

Conservation Priorities for Tree Crop Wild Relatives in the United States¹

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Abstract

Crop wild relatives native to the United States have proved useful as genetic resources in breeding more productive, nutritious, and resilient crops. Their utilization is expected to increase with better information about the species and improving breeding tools. But this utilization may be constrained by their limited representation in genebanks and the ongoing loss of wild populations to habitat modification, invasive species, pollution, over-collecting, and climate change. We report on a series of related initiatives contributing to conservation of crop wild relatives in the United States. An inventory of wild relatives has documented taxa related to a broad range of food, forage and feed, medicinal, ornamental, and industrial crops. Valuable species are threatened in the wild, and few accessions of these taxa are currently conserved *ex situ*. Potential distribution models based on historical occurrence information are clarifying where the species diversity of wild relatives is likely to be concentrated, and a gap analysis methodology is facilitating efforts to identify those taxa and geographic areas of particular conservation concern. A novel collaboration between the U.S. Department of Agriculture (USDA) Forest Service and USDA Agricultural Research Service (ARS) is making progress studying, collecting for genebank conservation, and protecting *in situ* a number of crop wild relative species. We discuss the value of broadening partnerships between agencies and aligning with ongoing regional and international initiatives to conserve, research, and utilize crop wild relative diversity.

Crop Wild Relatives- Useful but Threatened

Crop wild relatives—wild plants closely related to domesticated species—have proved useful as genetic resources in breeding more productive, nutritious, and resilient cultivars. Wild relative species native to the United States are no exception, with important contributions—especially to pest and disease resistance and stress tolerance—for corn (*Zea mays* subsp. *mays*), wine grape (*Vitis vinifera*), sunflower (*Helianthus annuus*), and English walnut (*Juglans regia*), among many others (Khoury et al. 2013).

The use of crop wild relatives is expected to increase with better information about the species (Castañeda-Álvarez et al. 2016, Wiersema et al. 2012) and improving breeding tools (Ford-Lloyd et al. 2011). But their use may be constrained by their limited representation in genebanks and the ongoing loss of wild populations to habitat modification, invasive species, pollution, over-collecting, climate change and other impacts (Castañeda-Álvarez et al. 2016). This is why the most important global agreements on agriculture, development, and conservation, such as the Sustainable Development Goals (Target 2.5) (United Nations Sustainable Development Platform 2016) and the Aichi Biodiversity Targets (Target 13) (Convention on Biological Diversity 2016), have explicitly highlighted the need to fully conserve crop wild relative diversity within the next few years. The United States has been recognized as one of the most important hotspots of crop wild relative diversity worldwide because it is home to many important native species that are inadequately represented in genebanks and are facing considerable threats *in situ* (Castañeda-Álvarez et al. 2016, Volk et al. 2015).

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One major challenge to overcome is that these unique sources of indirect ecosystem services have historically been given relatively low conservation priority in agricultural research, biodiversity, and natural resources management agencies' and organizations' mandates. Crop wild relatives have therefore been slipping between the cracks in conservation systems even while their characterization and use in crop breeding has been increasing. Information sharing and cooperation across different conservation approaches is needed to comprehensively resolve these deficiencies. The good news is that numerous recent initiatives are beginning to address conservation gaps for crop wild relatives through innovative collaborations among research and management organizations.

Crop Wild Relatives of the United States

The relatively short list of important crops originating in the United States includes squash (*Cucurbita pepo*) and sunflower (*Helianthus annuus*), which were domesticated before European contact, as well as blueberry (*Vaccinium* section *Cyanococcus*), cranberry (*Vaccinium* section *Oxycoccus*), blackberry (*Rubus fruticosus*, sensu lato and hybrids), and pecan (*Carya illinoensis*), which were first cultivated more recently. The number of crop wild relatives native to the country would thus at first glance appear likely to be fairly small (Vavilov 1926).

Three additional factors lead to a considerably larger number of potentially valuable wild relatives documented in the region. The relatives of Mesoamerican crops, including species related to corn (*Tripsacum*), bean (*Phaseolus*), chili pepper (*Capsicum*), and cotton (*Gossypium*) are distributed in the southern regions of the United States. A number of crops domesticated in other temperate regions of the world are congeneric with wild species occurring in the country, for example onion (*Allium*), grape (*Vitis*), apple (*Malus*), strawberry (*Fragaria*), hops (*Humulus*), and walnut (*Juglans*). In addition, populations of introduced relatives of important staples such as wheat (*Aegilops*), oat (*Avena*), and sugar beet (*Beta*) have become quite successfully established (Khoury et al. 2013).

Taking a broad perspective both on what species can be considered crop wild relatives and what types of crops may be of interest (e.g., food, forage and feed, medicinal, ornamental, and industrial), a recent inventory of wild relatives occurring in the United States recognized 2500 taxa from 160 genera and 56 plant families (Khoury et al. 2013). Of these, ca. 250 native wild relative species were prioritized as close relatives of important food crops, including tree crop wild relatives of apricot, cherry, peach, and plum (*Prunus*), chestnut (*Castanea*), fig (*Ficus*), guava (*Psidium*), hazelnut (*Corylus*), mate (*Ilex*), pecan (*Carya*), persimmon (*Diospyros*), pistachio (*Pistacia*), sugar maple (*Acer saccharum*), and walnut.

Several well-documented examples of use of native wild relatives in crop breeding exist. North American wild grape germplasm proved critical in providing resistance to phylloxera (*Phylloxera vitifoliae*) as a rootstock in European grape production in the late 1800s, and these stocks continue to provide the basis for protection worldwide. Genes for resistance to rust, downy mildew, powdery mildew, broomrape, sclerotinia head and stalk rot, and sunflower moth have been successfully transferred from wild sunflowers into cultivars (Khoury et al. 2013). The foundation English and European hops cultivar "Brewer's Gold" is a hybrid carrying important introgressions from a North American species (*Humulus lupulus* var. *lupuloides*) (Townsend and Henning 2009). Tree crop wild relatives have primarily been utilized as pest and disease resistant and stress tolerant rootstocks, notably including American filbert (*Corylus americana*), Oregon crab apple (*Malus fusca*), northern California walnut (*Juglans hindsii*), and desert peach (*Prunus andersonii*) (Khoury et al. 2013).

Conservation Gaps

Sixty-two crop wild relative taxa native to the United States are listed endangered under the Endangered Species Act; 10 taxa as threatened; and 11 as candidates for listing. NatureServe, a non-profit organizational source of threat status information, has assessed eight native wild relative taxa as known or presumed extinct in the wild, 115 as globally critically imperiled, 111 as imperiled, and 337 as vulnerable. Threatened species with known or high potential value for crop breeding include northern California

walnut, which is used as a primary rootstock for English walnut and is critically imperiled in its native habitat, and Pecos sunflower (*H. paradoxus*) (fig. 1), a source of salt tolerance, as well as close relatives of squash, cotton, currant (*Ribes*), raspberry (*Rubus*), onion, wild rice (*Zizania* spp.), and plum (table 1) (Khoury et al. 2013).



Figure 1—Pecos sunflower (*Helianthus paradoxus*) at Blue Hole Cienega, Santa Rosa, New Mexico. Pecos sunflower is a source of salt tolerance for cultivated sunflower, and is listed threatened under the Endangered Species Act and globally imperiled in NatureServe (Khoury et al. 2013). (Photo by Laura Marek)

Table 1—Threatened United States wild relatives of major crops

Taxon	Endangered Species Act^a	NatureServe	Number of accessions^b
<i>Allium munzii</i>	LE	G1	4
<i>Allium obtusum</i> var. <i>conspicuum</i>		T2-3	0
<i>Allium scilloides</i>		G2-3	0
<i>Cucurbita okeechobeensis</i>	LE	G1	1 (+ 43 of subspecies)
<i>Fragaria chiloensis</i> (L.) subsp. <i>sandwicensis</i>		T2	2
<i>Gossypium tomentosum</i>		G2	41
<i>Helianthus carnosus</i>		G1-2	6
<i>Helianthus niveus</i> subsp. <i>tephrodes</i>		T2	15
<i>Helianthus nuttallii</i> subsp. <i>parishii</i>		TH	0
<i>Helianthus paradoxus</i>	LT	G2	22
<i>Helianthus smithii</i>		G2	10
<i>Helianthus verticillatus</i>	LE	G1	2
<i>Hordeum arizonicum</i>		G2-4	1
<i>Ipomoea microdactyla</i>		G2	2
<i>Juglans hindsii</i> (Jeps.)		G1	19
<i>Lathyrus grimesii</i>		G2	3
<i>Lathyrus holochlorus</i>		G2	1
<i>Leymus pacificus</i>		G2-3	0
<i>Manihot walkerae</i>	LE	G2	1
<i>Phaseolus texensis</i>		G2	0
<i>Prunus eremophila</i>		G1	0
<i>Prunus geniculata</i>	LE	G3	3
<i>Prunus murrayana</i>		GH	0
<i>Ribes binominatum</i>		G2-3	3
<i>Ribes echinellum</i>	LT	G1	3
<i>Ribes erythrocarpum</i>		G2	18
<i>Rubus aliceae</i>		GH	0
<i>Rubus hawaiiensis</i>		G2-3	14
<i>Rubus macraei</i>		G2	0
<i>Solanum incompletum</i>	LE	G1	0
<i>Solanum nelsonii</i>	PE	G2	0
<i>Solanum sandwicense</i>	LE	G1	0
<i>Solanum wallacei</i>		G2	0
<i>Tripsacum floridanum</i>		G2	1
<i>Vanilla mexicana</i>		G2-4	0
<i>Vicia menziesii</i>	LE	G1	0
<i>Vicia ocalensis</i>		G1	1
<i>Zizania texana</i>	LE	G1	0

Data from Khoury et al. (2013), NatureServe (2016), and USDA NPGS Genetic Resources Information Network (2016).

^a Taxa listed as endangered (LE), threatened (LT), or proposed endangered (PE) under the United States Endangered Species Act, and/or listed as known or presumed extinct in the wild (GH), globally critically imperiled (G1), imperiled (G2), vulnerable (G3), or apparently secure (G4) in NatureServe. T denotes global listing at the infraspecific level.

^b Number of accessions denotes active USDA National Plant Germplasm System accessions.

Species distribution models of the ca. 250 prioritized crop wild relatives based upon historical occurrence records have indicated a surprisingly high concentration of taxa in the northeastern and eastern United States, upper Midwest, and Gulf coast regions (fig. 2). As these are areas of particularly high human population density, further analyses are urgently needed to verify extant populations and to prioritize zones of important crop wild relative genetic diversity for conservation. Preliminary assessments of the state of representation of these species in the U.S. Department of Agriculture (USDA) National Plant Germplasm System and other *ex situ* conservation programs indicate that considerable further collecting is needed to comprehensively represent native crop wild relatives in genebanks. Some 209 taxa related to 36 food crops were assessed through a gap analysis as high priority for further collecting due to very limited or no representation *ex situ*. States with the greatest numbers of under-represented taxa include New York, Virginia, Tennessee, Texas, North Carolina, West Virginia, Pennsylvania, Ohio, Illinois, Georgia, New Jersey, and Indiana, although collecting gaps were identified in all 50 states as well as Washington DC.

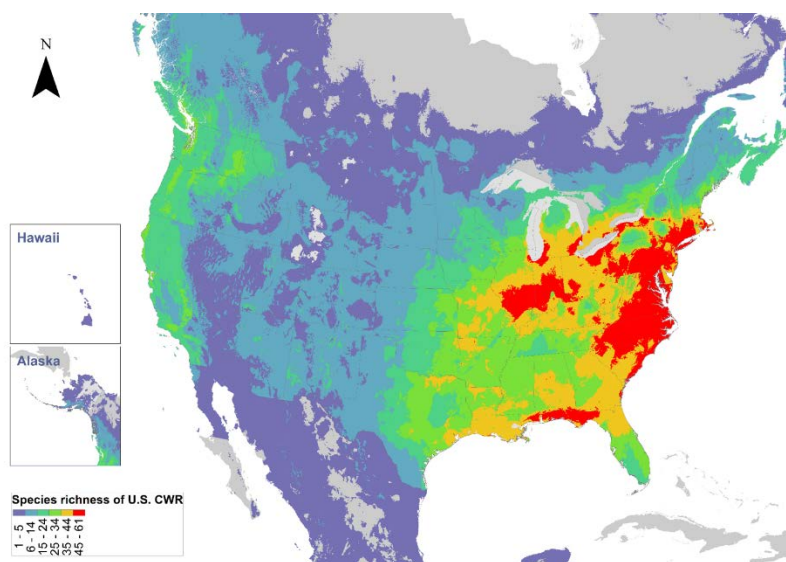


Figure 2—Priority crop wild relative taxon richness map. Areas colored light green, yellow, and red potentially possess the highest concentrations of species.

Progress Through Innovative Collaborations

Current efforts to collect crop wild relatives in the United States include the USDA ARS Plant Exploration Program, and the Bureau of Land Management Seeds of Success Program. A handful of conservation areas explicitly created to manage wild relatives *in situ* have been established, including for wild chilies (*Capsicum annuum* var. *glabriusculum*) in southern Arizona (USDA Forest Service 2016a). But given the considerable threats to wild relative populations in the United States and their relatively low level of representation in genebanks, both the urgent collection for *ex situ* conservation and the active management of taxa in conservation areas need to be enhanced considerably. Only a major increase in conservation action will enable the country to reach the global targets prioritized for completion by 2020.

In order to achieve these goals for the diversity of prioritized taxa, broad partnerships and networks between the federal, state, tribal and non-governmental organizations pursuing conservation activities are needed. An innovative example of such collaborations is current work on the conservation of wild cranberry by the USDA Forest Service (FS) and the ARS. Under the Strategic Framework on the Conservation and Use of Native Crop Wild Relatives in the United States established by the agencies (USDA Forest Service and USDA Agricultural Research Service 2014), populations of the two close

relatives of the crop are being collected for *ex situ* conservation in the National Plant Germplasm System, and assessed for unique genetic diversity in order to guide *in situ* conservation priorities (USDA Forest Service 2016b).

Such collaborations need to be extended to achieve comprehensive conservation. Moreover, because many of the taxa are distributed across national borders and the genetic resources of such species are potentially valuable globally, these efforts should be aligned with neighboring national strategies and with regional and global initiatives to conserve and provide access to crop wild relative diversity.

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