MARIGENE®
EXPLORING CANNABIS GENETICS

Open_Source

|	
SGID	030-0006
Date	Mon Aug 20 14:22:46 MDT 2018
PlateUID	J.14
PipelineMD5	fdde89a8c2512a0d9828235412084fc6

Stability

Greater genetic homozygosity leads to greater phenotypic stability which is the goal when breeding a consistently superior strain. Open_Source tested as 64.49 % homozygous (stable) and would be over 90% stable after 5 generations of sibling crosses.
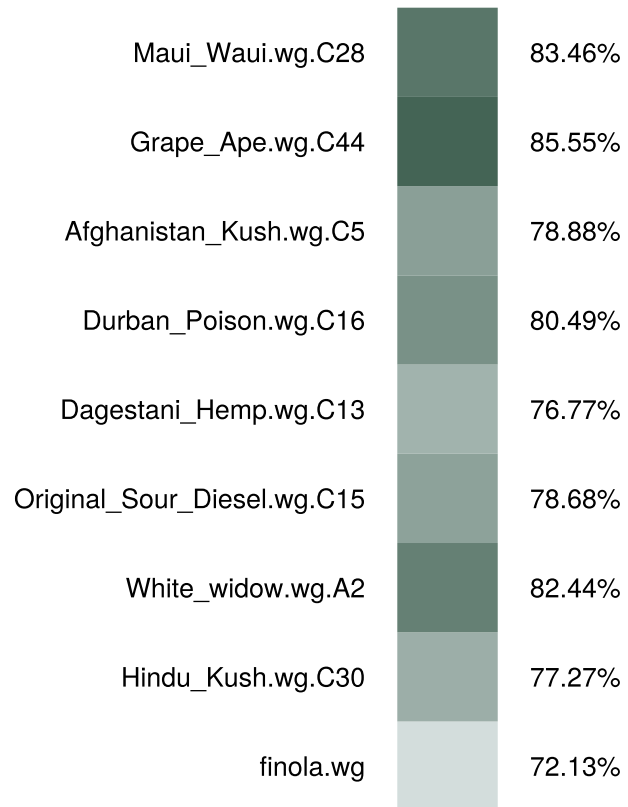

% Heterozygous   % Homozygous

Ancestry

Ancestry is a description of how Open_Source partitions into the four major clades currently identified within *Cannabis*. The pedigree of Open_Source is 25.93 % NLDT1 (similar to the Durban Poisons and Haze), 33.75 % NLDT2 (Hawaiian types fall into this clade), 4.43 % BLDT (Afghan and/or Kush genetics), and 35.89 % Hemp (like Carmagnola and USO-31).


NLDT1   NLDT2   HEMP   BLDT
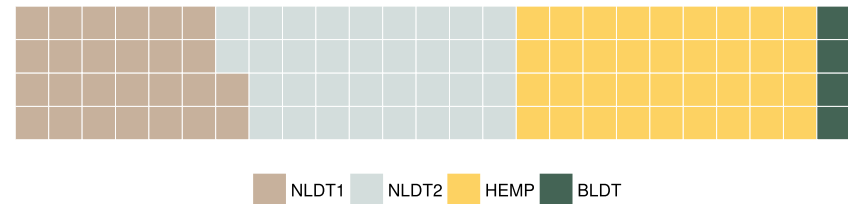
Similarity

The heat map represents how similar at the DNA level Open_Source 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		83.46%
Grape_Ape.wg.C44		85.55%
Afghanistan_Kush.wg.C5		78.88%
Durban_Poison.wg.C16		80.49%
Dagestani_Hemp.wg.C13		76.77%
Original_Sour_Diesel.wg.C15		78.68%
White_widow.wg.A2		82.44%
Hindu_Kush.wg.C30		77.27%
finola.wg		72.13%

Evolution

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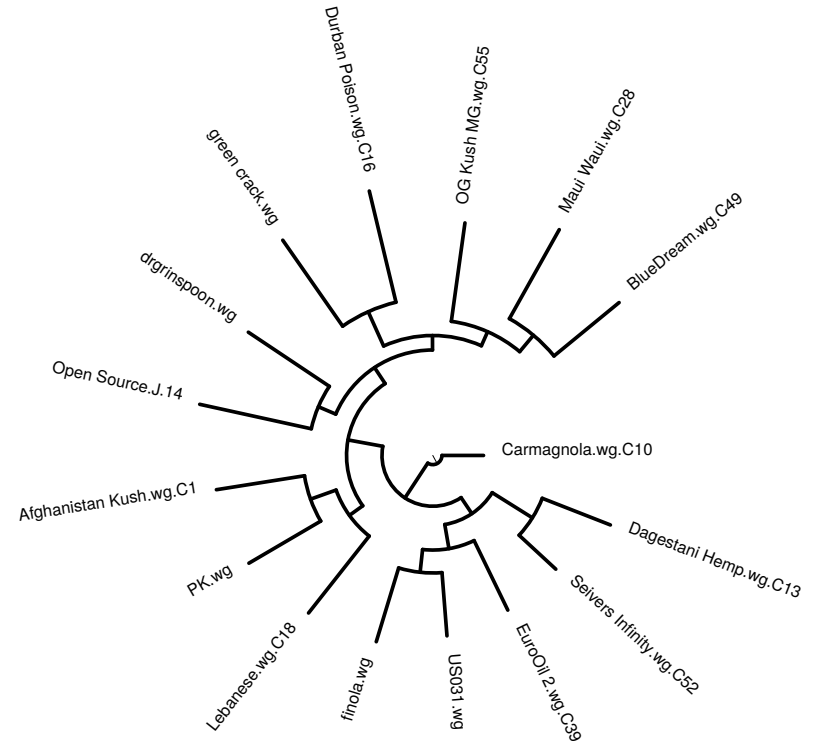
Population Structure

The population structure is similar to the ancestry analysis, but shows Open_Source in the broader context of our reference database. Bars of a single color indicate strains with the smallest degree of admixture.
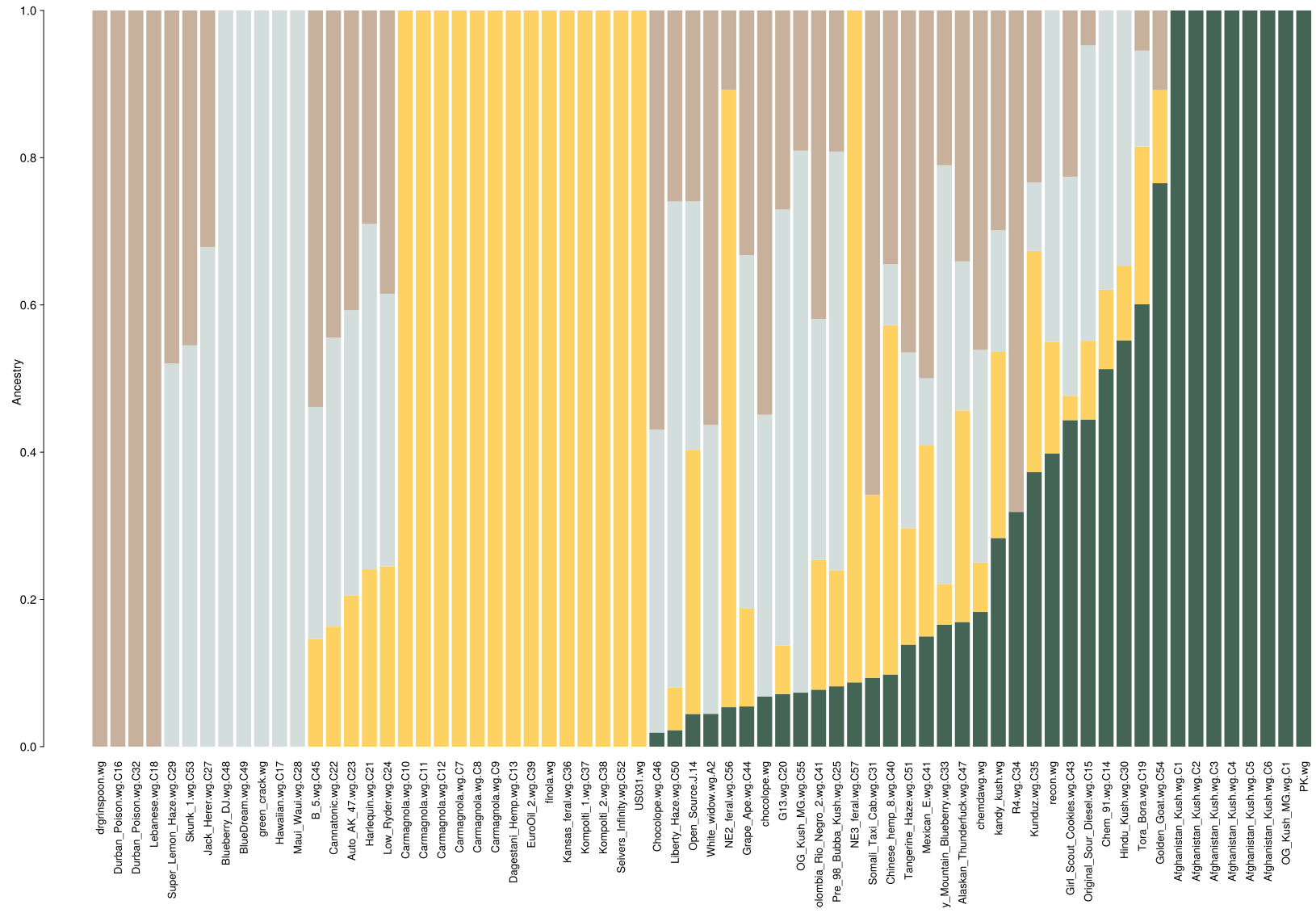
Cannabis is a diverse plant taxa with a complex breeding history. This star chart illustrates hybridization events leading to the modern strains. Evolutionary distance is measured outwards from the inside of the star. Connections between rays indicate the degree of hybridization between lines.
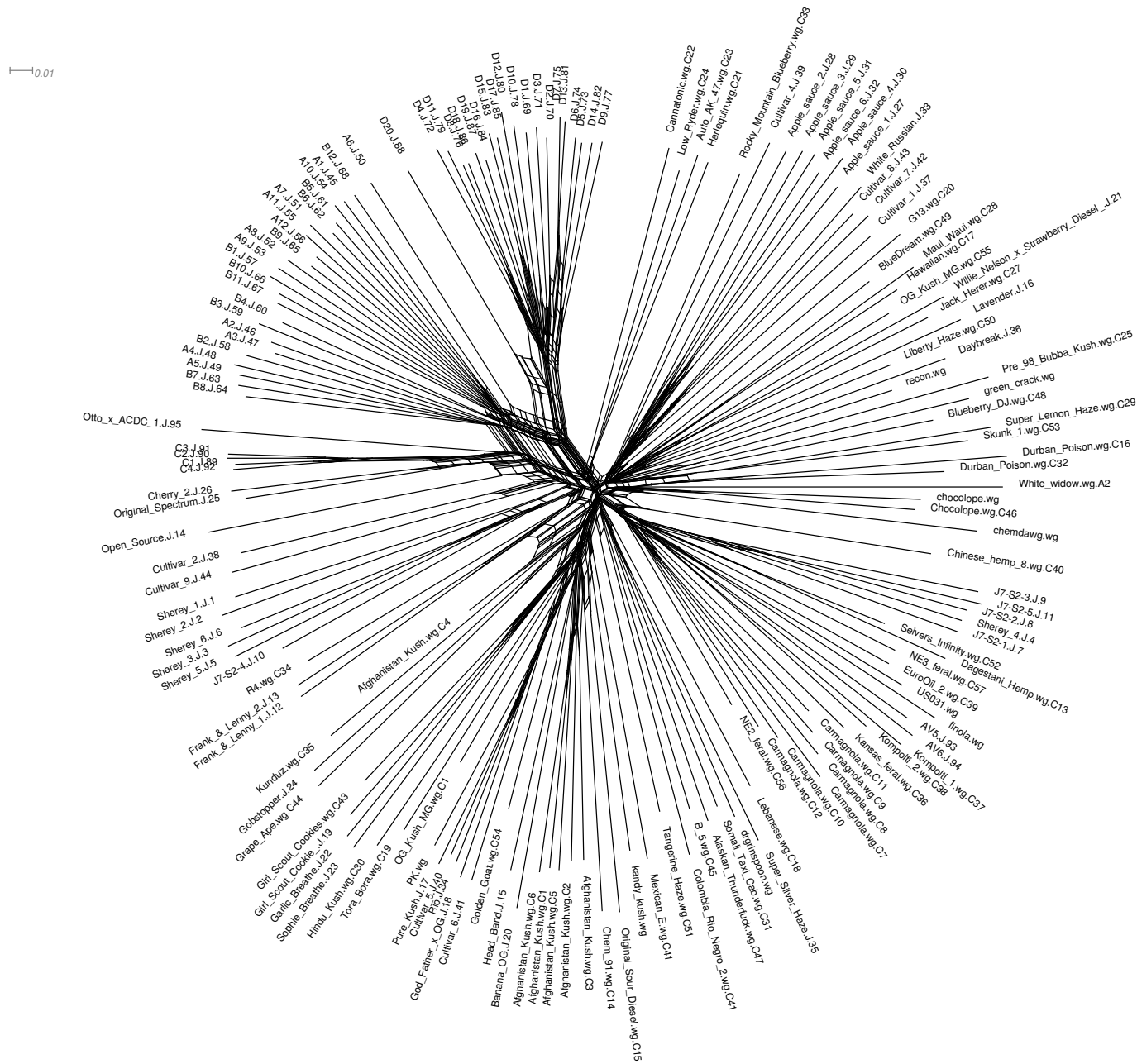
We read thousands of genetic markers from Open_Source and compared them to hundreds of other plants. Next, we reduced this deluge of data down to the most informative principle components (PCs) - dimensions of variation. Three of the most important PCs are represented by one axis in the three below. 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. Open_Source 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.

PC1
7.58%

OpenSourceJ14

CSPI07

US031wg

A10J54

JackHererwgC27

D3J71

AJSDGI27

PC2
3.06%

PC3
2.91%

```
NEIGHBOR                    : DISTANCE
OttoxACDC1J95               :    0.369
OriginalSpectrumJ25         :    0.38
Cherry2J26                  :    0.489
B8J64                       :    0.529
A5J49                       :    0.541
```