MARI GENE®
EXPLORING CANNABIS GENETICS

Apple_sauce_#2

|	
SGID	030-0020
Date	Mon Aug 20 14:22:46 MDT 2018
PlateUID	J.28
PipelineMD5	fdde89a8c2512a0d9828235412084fc6

Stability

Greater genetic homozygosity leads to greater phenotypic stability which is the goal when breeding a consistently superior strain. Apple_sauce_#2 tested as 68.69 % homozygous (stable) and would be over 90% stable after 4 generations of sibling crosses.

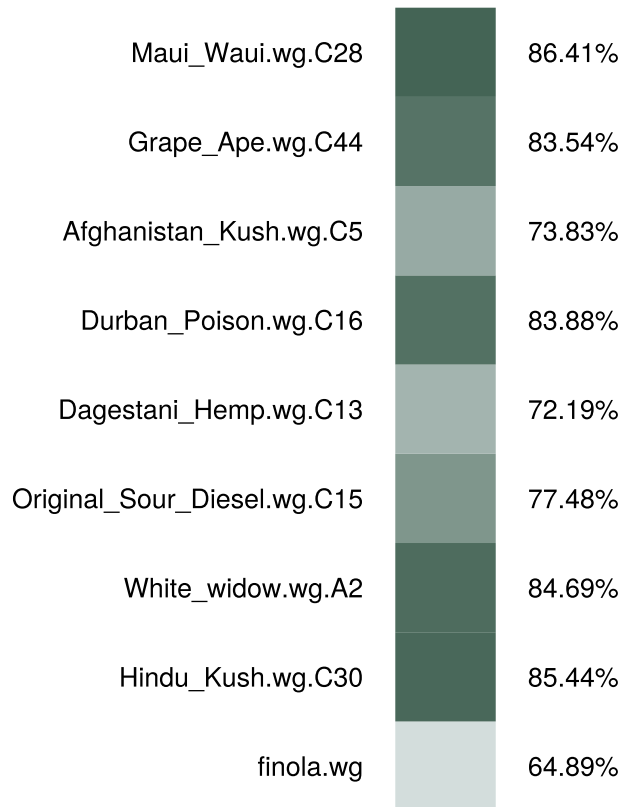% Heterozygous   % Homozygous
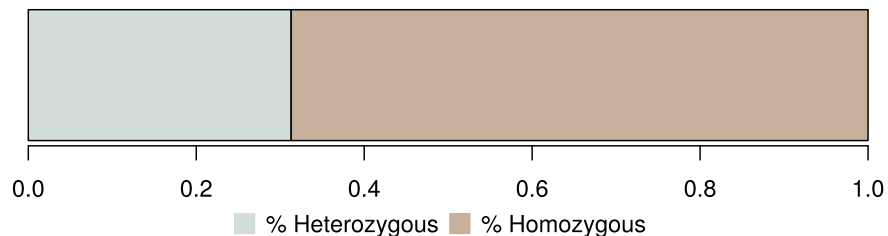
Ancestry

Ancestry is a description of how Apple_sauce_#2 partitions into the four major clades currently identified within *Cannabis*. The pedigree of Apple_sauce_#2 is 17.95 % NLDT1 (similar to the Durban Poisons and Haze), 69.60 % NLDT2 (Hawaiian types fall into this clade), 2.64 % BLDT (Afghan and/or Kush genetics), and 9.81 % Hemp (like Carmagnola and USO-31).


NLDT1   NLDT2   HEMP   BLDT
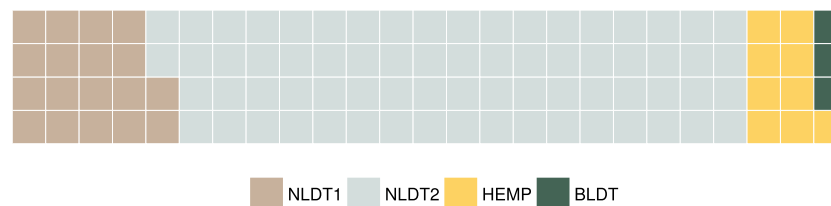
Similarity

The heat map represents how similar at the DNA level Apple_sauce_#2 is in relation to those in our reference database. The most similar strains (darker) are more recently related strains.

| Strain		Similarity
Maui_Waui.wg.C28		86.41%
Grape_Ape.wg.C44		83.54%
Afghanistan_Kush.wg.C5		73.83%
Durban_Poison.wg.C16		83.88%
Dagestani_Hemp.wg.C13		72.19%
Original_Sour_Diesel.wg.C15		77.48%
White_widow.wg.A2		84.69%
Hindu_Kush.wg.C30		85.44%
finola.wg		64.89%

Evolution

The figure shows the closest relatives to Apple_sauce_#2 and it's most likely relation to fifteen popular and well-defined strains. Branch lengths are proportional to evolutionary distance.
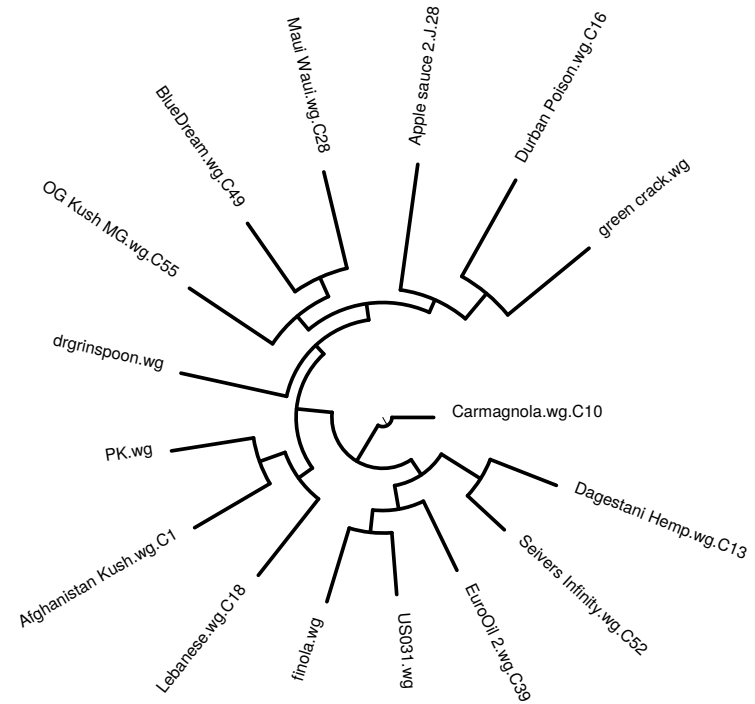
Population Structure

The population structure is similar to the ancestry analysis, but shows Apple_sauce_#2 in the broader context of our reference database. Bars of a single color indicate strains with the smallest degree of admixture.
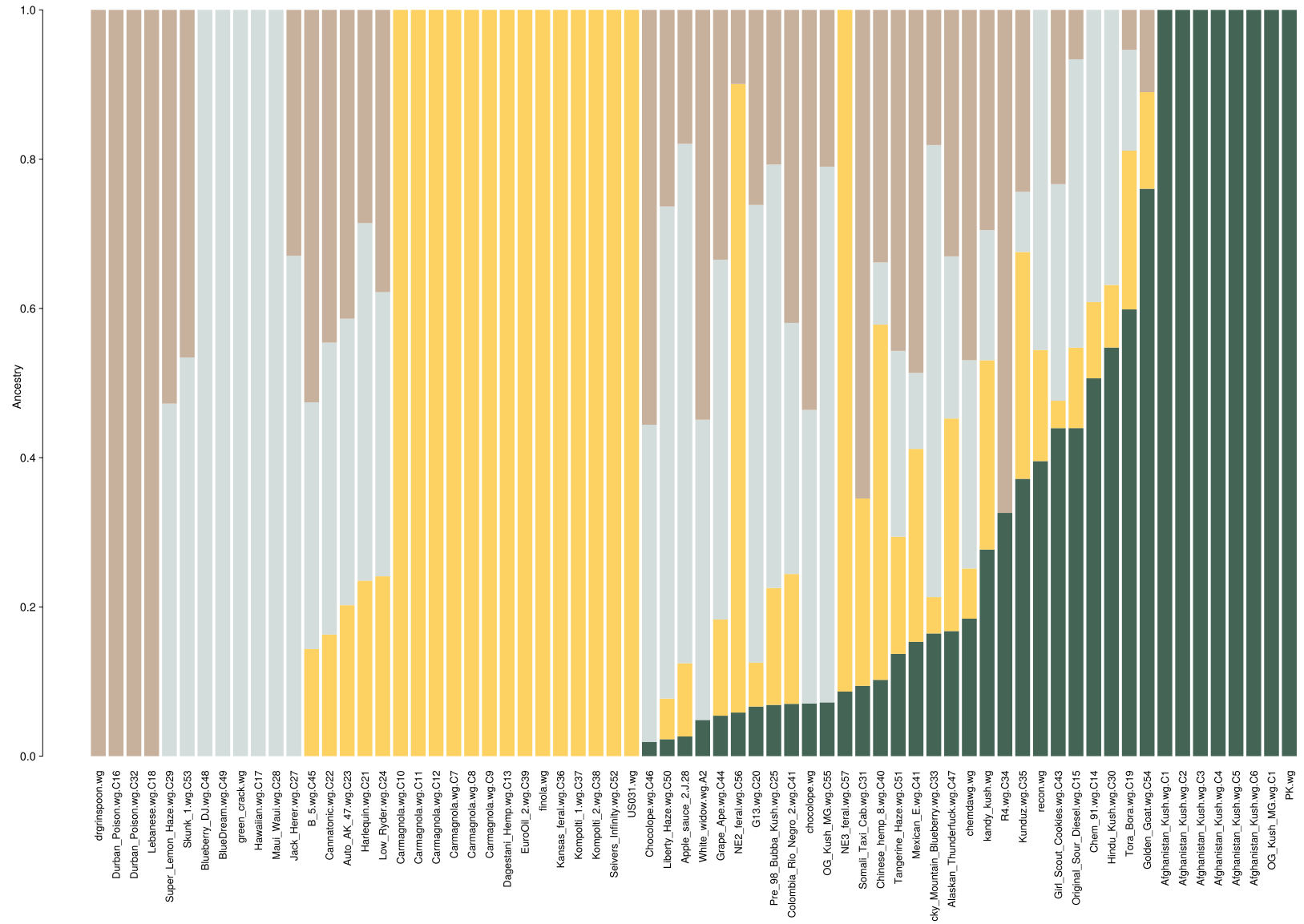
Cannabis is a diverse plant taxa with a complex breeding history. This star chart illustrates hybridization events leading to the modern strains. Evolutionary distance is measured outwards from the inside of the star. Connections between rays indicate the degree of hybridization between lines.
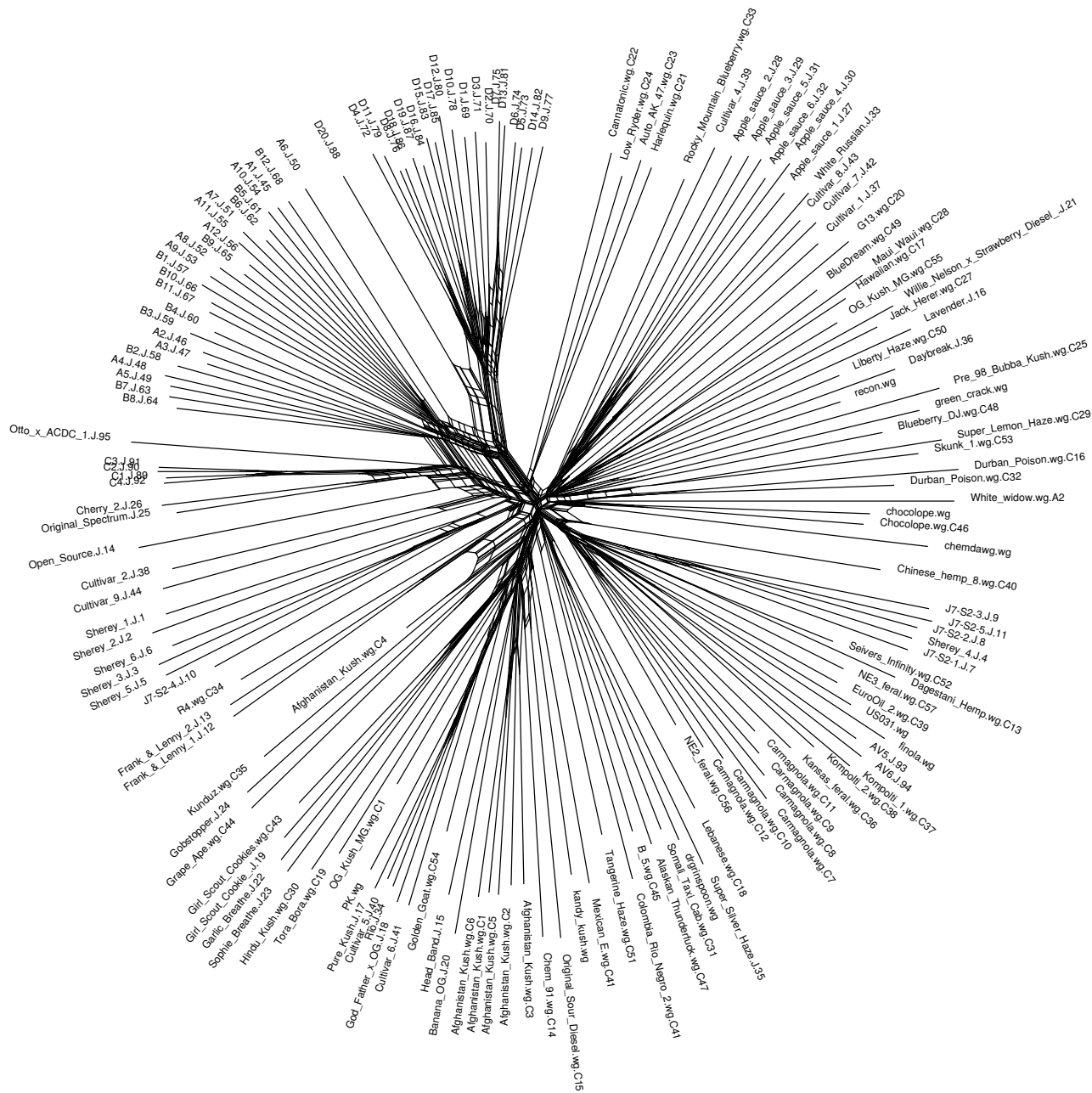
We read thousands of genetic markers from Apple_sauce_#2 and compared them to hundreds of other plants. Next, we reduced this deluge of data down to the most informative principle components (PCs) - dimensions of variation. Three of the most important PCs are represented by one axis in the three below. The plants are partitioned into six groups based on how they cluster in this PC space. Each cluster is assigned a color and the arrows point to plant that is closest to each cluster's center. Apple_sauce_#2 is marked with a cannabis leaf in each figure and its five nearest neighbors are listed in the table at the bottom. Note that each figure displays two PCs. The upper two figures both have PC1 running horizontally and the two rightmost figures have PC3 running vertically. PC2 runs vertically through the top-left figure, horizontally through the bottom-right figure, and is absent from the figure in the corner. The percent of variation explained by each component is listed under its label.


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NEIGHBOR                 : DISTANCE
Applesauce5J31           :    0.284
Cultivar4J39             :    0.464
Applesauce3J29           :    0.471
Applesauce6J32           :    0.483
chocolopewg              :    0.499
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