



## Utilization of Crop Wild Relatives in the Breeding Programmes: Progress, Impact and Challenges

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The Crops Wild Relatives (CWR) includes wild forms, progenitors and those species that are closely related to cultivated crops. The concept of CWR is relative in the sense that all the related species may not have equal potential as gene donors to crops (Maxted *et al.*, 2006); their relative status is very often inferred rather than based on direct evidence (Heywood *et al.*, 2007). The gene pool system devised for understanding genetic relationship between crops and related species by Harlan and de Wet (1971) facilitated beneficial gene and traits transfer from wild to cultivated. Historically, the conservation of plant genetic resources (PGR) has focused almost explicitly on cultivated plants (Maxted *et al.*, 2008), however, in the recent past the importance of CWR have been recognized globally for breeding high yielding varieties to feed increasing population and to tolerate variety of stresses arising due to climate change. Thus, future crops species will need to be able to thrive in a drier, warmer, and more variable climate and in an environment increasingly populated by new pathogenic organisms. To meet these challenges we need broader crop gene pools and CWR has greater role to play in it.

### Crop Wild Relatives in India

India is one of the 12-mega diversity centres, accommodates part of four hot-spots—the Himalaya, Western Ghats, Indo-Burma and Sundaland out of 35 identified the world over and is immensely rich in agricultural biodiversity. Indian gene centre is rich in domesticated crops diversity having 168 species out of 2489 species distributed in 12 regions of diversity of cultivated plants (Zeven and de Wet 1982). Among CWR, 326 documented species have originated and/or developed diversity in different phyto-geographical regions of India (Pandey and Arora, 2004). However, Pradheep *et al.*, 2014 have made a pragmatic exercise to further shortlist and update the CWR of 168 native

crops, which resulted into 817 taxa belonging to 730 species, including wild/weedy form(s) or populations of 142 crop species, occurring in India (Table 1).

### Importance of CWR

The increasing genetic uniformity of crop varieties combined with climate change effects makes crops more vulnerable to various biotic and abiotic stresses. There had been examples of large scale devastations of crops due to genetic uniformity, for instance potato famine of the 1840s due to late potato blight epidemic across Ireland, Europe and North America; 1970s southern corn blight outbreak in the US maize and rice losses due to blast in the Philippines, Indonesia and India leading to the great Bengal famine. Intensive modern breeding efforts have contributed to a narrowing of the gene pool by concentrating more on favorable alleles already present in early domesticates (Debouck, 1991). CWR are therefore important for maintaining genetic diversity for and preventing such losses, which may have serious consequences for food, nutrition and environmental security. Advancement in the molecular biology in the study and utilization of species as gene source has made CWR a priority in PGR management and crop improvement. At the same time, post-CBD concerns of habitat loss, genetic erosion, policy issues related to access and benefit sharing and sovereign rights have also come in the forefront.

### Utilization in India Breeding Programmes

Despite having valuable genes with immense value for crops improvement and adaptation to changing environmental conditions, utilization of CWR has enjoyed a great success only in few crops, while disappointing for numerous others. Many genes are still lies untapped in these genetic resources, presumably due to the lack of useful genetic information and genetic bottlenecks as well. Scientists, the world over have argued that breeders were not fully exploiting the potential of

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**Table 1. Summary of crop-group-wise native CWR occurring in India**

Crop-group (crops**)	No. of CWR species*	Taxa	Crop-group (crops**)	No. of CWR species*	Taxa
Cereals and millets (13)	72 (2)	83	Vegetables (25)	76 (11)	87
Pseudocereals (3)	13 (1)	13	Spices and condiments (12)	50 (7)	54
Grain legumes (10)	49 (4)	57	Ornamentals (13)	141 (61)	152
Oilseeds (4)	9 (1)	10	Medicinal & aromatic plants (20)	70 (19)	81
Fibres (5)	18 (3)	20	Plantation crops (3)	12	14
Forages (16)	58 (14)	63	Others (8)	35 (7)	39
Fruits and nuts (36)	127 (12)	144	Crops: 168	730 (142)	817

\*Figures in parenthesis is crop species with wild/weedy form(s) or populations occurring in India, which are also included for counting as CWR;

\*\*One crop may involve more than one species

CWR; historically they relied on searching genes for beneficial traits associated with certain CWR rather than searching more generally for beneficial genes. Hajjar and Hodgkin (2007) while reviewing the utilization of CWR in 20 years found that over 60 wild species were used in 13 major crops and >100 beneficial traits derived from them.

Although, utilization of CWR in crop improvement is limited still many wild species have used successfully. Some of the examples include; use of *Oryza nivara* genes provided long-lasting resistance to grassy stunt virus (Brar and Kush, 1997) and use of *O. spontanea* as the source of wild abortive cytoplasmic male sterility, which has provided the cornerstone for today's hybrid rice (Li and Zhu 1988). Many unique traits such as weed competitiveness, drought tolerance and the ability to grow under low input conditions has been transferred from *O. glaberrima* to *O. sativa* and combined with high yield to develop NERICA (NEw RICE for AFriCA), which is high yielding, drought and pest resistant and adapted to the growing conditions of West Africa (Sarla and Mallikarjuna, 2005). Molnar-Lang *et al.* (2013), have given comprehensive review on intergeneric breeding of *Hordeum* species (cultivated and wild) with wheat. They found that wheat-barley hybridization has the potential to incorporate earliness, salt and drought tolerance, desired amino acid integration, and high tillering ability of barley into wheat, whereas the favourable characteristics of stem strength and winter hardiness of wheat can be introgressed into barley. Resistance to stem and leaf rust have been transferred from *Agropyron elongatum* and *Aegilops umbellulata* in wheat (Prescott-Allen and Prescott-Allen 1986) and spring wheat germplasm lines derived from *Aegilops tauschii* provided or resistance to Hessian fly (Suszkiw 2005). The most well known introgression is the rye (*S. cereale*) 1RS translocation that harbors genes involved in multiple disease resistance (*Pm8/Sr31/Lr26/Yr9*; Mago *et al.*, 2005) and improved

root structure (Sharma *et al.*, 2011), as well as additional positive agronomic characteristics (Rajaram *et al.*, 1983). Also, using marker assisted selection, one APR gene for leaf rust and stripe rust has been transferred from *T. monococcum* to bread wheat WL711 and one gene for leaf rust has been transferred to PBW343 background (Singh *et al.*, 2007).

In potato, *Solanum demissum* provided resistance to late blight (National Potato Council 2003) while in tomato >40 resistance genes have been derived from *S. peruvianum*, *Solanum pennellii* Correll var. *pennellii*, *Lycopersicon cheesmanii*, *L. pimpinellifolium* for traits such as increased soluble solid content, fruit colour, and adaptation to harvesting (Rick and Chetelat 1995). Broccoli varieties producing high levels of anti-cancer compounds have been developed using genes obtained from wild Italian *Brassica oleracea*. The species of *Solanum* complex such as *S. incanum*, *S. viarum*, *S. melongena* var. *insanum*, *S. khasianum* have provided gene for resistance to *Fusarium* wilt, bacterial wilt, frost tolerance and fruit & shoot borer. The wild species of okra *Abelmoschus tuberculatus* to YVMV and wild cucumbers *Cucumis hardwickii* and *C. callosus* have resistance to downy mildew and fruit fly, *Cucumis melo* var. *chito* for *Fusarium* wilt resistance.

Among pulses, *Vigna tribolata*, *V. mungo* var. *sylvestris*, *V. radiata* var. *sublobata* have provided resistance to yellow mosaic virus, *V. vexillata* has high protein and resistance to cowpea pod sucking bug and buchids and is crossable with *V. unguiculata* and *V. radaita*. Cytoplasmic male sterile systems were developed for pigeon pea exploiting the cross-pollination mechanism and utilizing wild *Cajanus* species (Mallikarjuna *et al.*, 2012). High protein and seed size breeding lines such as HPL 2, HPL 7, HPL 40 and HPL 51 were developed from *C. sericeus*, *C. albicans* and *C. scarabaeoides* (Saxena *et al.*, 1987, Jadhav *et al.*, 2012). *Phaseolus*

*coccineus* is a source of resistance to anthracnose as well as root rots, white mold, and BYMV in common bean (Sharma and Rana, 2012). In chickpea, productivity enhancement related traits have been introgressed from *C. reticulatum*, *C. echinospermum*, (Sandhu *et al.*, 2006; and for resistance to *Ascochyta* blight, pod number and short internode from *C. reticulatum*, *C. echino* (Singh *et al.*, 2015). *Cicer microphyllum* have been identified to carry genes for cold hardiness, drought tolerance and seeds/pod (Rana *et al.*, 2009). Stable Recombinant Inbred Lines (RILs) were developed for resistance to rust, powdery mildew and pod number from *Lens orientalis*, *L. odomensis* and *L. ervoides* (Singh *et al.*, 2013)

Gene sources have also been identified in *Sesamum laciniatum* to leaf phyllode, *S. malabaricum*, *S. mulyanum* and *S. alatum* for powdery mildew; *Linum perenne* for drought and cold hardiness, *L. grandiflorum* for linseed bud fly and alternaria blight; *Brassica oxyrhina*, *Moricandia arvensis*, *Trachystoma balli*, *Diplotaxis catholica* as sources of CMS, *B. tournefortii*, *Diplotaxis acris*, *D. harra*, *Eruca sativa* for drought tolerance in *Brassica*; *Corchorus aestuans*, *C. tridens*, *C. fascicularis* resistant to Jute semi-looper and *Macrophomina* sp., *C. olitorius* for yellow mite, *C. capsularis* for stem rot and anthracnose, *C. depressus* for drought tolerance and *Erianthus* sp. have gene for cold and drought tolerance, high yield for *Saccharum* improvement.

Among fruits, *Malus baccata* in apple; *Pyrus pashia* and *P. pyrifolia* in pear; *Prunus cerasoides* in cherry and *P. mira* in peach are used as rootstocks with multiple disease and insect resistance and drought tolerance. In Citrus, *Citrus jambhiri*, *C. limonia* and *C. karna* are used as rootstocks for cultivated species and are tolerant to citrus tristeza virus and most promising rootstocks for mandarin, orange and Kinnow in the lower hills. *Musa acuminata* ssp. *burmannica* found resistant to leaf spot and Foc wilt and *Rhodochlamys* such as *M. laterita*, *M. velutina*, *M. ornate* and *M. aurantiaca* have resistance to leaf spot, wilt and tolerance to nematodes. *Phyllanthus acidus* has tolerance for rust and frost. *Vitis parviflora* showed multiple disease resistance while *V. himalayana* is cold hardy, drought tolerant and late ripener, hence escape fruit cracking in rainy season in grapes.

## Conclusion

Wild species/species complexes that have studied and utilized are few considering the large number of

native economically important taxa in India. Also, species introduced for their potential importance are another large resource, which needs to be conserved on a priority basis as future introductions are likely to be few especially since these are now exchanged only with prior consent and under material transfer and benefit-sharing agreements. To cope with problems arising from intensive modern agriculture and climate change, it is essential to maintain genetic diversity within crop gene pools. In the past crop breeders had been struggling with the problem of linkage drag while dealing with CWR. Nevertheless, now the advances in DNA sequencing technology particularly combination of de novo sequencing and resequencing are being used efficiently to explore useful genetic variation in CWR. Therefore, plant breeders have to work closely with genetic engineers to develop new cultivars. There is need to design altogether new crops, plant types and varieties, which have the ability to perform well under adversities. Breeders should be well equipped with the genes to keep themselves one-step ahead of the rapidly evolving pests and diseases and even new climate regimes. The value of diversity in crops is similar to the value of a diversified portfolio to an investor. If one stock fails, the investor does not lose everything. Nature does not produce individual plants resistant to all diseases, pests and environmental stresses, and neither can the breeder. It is natural genetic diversity, in which many individuals, each somewhat different genetically, thrive together, allows a population to withstand challenges to its survival and produce traits of needs.

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