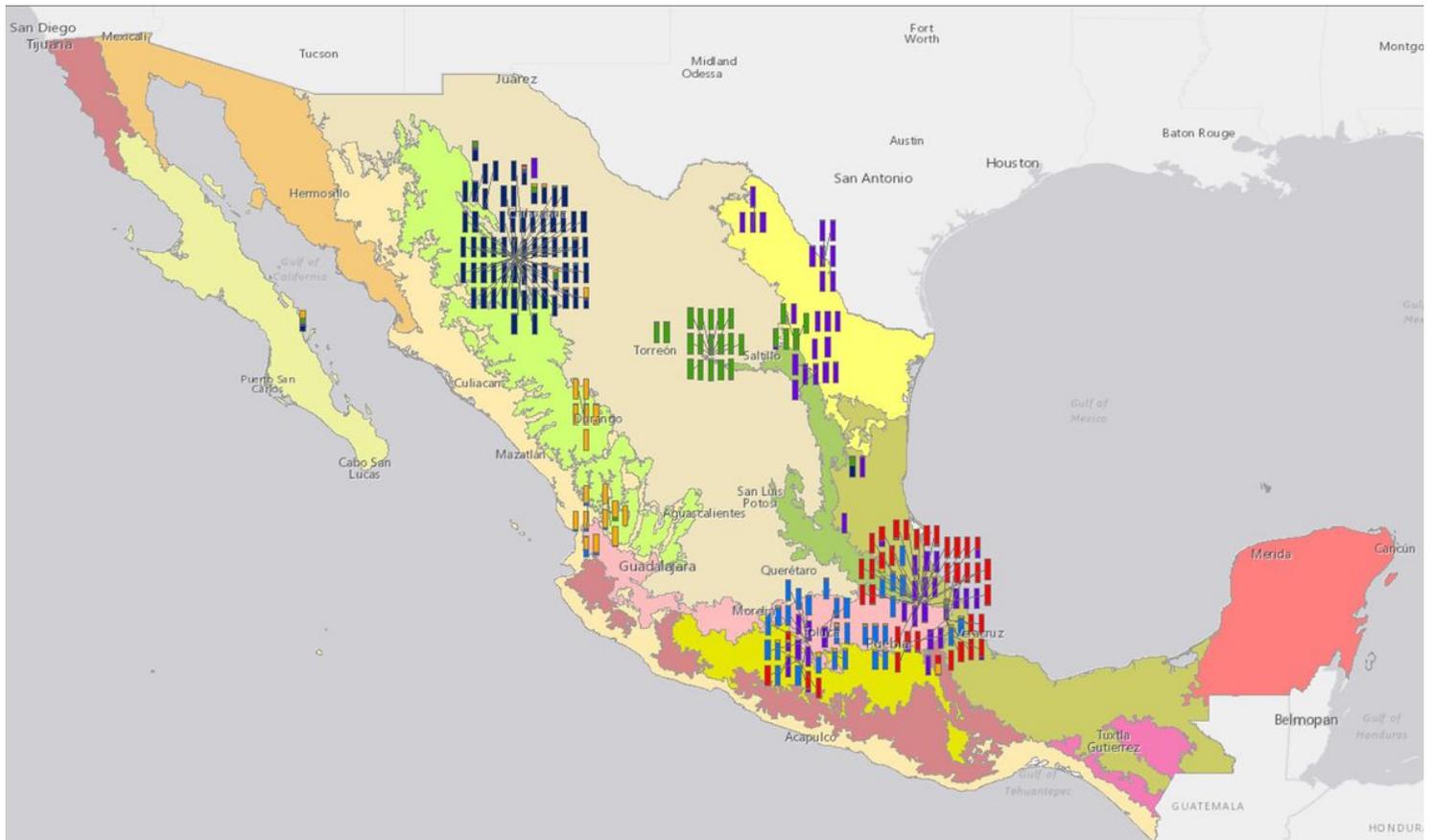


Figure 2

Geographical distribution of accessions used in this study and their STRUCTURE results (K=6). Every colored bar represents one accession and the proportion of Q in each of the six genetic groups. Accessions without reported GPS data were unable to be plotted on the map. Bar colors represent group assignment. Colors in the map represent biogeographical provinces obtained from previous studies. Note: The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.

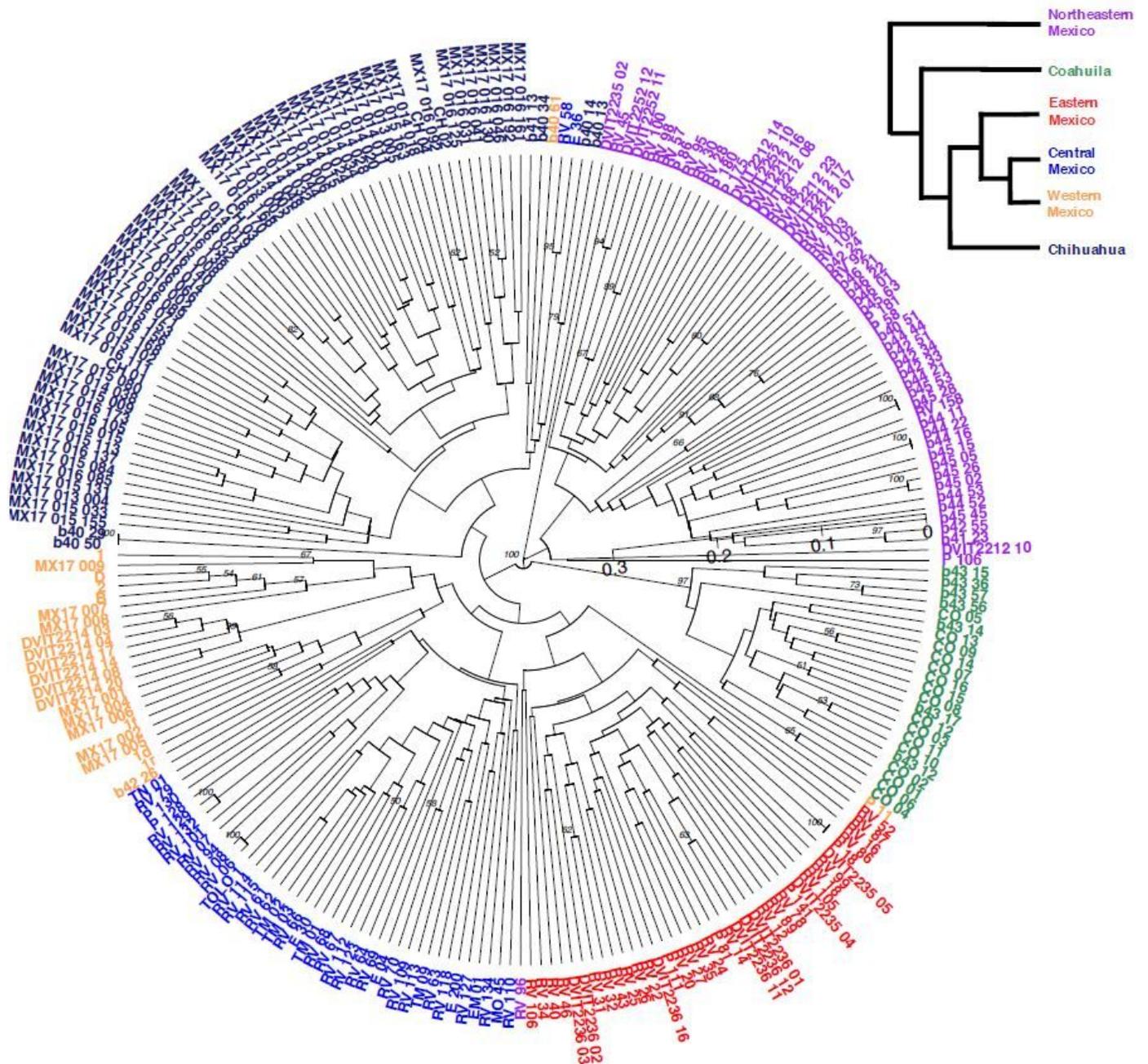


Figure 3

UPGMA rooted dendrogram based on Bruvo's genetic distance from 15 SSR markers. Colors denote the group assignment previously obtained by STRUCTURE. Accessions placed outside of their color block are admix. Bootstrap values are indicated at the node. Red: Eastern Mexico; Purple: Northeastern Mexico; green: Coahuila; navy blue: Chihuahua; gold: Western Mexico. Upper right: simplified dendrogram. Branch length in the dendrogram does not depict any genetic distance.

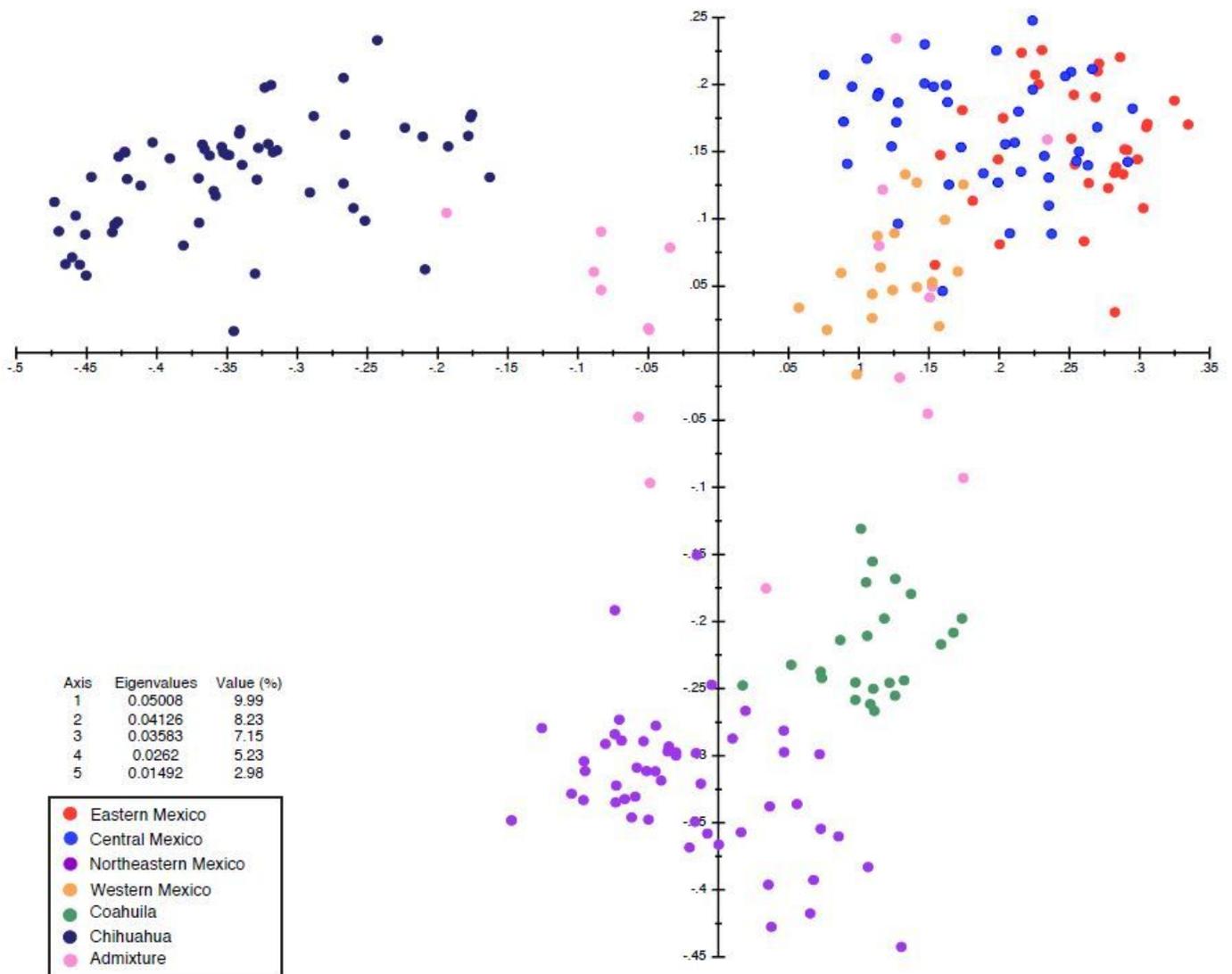


Figure 4

Principal Coordinate Analysis (PCoA) of 247 accessions based on 15 SSR markers using DARWIN software. Accessions were labeled with the corresponding color for the group to which they belong. Eigenvalues for the four axes are shown below. Shown axes 1 and 2 explain 9.99 and 8.23% of the variation, respectively.

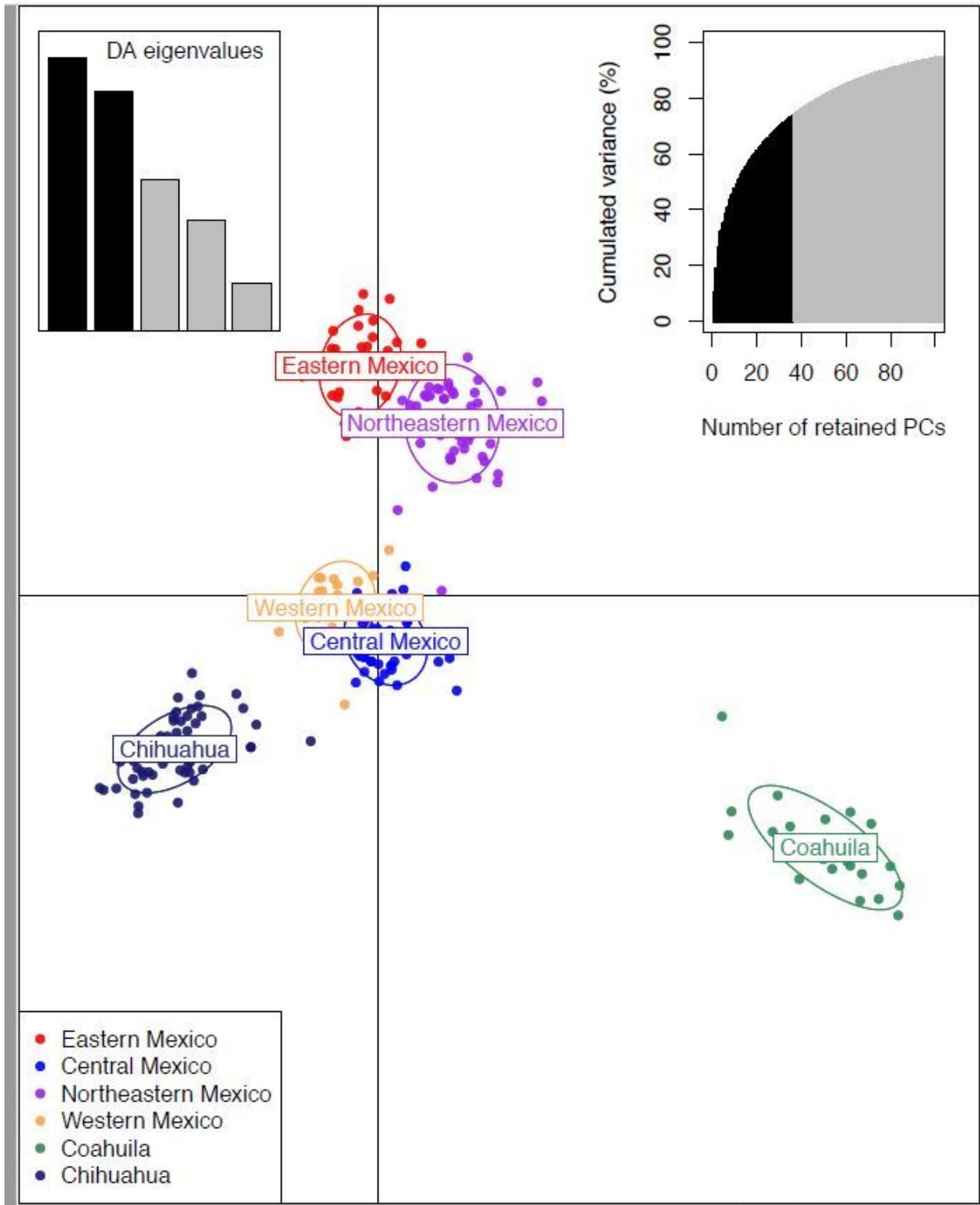


Figure 5

Discriminant Analysis of Principal Components. DAPC maximized the difference between genetic groups and minimized differences within individuals in the same group. A total of 36 Principal Component (PCs) (top right) were retained during the analysis with a cumulated variance of 73.7%. Two out of the five axes retained in the Discriminant Analysis (DA) are highlighted in black (top left) corresponding to the horizontal and vertical axes.

Supplementary Files

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