**Apple Crop Germplasm Committee: Update to the Apple Crop Vulnerability Statement**

**August 18, 2020**

This is an update/addendum to the published 2015 Apple Vulnerability Statement:

Volk, G. M., Chao, C. T., Norelli, J. L., Brown, S., Fazio, G., Peace, C., McFerson, J., Zhong, G.-Y. and Bretting, P. 2015. The vulnerability of U.S. apple (*Malus*) genetic resources. Genetic Resources and Crop Evolution. 62:765-794.

**Collection composition**

The USDA-ARS National Plant Germplasm System apple collection maintained by the Plant Genetic Resources Unit in Geneva, NY is currently comprised of 6,002 unique accessions in the field and 1,934 seed accessions representing *M. domestica*, 35 *Malus* species, and 15 hybrid species. Of the trees in the field, 2,793 are grafted and are represented by a core collection of 258 individuals. A significant change in the collection was the removal of the K1 orchard in 2016, comprised of 1,200 *Malus sieversii* trees grown from seeds collected from the wild in Central Asia. Prior to removal, representative genetic diversity from the K1 orchard was grafted onto rootstocks and added to the grafted collection at the PGRU. At this time (2020), the W3 seedling orchard comprised of 10 wild *Malus* species is still available at the PGRU. Recent collection trips within the United States have resulted in additional seed accessions of *Malus angustifolia, Malus coronaria*, and *Malus ioensis*. In addition, a plant exploration trip to Romania resulted in the addition of *Malus sylvestris* seed accessions and a plant exploration trip to collected *Malus doumeri*, maintained as cryopreserved seeds at the National Laboratory for Genetic Resources Preservation (NLGRP, Fort Collins, CO) and as trees at the USDA-ARS National Plant Germplasm System Corvallis, OR and Parlier, CA locations. The NLGRP has 2052 accessions of dormant budwood from the NPGS Apple collection cryopreserved as secure back-ups (Volk et al. 2017).

**Molecular tools and collection characterization**

Apple breeding and research programs have been significantly impacted by the development of and access to genomic tools for apple genetic resources. Microsatellite genetic fingerprinting datasets for the NPGS Apple collection have been used to identify historic trees on public lands to help document cultural heritage (Routson et al. 2009). Single nucleotide polymorphism (SNP) arrays have facilitated comparisons among apple collections from around the world. They have also been used to determine pedigrees of breeding program materials and genebank accessions, and have been used for marker-assisted breeding (Howard et al. 2017; Muranty et al. 2020).

Genome based sequencing (GBS) genetic analyses are most applicable to domesticated *Malus,* close crop wild relatives and progenitor species. GBS data have been used to assess population structure, pedigree relationships, and ploidy levels in germplasm collections (Larsen et al., 2018). GBS has been used to perform GWAS using accessions in the USDA National Plant Germplasm System apple collection and possible SNPs linked to harvest date and fruit skin color were identified (Migicovsky et al., 2016). In addition, the USDA apple collection was also the source of materials used to identify QTL for blue mold resistance in apple using GBS (Norelli et al., 2017).

Chloroplast sequence data have provided insights with regard to genetic relationships among species, particularly *Malus* species that are distant from *Malus domestica* (Nikiforova et al., 2013; Volk et al., 2015). These species-level genetic relationships help identify gaps in collections for improved collection management and targeted collection expansions. Genomic sequence data obtained from *Malus* accessions revealed domestication relationships between wild *Malus s*pecies and Chinese landraces (Duan et al., 2017). An understanding of the relationships between domesticated apples and related landraces and progenitors may help genebanks and user communities identify novel genetic resources that can be easily integrated into breeding programs.

**U.S. Apple Breeding**

Apple breeding in the U.S. continues to develop superior cultivars and rootstocks. Demand from consumers and growers for high quality, sustainably produced fruit drives innovation for breeders. Advancement of elite germplasm with durable disease resistance is a target of breeding programs (Luo et al. 2020). However, utilization of wild *Malus* for resistance genes tends to negatively impact fruit quality, slowing cultivar development. Development of genetic and genomic resources for apple allows for marker-assisted breeding (MAB) for traits related to fruit quality, tree architecture and development, and disease resistance (Evans and Peace, 2017). Additionally, long breeding cycles may be shortened through genomic selection (Kumar et al. 2012). Both MAB and genomic selection facilitate the introduction of broad genetic diversity in breeding and pre-breeding programs (Kumar et al., 2020).

**A Global Conservation Strategy for the Conservation and Use of Apple Genetic Resources**

In 2019, a global conservation strategy for apple (Malus) genetic resources was released: https://cdn.croptrust.org/wp/wp-content/uploads/2019/11/Apple-Conservation-Strategy.pdf

This document includes information about locations, composition, maintenance, and distribution of international apple collections and is based on information obtained through surveys and in-person meetings. It proposes the development of a global platform in which information about apple genetic resources conservation and use can be shared.

**Documentation**

Public access to genetic and genomic data for apple collections is becoming increasingly important to user communities. The classic version of the Genetic Resources Information Network (GRIN) was updated to GRIN-Global in 2011 (Postman et al., 2010; Genetic Resources Information Network, 2020). GRIN-Global has been adopted by genebanks worldwide as an inventory management and tracking database that provides public information about genebank accessions. The data in GRIN-Global regarding the apple collection continue to be updated, as new information becomes available. Phenotypic data are recorded in GRIN-Global, but they are usually limited to unreplicated data collection events that may have been collected over multiple years, often in the 1990s or early 2000’s. NPGS Apple collection microsatellite data are available (and recently updated) in the GRIN-Global database. Some additional genetic and genomic data for the NPGS Apple collection are publicly available in the Genomic Database for Rosaceae (Jung et al. 2014). Increased public access to organized accession-level genetic data produced using consistent markers or platforms will greatly enhance communication between germplasm collections, which in turn would improve application by end-users.

**References**

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