Using genetic markers to identify unknown apple trees

Briana L. Gross[1] and Cindy Hale[2]
University of Minnesota Duluth, [1]Department of Biology and [2]Sustainable Agriculture Program and the Natural Resources Research Institute

Goals

The UMD Seedling Trial Orchard and surrounding landscape contain many apple (*Malus* × *domestica*) trees without known cultivar designations. Many of these trees have valuable traits, such as excellent flavor and texture, cold hardiness, and high yield in stressful years. **Our goal is to use a set of known genetic markers to identify these trees**, either by matching them to cultivars in the USDA national collection or by identifying new varieties that are unique to northern Minnesota.

How it works

Recent work on the USDA national apple collection has provided us with genotypes (genetic fingerprints) of 1,910 apple varieties, including **1,131 domesticated apples** (Gross et al., 2012). In order to identify unnamed trees, we will extract DNA from healthy leaves, genotype the trees at nine known molecular markers, and compare the finished genotypes to the existing dataset to look for matches. We will also look for repeated genotypes, even if they are not present in the USDA collection, to see which local cultivars are most popular and best adapted to the area.

Want to participate?

Are you interested in finding out what kind of apple tree is in your orchard or in your backyard? **Please sign up** and we'll contact you for leaf samples. Additional written descriptions the history of the trees and photos of the fruit or tree are also welcome.

Contact Information:
Briana L. Gross – blgross@d.umn.edu
Cindy Hale – cmhale@d.umn.edu

Apple leaves

DNA extraction

DNA

PCR amplification

Genotypes

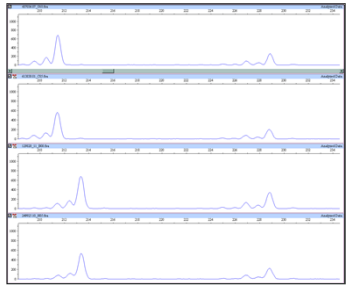

Figure 1. Genotypes at marker CH02d08 for two sets of duplicated *Malus* × *domestica* genotypes. The first two are PI# 437036 and PI# 613830 (cultivars Aromat de Vara and Inducoa No. 11), with alleles of length 212 and 230 base pairs. The second two are PI# 129820 and PI# 249925 (cultivars Cole and King Cole), with alleles of length 214 and 230 base pairs.

Repeat
>1000 times

Dataset with low Probability of Identity

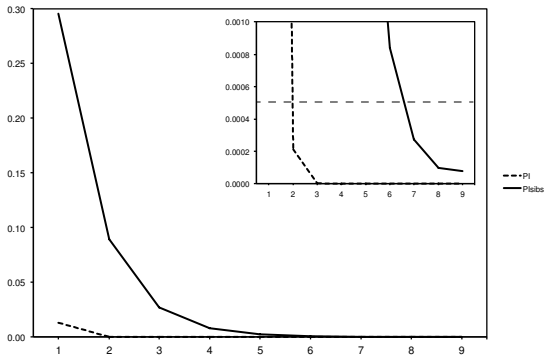

Figure 2. Probabilities of identity (PI) for increasing combination of loci arranged in decreasing order of PI for each locus. Dashed lines show the standard PI, and solid lines show the more conservative PI_{sibs}. Horizontal dashed line in the inset graph shows the reciprocal of the sample size (0.00052), representing the cutoff below which duplicated genotypes are likely to be due to true identity rather than to chance.

Compare all genotypes

Identify duplicates or unknown trees

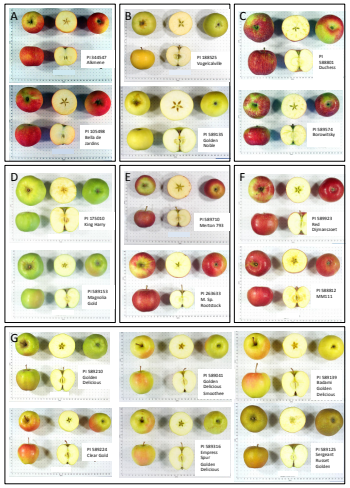

Figure 3. Representative sets of *M.* × *domestica* fruit from the USDA national collection identified as sharing identical genotypes based on nine genetic markers. PI# and cultivar names are provided on the figure for pairs of accessions with matching genotypes and different names (A, B, C, D), cultivars matching rootstock accessions (E,F), and a portion of the Golden Delicious sport family (G). Fruit are arranged on 1 cm^2 grids.

Add new genotypes
back to dataset

Figures taken from: Gross, BL, GM Volk, CM Richards, PL Forsline, G Fazio, CT Chao. 2012. Identification of "Duplicate" accessions within the USDA-ARS National Plant Germplasm system *Malus* collection. *Journal of the American Society for Horticultural Science* 137: 333-342.