UCONN
COLLEGE OF AGRICULTURE, HEALTH AND NATURAL RESOURCES

Aronia Breeding: The next generation of antioxidant-rich pome fruits

Jonathan D. Mahoney[1], Peter V. Apicella[1], Jacob A. Griffith Gardner[1], Liam A. Iorio[1], Huanzhong Wang[1,2], Mark H. Brand[1]
[1]Department of Plant Science and Landscape Architecture, University of Connecticut, Storrs, CT 06269
[2]Institute for Systems Genomics, University of Connecticut, Storrs, CT 06269

Aronlomics

Introduction

- The genus *Aronia* is a group of deciduous shrubs in the Rosaceae family and are native to eastern regions in North America (**Fig. 1**).
- *Aronia* fruits contain high levels of dietary polyphenols and anthocyanins.
- The sugar and polyphenol content of *Aronia* fruit are two of the primary traits perceived by consumers.

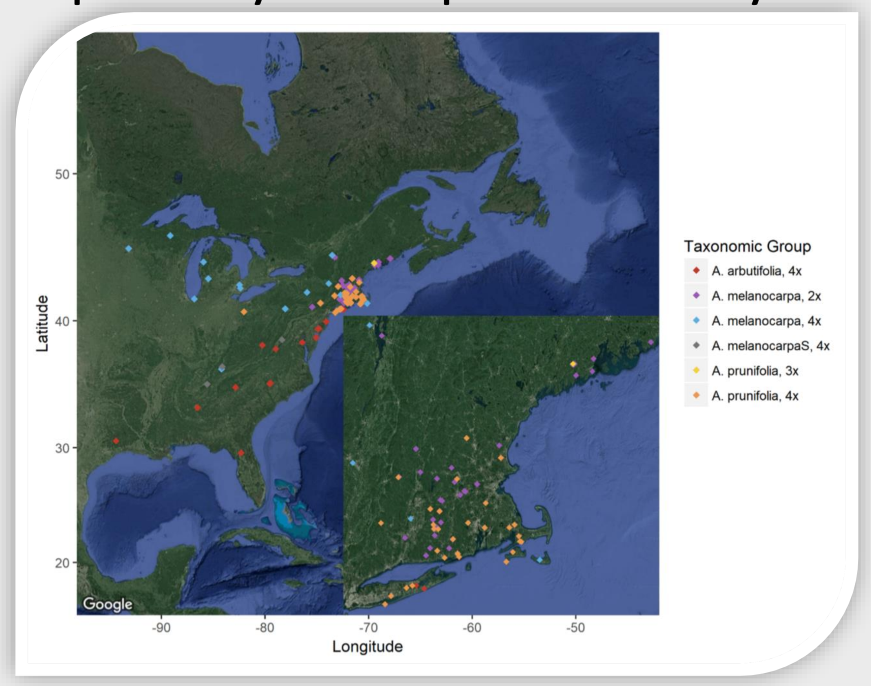

Figure 1. Distribution of wild *Aronia* germplasm.

Objectives

I. **Characterize fruit biochemical profiles of wild and cultivated *Aronia* germplasm.**
II. **Identify candidate genes involved with polyphenol biosynthesis in *Aronia melanocarpa*.**
III. **Breed new *Aronia* germplasm for the commercial fruit industry.**

Materials & Methods

I. 123 *Aronia* accessions maintained at the UConn Research Farm (Storrs, CT) were collected at peak ripe (stage 2) (**Fig. 2**) and analyzed for soluble solids and titratable acidity.

II. 6 *A. melanocarpa* (2x) accessions were collected at four developmental stages (**Fig. 2**) and used for anthocyanin analysis and RNA-sequencing.

III. Controlled pollinations were conducted in a greenhouse and seedlings were regenerated *in vitro*. Progeny were genotyped using genetic markers and ploidy levels were estimated using flow cytometry.

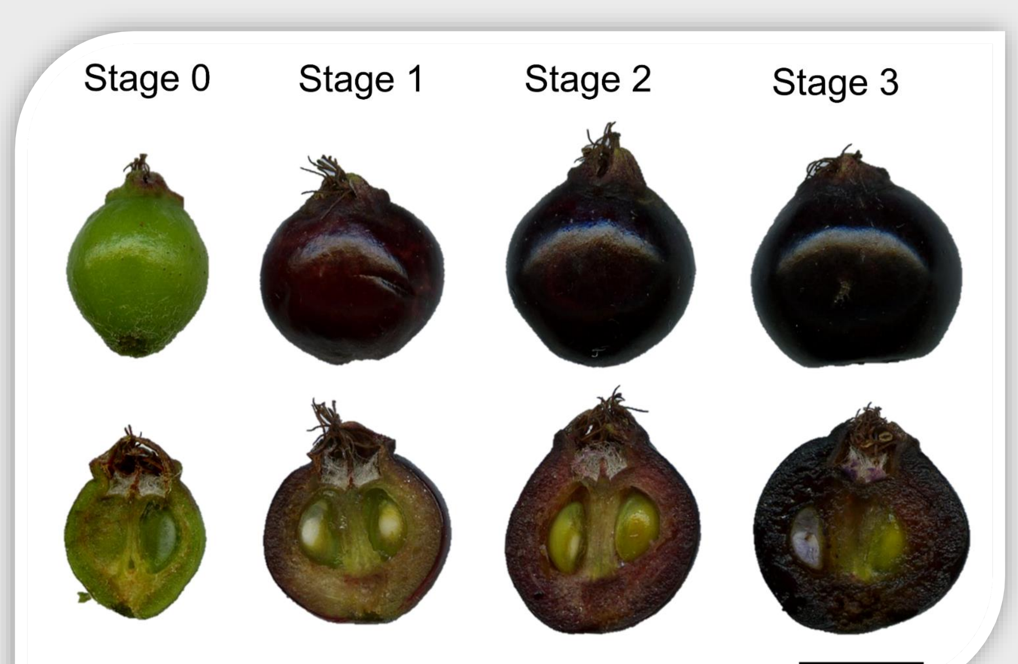

Figure 2. Developmental stages of *A. melanocarpa* fruit. (Bar = 5 mm).

Results

I) Fruit biochemistry

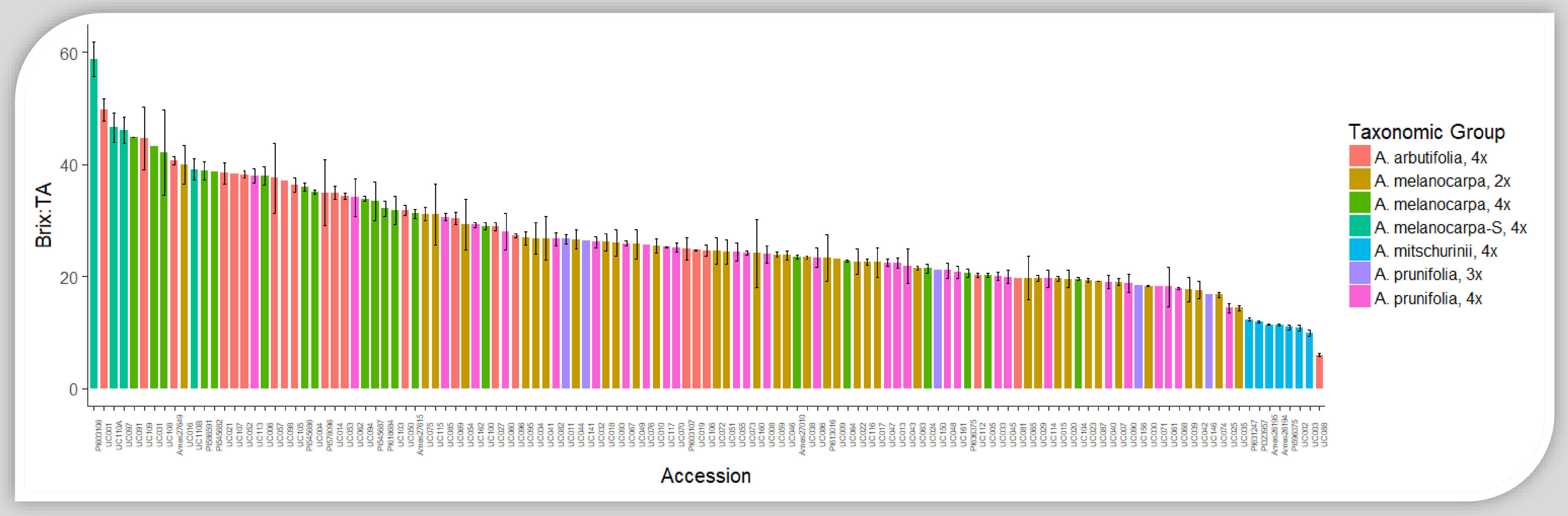

Figure 3. Brix:TA ratios for 123 accessions collected at peak ripe (stage 2). Bars represent standard error.

- The significant variation in brix:TA ratios among wild *Aronia* accessions make this germplasm useful in selecting elite parental material (**Fig. 3**).
- Anthocyanin content of *A. melanocarpa* tended to increase at each developmental stage (**Fig. 4**).
- Cyanidin-3-galactoside is the most abundant form of anthocyanin found in *Aronia*.

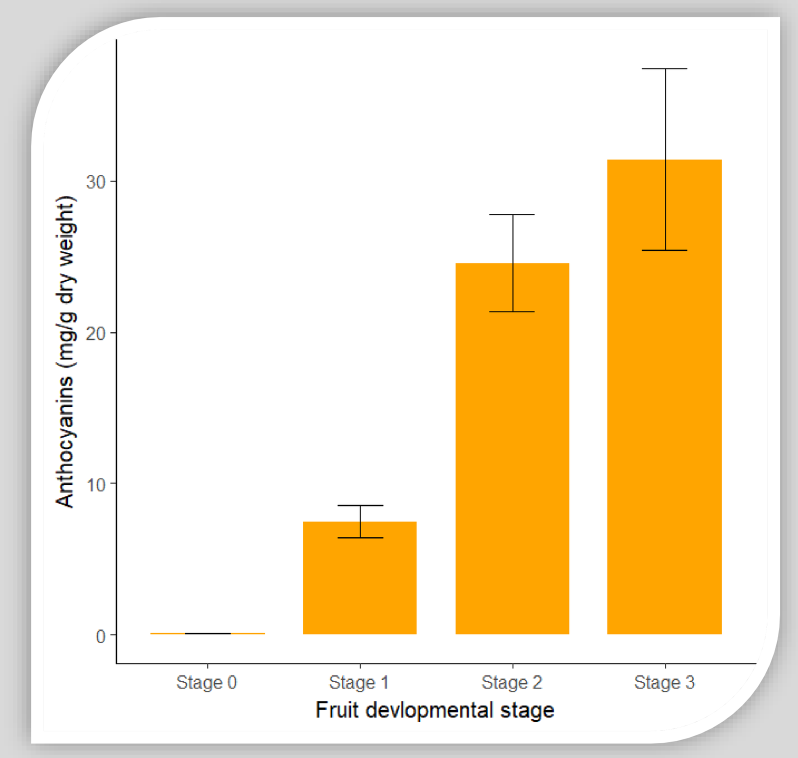

Figure 4. Total anthocyanin content of *A. melanocarpa* at four developmental stages. Bars represent standard error.

II) Functional genomics of polyphenol biosynthesis

- 5363 differentially expressed genes (DEGs) were identified between the four developmental stages.
- Four DEGs were selected as candidate genes in the flavonoid pathway MYB114, CHI, F3H and LAR (**Fig. 5**).

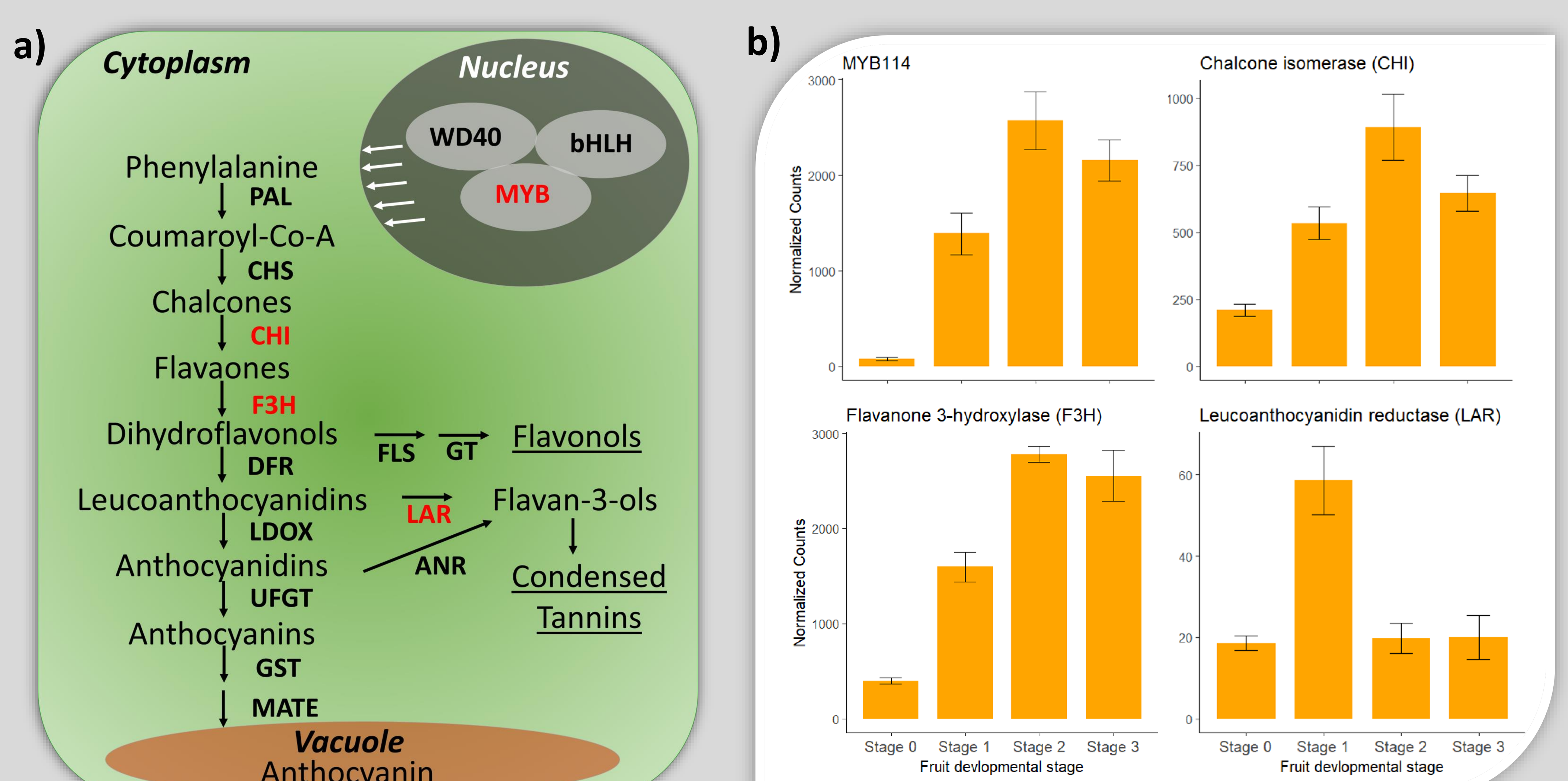

Figure 5. a) Diagram of the flavonoid/anthocyanin pathway. Transcription factor and proteins shown in red are a subset of putative candidate genes. b) Expression levels of putative candidate genes involved with the flavonoid pathway from fruit of *A. melanocarpa* (n=6) at four developmental stages. Bars represent standard error.

III) Genetic enhancement

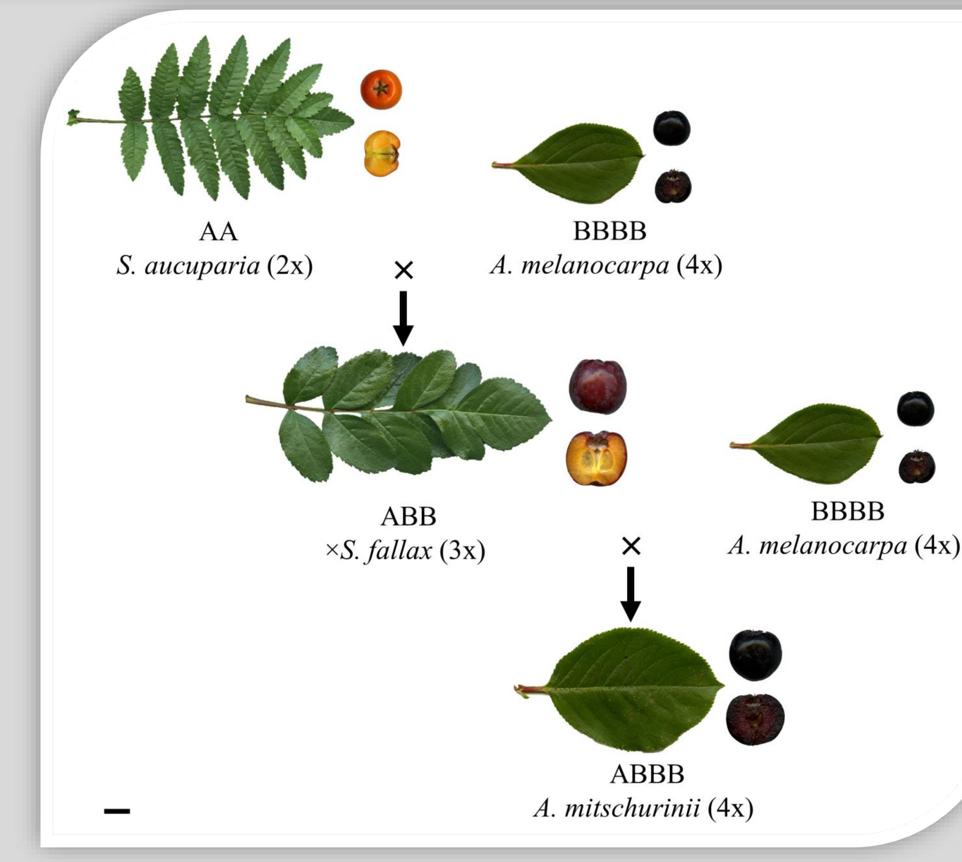

Figure 6. Proposed pedigree framework of allopolyploid *A. mitschurinii* illustrating the ABBB genome was derived from a polypoloidization event between the diploid A and tetraploid B genome. (Bar = 5 mm).

- 136 new *A. mitschurinii* genotypes have been developed by hybridizing novel sources of wild *A. melanocarpa* (4x) genotypes with ×*S. fallax* (3x) (**Fig. 6**).
- All *A. mitschurinii* cultivars, except for PI-652520, are genetically identical (**Fig. 7**).
- New *A. mitschuinii* genotypes (GH15/009-1 and GH15/009-2), bred at UConn, are genetically different from what is currently available for commercial production (**Fig. 7**).

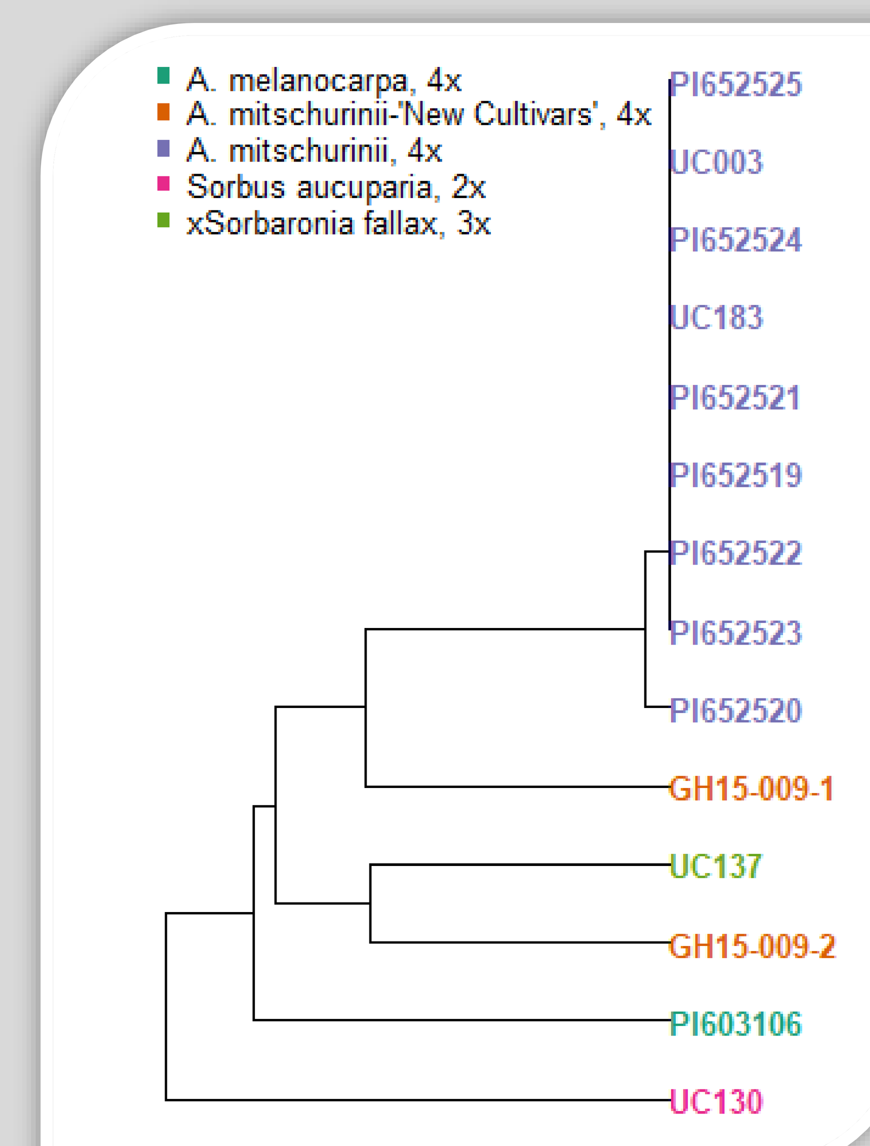

Figure 7. Phenogram created using the unweighted pair group method with arithmetic averages based on Jaccard's coefficient of dissimilarity.

USDA