

Travels To Gather, Improve Apples Start To Bear Fruit

Most of the genetic base presently used for breeding new varieties of apples is known as the “North America gene pool.” It dates back to seedling orchards planted when settlers first arrived here, between the 17th and 19th centuries.

This source is often referred to as the “Johnny Appleseed gene pool.” This alludes to John Chapman, who during America’s infancy spent nearly 50 years planting apple seeds throughout the wilderness of Pennsylvania, Ohio, Indiana, and Illinois.

Many common varieties—including Red Delicious, Golden Delicious, Jonathan, and McIntosh—were discovered as chance seedlings from this pool. And breeders have made great strides already using them to produce new ones that are now in the world marketplace.

But the fact is that this gene pool is very narrow compared to what can be found by tracing further back, through Western Europe, to central Asia. Indeed, the mother lode of apple genes is in central Asia, the apple’s center of origin.

From 1989 to 1996, USDA sponsored expeditions to central Asia to collect seeds and tree samples related to these unique apples. And today, it is becoming clear that these studies—and later ones by ARS, Cornell University, and other institutions—may have an impact on this fruit’s domestic production that will rival that of Chapman’s.

For while Chapman’s iconic work did much to spread apples across North America, recent findings in wild apple germplasm from central Asia—Kazakhstan in particular—may help apple growers breed trees that do a better job of defending themselves against diseases. (See article on page 4.)

I took part in seven of these expeditions. Four of them were to central Asia to collect *Malus sieversii*, the main progenitor of the commercial apple, *M. x domestica*. Our findings greatly enhanced the known gene pool of *Malus*.

We collected this apple species across its entire range in the Tien Shan mountains, in latitudes ranging from 38°N to 48°N. As a result, we now have well-characterized *Malus* genetic resources with traits representing a long period of adaptation to their environment. The potential impact of this can only be described as major.

As curator at ARS’s Plant Genetics Research Unit (PGRU) in Geneva, New York, I oversee one of 34 stations that are part of the National Plant Germplasm System. Geneva is tasked with preserving and safeguarding about 20,000 samples of apples, vegetable crops, cold-hardy grapes, and tart cherries, to ensure they will be around for generations to come.

The seeds gathered on the trips increased PGRU’s apple collection by 1,140 samples, to over 3,900. The visits to Kazakhstan and Kyrgyzstan alone added 949 accessions of *M. sieversii*.

This work has been a boon to ARS programs aimed at improving and making forever accessible the plants we need to support our food supply.

The research has helped these programs by preserving samples in the field and in cryogenic storage here and at ARS’s National Center for Genetic Resources Preservation at Fort Collins, Colorado. It has also allowed for distribution of collected seeds to 24 cooperators in places such as New Zealand, Germany, South Africa, and Norway for grow-out and evaluation.

A big part of this success has come from working with other ARS facilities. Collaboration with the Fort Collins lab, for example, involves intercrossing populations of seedlings in the flowering/fruitlet stage that are from specific sites in Kazakhstan. The result will be increased supplies of seeds. And we recently started a project with ARS’s Appalachian Fruit Research Station in Kearneysville, West Virginia, to identify *M. sieversii*’s resistance to insects.

Soon, the usefulness of *M. sieversii* germplasm in cooperators’ breeding programs will be widely known. The Midwest Apple Improvement Association is already evaluating lines of *M. sieversii* and its hybrids for spring frost avoidance and superior horticultural traits.

There are several reasons that this germplasm should present growers with useful genetic diversity. First, the extensive ecological variation of this species in its native habitats is truly impressive. Since samples were collected from diverse ecosystems, they should offer environmental adaptation as rootstocks or scions for most other apple-producing regions.

Second, *M. sieversii* in its native habitat has co-evolved with several organisms that cause problems in orchards. Apple scab and codling moth were especially noted at collection sites. Multigene scab resistance that has been observed in collaboration with scientists at Cornell, the University of Minnesota, and HortResearch in New Zealand is very important. And *M. sieversii* is showing much promise for use in breeding new rootstocks with resistance to apple replant disease.

Third, some *M. sieversii* genotypes will be immediately useful because they are similar to commercial cultivars in phenotype for many critical horticultural traits. Elite clonal accessions and similar seedlings discovered during evaluation may contribute to new cultivars without extensive backcrossing.

All of this—and forthcoming findings—may one day put the impact of the ARS apple-gathering excursions to central Asia on a par with that of John Chapman’s legendary work. Such a result would represent a dream realized at ARS.

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