

Wild Relatives as A Source of Resistance to Biotic and Abiotic Factors

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Introduction

Wild relatives are cousins of cultivated crops. Crop wild relatives (CWR), which include the progenitors and wild/weedy relatives (primary gene pool) and distinctly related taxa, having potential for crop improvement (secondary and tertiary gene pools). These are important but scarcely exploited component of the gene pool, have been undeniably beneficial to modern agriculture, providing plant breeders with broad pool of potentially useful genetic resources. Have novel factors for wider adaptability, tolerance/ resistance to disease, pests, yield, quality attributes, sources of male sterility and abiotic traits. CWR contain a wealth of genetically important traits due to their adaptation to a diverse range habitats and the fact that they have not passed through the genetic bottlenecks of domestication.

Biotic stress resistance

Over 80% of the beneficial traits conferred by CWR genes in this survey involved pest and disease resistance. Breeders have exploited wild relatives for resistance to diseases for over a century, and they continue to search extended gene pools for genes that convey resistance to major crop pests and diseases. Of the 13 crops with incorporated wild genes in released cultivars, all except barley and chickpea have cultivars with disease resistances derived from wild relative genes. However, only maize, banana and groundnut have disease resistance as the only beneficial trait derived from the wild.

- Prior to the mid-1980s, stories about wild genes preventing devastation by pests and diseases were dominated by a handful of crop success stories. Most prominent among these were: *Oryza nivara* providing resistance to grassy stunt virus in rice; *Solanum demissum* providing resistance to potato late blight; the many tomato disease



resistances introgressed from wild species, mostly from *Lycopersicon pimpinellifolium* and stem and leaf rust resistance from *Agropyron elongatum* and *Aegilops umbellulata* respectively, in wheat.

- Since then, the discovery and use of new resistance genes from the wild have steadily increased in these crops and others. Resistances found in tomato wild relatives have been reported at a rate of about one per year since 1982, with virtually all disease resistance genes currently in commercial cultivars having been bred from wild genetic resources. Over 40 resistance genes have been derived from *Lycopersicon peruvianum*, *L. cheesmanii*, *L. pennellii*, and several other wild relatives.
- In rice, *Oryza nivara* genes still provide strong and extensive resistance to grassy stunt virus on millions of hectares of rice fields in south and south-east Asia, and resistance to at least six other major diseases in rice have been obtained from different wild species. In potatoes, besides several new resistances from other wild relatives, resistance to potato late blight obtained from *Solanum demissum* and *S. stoloniferum* continues to be effective in some areas, and currently 40% of the total area of the most popular potato cultivars in the United States have *S. demissum* in their ancestry, a considerable increase from 11% of the total area in 1986. Along with these wild relatives, *S. chacoense*, *S. acaule*, *S. vernei* and *S. spegazzinii* have provided resistance to several viruses and pests.
- Breeders continue to isolate and introgress genes from wheat wild relatives for resistance to leaf and stem rust, yellow dwarf virus, root lesion nematode, powdery mildew and wheat streak mosaic virus. Spring wheat germplasm lines derived from *Aegilops tauschii* for resistance to Hessian fly, a major insect pest causing multimillion dollar crop losses in the US, have recently become available to breeders.
- Disease resistances in wild sunflowers have been exploited for decades, with multiple sources of genetic resistance to all the known races of downy mildew, as well as rust, verticillium wilt, and broomrape, continually being transferred from wild *Helianthus annuus* L. and *H. praecox* into new sunflower hybrids. Resistance to new strains of downy mildew continue to be found in the wild relative, with several of these resistant cultivars having been released in 2005 alone. The most recent trait from wild *H. annuus* L. is herbicide resistance to imidazolinone and sulfonylurea chemicals used to control



broomrape. These resistance genes have been transferred into cultivated hybrids under the trade name 'Clearfield', and are expected to be worth millions of dollars globally.

- In millets, rust and *Pyricularia grisea* resistances were introgressed from wild relatives. Although the rust resistance was overcome quickly, *Pyricularia* resistance is still effective. Striga resistance has been identified in millet's primary gene pool, but the work remains at the early stages of gene transfer. In sorghum, recent success in hybridization between *Sorghum macrospermum* and *S. bicolor* promises to help in introducing several pest and disease resistance traits to cultivars.
- In bananas, 'Calcutta 4' (*Musa acuminata*), a wild, non-edible diploid banana has been used as a source of resistance in banana hybrids to black Sigatoka, the most serious constraint to banana production globally caused by the fungus *Mycosphaerella fijiensis*. The new generations of these hybrids, distributed since the 1990s, are resistant to black Sigatoka and *Fusarium* wilt. However, resistance to black Sigatoka has been overcome in the Pacific, and breeders have once again turned to wild *M. acuminata* for more resistance genes.
- The vast majority of modern lettuce cultivars have benefited from wild relatives. All lettuce downy mildew, *Bremia lactucae*, and lettuce aphid, *Nasonovia spp.*, resistance is derived from the wild. For downy mildew, cultivars with resistance derived from wild germplasm have been released regularly since the 1980s. Fungicides have limited effectiveness against the pathogen, thus without the introduced genes it would not be possible to grow lettuce in many parts of Europe. However, resistance genes appear to be overcome rapidly, and breeders are constantly returning to wild germplasm for new resistance genes.
- The use of wild genes in groundnut and maize has not been as successful so far. Groundnut cultivars with root knot nematode resistance derived from *Arachis cardenasii* were released, but were never grown on a significant area because of a lack of resistance to tomato spotted wilt. Introgression of genes from *Tripsacum L.* into maize cultivars has not had any successes since cultivars released between the 1950s and 1980s with resistance to *Helminthosporium* and *Puccinia*. However, both these crops have cultivars in the pipeline, with wild-derived disease resistant groundnut germplasm available to breeders, and rootworm resistant, drought and aluminum-



tolerant, nutritionally-enhanced maize cultivars with *Tripsacum* gene introgression currently being field tested.

- ☐ Soybean cyst nematode resistance has been successfully transferred from wild perennial soybean, *Glycine tomentella*, but cultivars are still in an experimental stage.
- ☐ Unsuccessful attempts have been made to transfer resistance to Maruca pod borer to cultivated cowpea from crosses with *Vigna vexillata*.
- ☐ Chickpea lines derived from *Cicer reticulatum* are being developed for resistance to root lesion nematodes and *Phytophthora* root rot, but these are still undergoing backcrossing programs to recover the domesticated phenotype.
- ☐ Phaseolus wild relatives are currently being screened for resistances to web blight, rust, white mold, bean golden yellow mosaic, bruchids, and seed storage insects.

Abiotic stress tolerance

Only a handful of examples of wild relatives contributing genetic resistance to abiotic stresses in crops have reached the stage of cultivar release although many wild relatives with potential have been described (e.g., Shannon 1997). Important recent advances in this field include the release of a chickpea cultivar with introgressed wild genes in 2004.

- ☐ Developed by the India Agricultural Research Institute, 'BG1103' drought and temperature tolerance are derived from *Cicer reticulatum*, and is already a leading cultivar in Northern India. Also in 2004, six barley cultivars with drought tolerance derived from *Hordeum spontaneum* were released for use in Syria by the International Center for Agricultural Research in Dry Areas.
- ☐ *Oryza rufipogon* genes have been exploited for tolerance of soils with high acidic-sulfate content in Vietnam, and *O. longistaminata* genes for drought tolerance in cultivars in the Philippines, allowing the spread of rice production to previously unusable lands.
- ☐ In tomatoes, *L. chilense* and *L. pennellii* genes have been used to increase drought and salinity tolerance.
- ☐ Sunflower and bean cultivars with genes from CWR will soon be released. Salt tolerant sunflower hybrids, which promise to yield 25% more in salt-impacted soils, are still under development although maintainer lines have already been released. Bean



cultivars with tolerance to low temperatures and salinity derived from wild *Phaseolus* are in the pipeline.