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Utilization of wild germplasm for vegetable improvement: a review

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Abstract

About 400 species constitute the total diversity in vegetable crops across the globe. Among the diversity rich regions of the world that represent the centers of origin and /or diversity as well the regions possessing maximum diversity are the tropical American, Tropical Asian and the Mediterranean region. In the tropical Asian region, both India and China hold maximum diversity. Nearly 80 species of major vegetables, apart from several wild/undomesticated types are native to Indian region and are mentioned under "Hindustani Centre". India has a long history of vegetable cultivation and Sanskrit equivalents are available for introduced vegetable crops indicating exchange of plant material with other countries well before the Christian Era e.g. bottle gourd and watermelon from Africa, and onion from Central Asia. Other species, having wide distribution in India are, *Trichosanthes, Momordica, Coccinia and Canavalia* etc. Overall, 20-25 vegetable crops are commercially important and these include both the indigenous and exotic species.

Germplasm acquisition from within and outside country is the first step in germplasm management programme. A large germplasm representing a broad spectrum of genetic diversity has been introduced from other countries. Several introduced varieties have been used directly for large-scale cultivation. Many introductions in vegetable crops have also been used as parents to develop new cultivars. Germplasm of wild species of crops like brinjal (47), chilli (87), okra (82), tomato (385), water melon (18) have been introduced by NBPGR from abroad in the past few years. Besides identifying donors form cultivated form, their wild allies called CWR does have valuable genes with immense value for crop improvement and adaptation to changing environmental conditions. Utilization of CWR has enjoyed a great success in few crops like okra, tomato, potato, cucumber.

Key words: Will germplasm, Vegetables, Relatives, Diversity, Environmental conditions

Global food security is increasingly threatened by a range of challenges, including population growth, habitat destruction, climate change, water scarcity, limited arable land, and soil degradation (Godfray & Garnett, 2014; Hengyou *et al.*, 2015). Over the past five decades, human activities have drastically reduced biodiversity, accelerating genetic erosion in crops and their wild relatives. The Food and Agriculture Organization (FAO, 2010) estimates that nearly 75% of crop genetic diversity has already been lost, posing a serious risk to agricultural resilience and long-term sustainability. Ongoing habitat destruction further exacerbates this issue by diminishing the genetic resources essential for food production and adaptation to shifting environmental conditions. Addressing these challenges is imperative to ensuring a secure and sustainable global food supply.

Present day's vegetable crops have evolved from its wild progenitors known as crop wild relatives (CWRs). These hidden reservoirs of valuable genes are crucial for developing resilient, climate-smart vegetable crop varieties, making them essential for global food security (Castaneda *et al.*, 2016; Singh *et al.*, 2018). The potential of CWRs as gene donors for crop improvement was first recognized by renowned Russian plant geneticist Nicolai Vavilov in 1920s and 1930s (Vavilov, 1926). the CWRs share a common ancestry with domesticated species and serve as sources of beneficial alleles for key nutritional and agronomic traits (Tanksley and McCouch, 1997; Guarino and Lobell, 2011; Fielder *et al.*, 2015). These wild relatives of vegetable crops enhance the adaptive capacity of agricultural systems worldwide due to their natural resilience to local environmental conditions. The use of CWRs for introducing genes conferring disease and pest resistance, as well as tolerance to abiotic stresses, dates back more than 60 years (Hajjar and Hodgkin, 2007). unfortunately, many CWRs of vegetable crops remain underutilized in breeding programs. It is, therefore, imperative to prioritize their conservation, particularly through *in-situ* preservation, allowing them to continue evolving and developing valuable adaptations for future agricultural challenges.

Over the past decade, international initiatives like the FAO treaty and UN programs have advanced efforts to conserve and share wild plant genetic resources. Key strategies, including the Global Strategy for Plant Conservation (CBD, 2010b) and the Aichi Biodiversity Targets (CBD, 2010a), emphasize comprehensive conservation. In India, the ICAR-NBPGR plays a vital role in collecting, conserving, evaluating, and sharing plant genetic resources with crop breeders for its utilization in crop improvement programmes.

The Indian subcontinent is rich in wild vegetable plant species with high nutritional, traditional, and social value. Collecting and characterizing wild vegetable

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species is crucial for identifying useful traits and conserving them for future breeding programs (Hajjar and Hodgkin, 2007 and Teso *et al.*, 2018). Advances in genomic tools, particularly high-density SNP markers, have transformed how breeders utilize genetic diversity, aiding in the discovery of valuable genes (Tanksley and McCouch, 1997 and Gayle and Christopher, 2011). Crop wild relatives (CWRs) play a key role in developing climate-smart genotypes with better adaptation, higher nutrition, and greater ecological flexibility. This review paper emphasizes the need for prioritizing, conserving and utilization of wild vegetable species in Indian gene banks to enhance food and nutritional security.

Gene pool

Wild relatives of crop plants constitute a part of the crop gene pool. The crop gene pool concept developed by Harlan and de Wet (1971) is used to classify genetic relationship between crops and related taxa (Fig.1). In crops where categorization of CWR into gene pools has not been done as per their crossability relationship, taxonomic classification can be useful. This method of classification is referred to as taxon group concept (Maxted et al., 2006). In brinjal, the primary gene pool (GP1) consists of cultivated and its wild ancestor (Fig.2) *Solanum insanum* L. (Ranil *et al.,* 2017) which can be crossed easily and produce normal fertile hybrids (Plazas *et al.*, 2016). The secondary gene pool (GP2) includes a large number (over 40) of *Solanum* species that can be crossed or are phylogenetically close to brinjal, but the success of the crosses and viability of the hybrids with Brinjal (*Solanum melongena* L.) may be reduced. For example, some interspecific hybrids derived from GP2 are partly sterile or weak due to reproductive barriers such as with *S. dasyphyllum, S. linnaeanum* Hepper and P.-M. L. Jaeger or *S. tomentosum* L. (Rotino *et al.*, 2014 and Kouassi *et al.*, 2016). The tertiary gene pool (GP3) of brinjal includes more widely related New World species which are used in its improvement programs for the transfer of resistance traits. For making successful crosses between these species, there is a need of follow specific breeding tools (e.g., *S. torvum* Sw., *S. elaeagnifolium* Cav., and *S. sisymbriifolium* Lam.; Kouassi *et al.*, 2016; Plazas *et al.*, 2016; Syfert *et al.*, 2016).

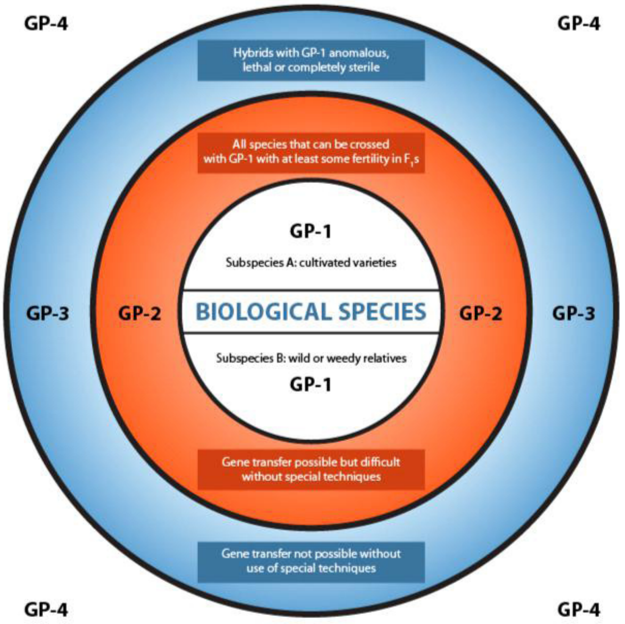


Fig 1: The modified "gene pool concept" adapted from Harlan and de Wet (1971)

Genus *Pisum* is comprises of mainly three species i.e. *P. sativum* L. with subsp. *sativum* (includes var. *sativum* and var. *arvense*), ssp. *elatius*, *P. fulvum* and *P. abyssinicum*. The widely used classification is given by Maxted and Ambrose, 2001 to which *Vavilovia formosa* was added to group four species (Smýkal *et al.* 2011). In pea, primary gene pool consists of *Pisum sativum* including wild *Pisum sativum* ssp. *elatius*, the secondary gene pool is composed of *Pisum fulvum* and the tertiary gene pool consisting only of *Vavilovia formosa*. This is the closest species to whole tribe Fabeae that holds significant interest and breeding value in leguminous crops in the world. Gepts and Papa (2003) modified the gene pool concept and gave an additional gene pool level known as quaternary gene pool which takes into account the biotechnological advances such as plant transformation and genomics. It harness the genes from wild species which otherwise are sexually incompatible with crop species. This type of gene pool can also contain synthetic nucleotide sequence that does not occur in nature.

Diversity in vegetable crops

Plant genetic resources of wild relatives of vegetable crops are important components of agro- biodiversity, therefore extremely useful for present and future generations. Characterization of genetic diversity of wild collections exhibit evidence of historical demography and natural selection (Gayle and Christopher, 2011). India is the primary centre of diversity for brinjal, Smooth gourd (*Luffa cylindrica* (L.) *M. Roem.* (*M.J. Roem.*)), ridge gourd (*Luffa acutangula* (L.) Roxb. Roxburgh (Roxb.)), bitter gourd (*Momordica charantia* L.), spine gourd (*Momordica dioica* Roxb), Sweet gourd (*Momordica cochinchinensis*) and cucumber (*Cucumis sativus* L..), and the secondary centre for cowpea (*Vigna unguiculata* (L.) Walp), okra (*Abelmoschus esculentus* (L.) *Moench*), chillies (*Capsicum annuum* and *Capsicum frutescens*), melons (*Cucumis melo* L), pumpkin (*Cucurbita moschata*), cluster bean (*Cyamopsis tetragonoloba*) and members of brassicaceae

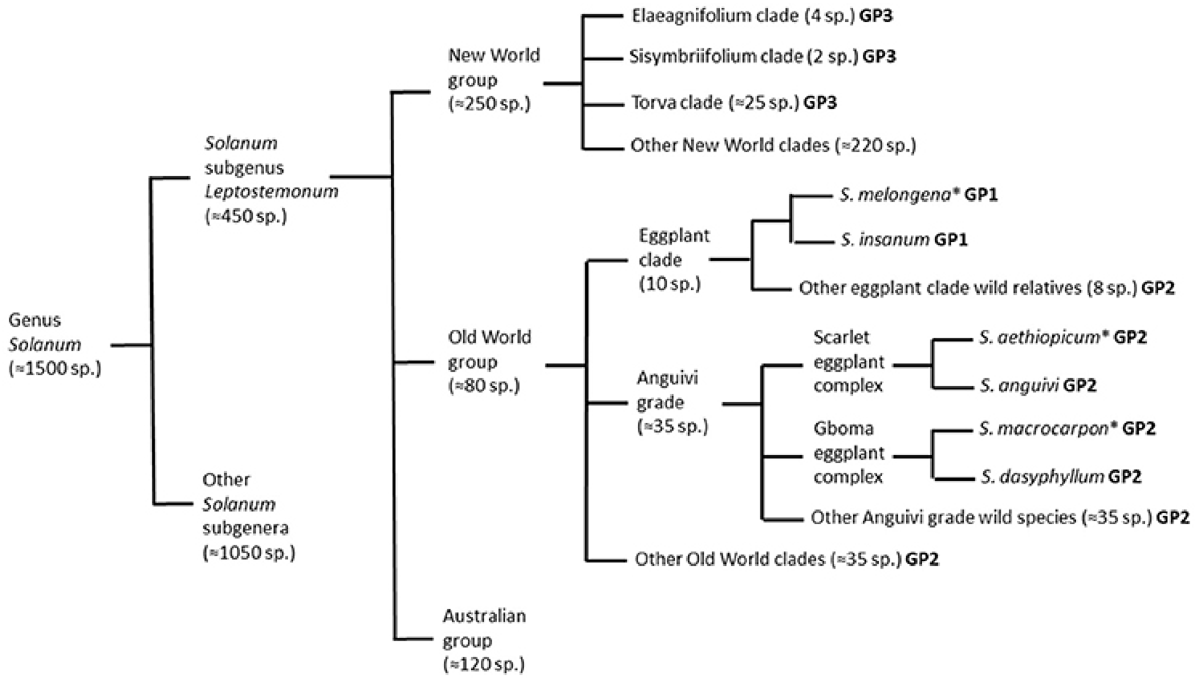


Fig.2. Schematic representation of taxonomic relationships between cultivated brinjal and other cultivated (scarlet eggplant, *S. aethiopicum*; and gboma eggplant, *S. macrocarpon*) and wild relatives from the genus *Solanum* based on Dalia *et al.* (2017), Nee (1999), Levin *et al.* (2006), Weese and Bohs (2010), Stern *et al.* (2011), Knapp *et al.* (2013), Syfert *et al.* (2016), and Vorontsova and Knapp (2016)

family. The distribution pattern of wild relatives of vegetable crops in different regions in India is presented in Table 1.

Table 1: Wild relatives of vegetable crops in different region of India

Region	Wild relatives of vegetables
Western Himalayas	*Cucumis sativus* var. *hardwickii, L. graveolens, Solanum incanum, S. indicum, Trichosanthes himalensi*
Eastern Himalayas	*Abelmoschus manihot, Cucumis hystrix, C. muriculatus*
North-eastern hills	*Abelmoschus, Alocasia macrorhiza, Amorphophallus bulbifer, Colocasia esculenta, Cucumix hystrix,, M. cochinchinensis, M. subangulata, Trichosanthes cucumerina, T. dioica, T. khasiana, T. ovata,*
Gangetic plains	*Abelmoschus tuberculatus, Luffa echinata, Momordica cymbalaria, M. dioica, Solanum incanum, S. indicum*
Indus plains	*Momordica balsamina, Citrullus colocynthis, Cucumis prophetarum*
Western peninsular tracts	*Abelmoschus angulosus, A. enbeepeegearense, A. moschatus, A. manihot, A. ficulneus, Cucumis setosus, C. trigonus, Momordica dioica, M. sahyadric Luffa graveolens, Solanum indicum, Trichosanthes anamalaiensis, T. bracteata, T. cuspidate, T. nerifolia, T. villosa*
Eastern peninsular tracts	*Amorphophallus campanulatus, Abelmoschus moschatus, A. crinitus, Colacasia antiquorum, Luffa acutangula* var. *amara, L. graveolens, L. umbellate, Momordica cymbalaria, M. dioica, M. subangulata, Trichosanthes bracteata, T. cordata,T. lepiniana, T. himalensis, T. multiloba*

The distribution pattern of wild relatives of vegetable crops in different phytographical regions and the areas of their occurrence and diversity is useful for germplasm collection and *in-situ* conservation.

The Base Collections are being maintained by NBPGR in the National Genegank (NGB) in form of seeds in Seed Genebank (where seeds dehydrated to ~5% moisture content and sealed in tri-layered laminated aluminum foil packets and conserved at -18^{0}C), in form of tissue culture in the *In vitro* Genebank and in Cryobank (-196^{0}C), and in form of live plants in Field Genebanks. The details of important vegetables crops maintained at National Genebank are presented in Table 2.

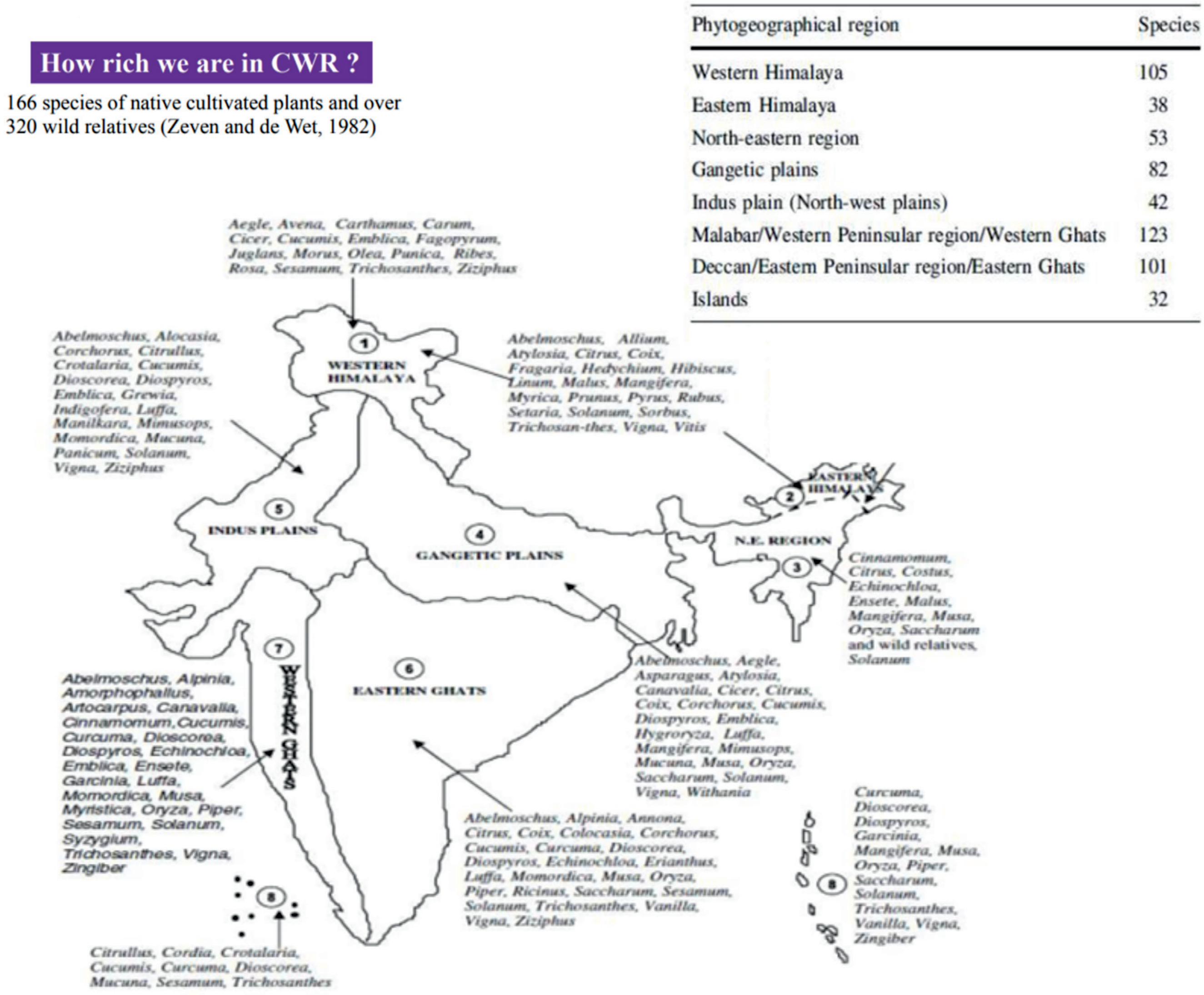
Utilization of wild species

In India, brinjal and some cucurbits are of Indian origin, whereas for tomato, okra and chilli, India considered as secondary centre of origin. *Solanum melongena* complex has three species, namely, the *S. melongena, S. incanum* and *S. melongena* var. *insanum.* Wild relatives of *Solanum viz. Solanum torvum, S. indicum, S. insanum, S. surattense, S. pubescens, S. gilo,* and *S. khasianum* are widely distributed in South India, Shivalik hills and North-eastern region. There are about 100 species of cucurbitacae family are reported to occur in India including 34 endemic species viz. *Cucumis hardwickii, C. trigonus, C. prophetarum, C. setosus, C. hystrix, Luffa graveolens, L. acutangula* var. *amara,*

Table.2: Status of cultivated and wild germplasm of major vegetable crops conserved in National Gene bank, India

Crop	Botanical name	No. of accession in NGB
Tomato and wild species	*Solanum lycopersicon, S. peruvianum, S. pimpinellifolium, S. lycopersicon var. cerasiforme, S. hirsutum, S. chilense*	2931
Brinjal and wild species	*Solanum melongena, S. aethiopicum, S. americanum, S. gilo, S. macrocarpum, S. melongena var. incanum, S. verbascifolium, S. viarum, S. melongena var. incanum, S. hispidum, S. incanum, S. melongena var. insanum, S. torvum, S. vagum, S. violaceum, S. albicans, S. anguivi, S. laciniatum, S. trilobatum,. S. pimpinellifolium, S. pubescens, S. seaforthianum, S. setosissimum, S. virginianum, S. xanthocarpum, S. aculeatissimum, S. aviculare, S. giganteum, S indicum, S. khasianum, S. nigrum, S. sisymbrifolium, S. surattense, S. lasiocarpum.*	4846
Chilli and wild species	*Capsicum annuum, C. baccatum, C. chinense, C. frutescense, C. annuum var. annuum, C. annuum var. grossum*	5402
Okra and wild species	*Abelmoschus esculentus, A. betulifolius, A. crinitus, A. ficulneus, A. manihot* spp. *manihot, A. manihot var. pungens, A. manihot var. tetraphyllus, A. moschatus var. tuberosus, A. pungens, A. tetraphyllus, A. tuberculatus, A. manihot, A. moschatus.*	4275
Ashgourd	*Benincasa hispida*	294
Bitter gourd	*Momordica charantia, M. charantia var. muricata, M.sahyadrica, M. tuberosa, M. cochinchinensis, M. dioica, Momordica subangulata* ssp. *renigera, M. balsamina.*	672
Bottle gourd	*Lagenaria siceraria, Lagenaria* sp.	800
Luffa spp. (Sponge gourd, Ridge gourd)	*Luffa echinata, Luffa pentandra, Luffa sp. Luffa tuberosa, Luffa acutangula, Luffa acutangula var. amara, Luffa hermaphrodita, Luffa aegyptiaca, Luffa cylindrica, Luffa graveolens*	988
Trichosanthes species (Snake Gourd)	*Trichosanthes tricuspidata, Trichosanthes dioica, Trichosanthes anguina, Trichosanthes cucumerina, Trichosanthes cucumeroides var. dicoelosperma, Trichosanthes palmata, Trichosanthes wallichiana, Trichosanthes bracteata, Trichosanthes cuspidata, Trichosanthes nervifolia, Trichosanthes lepiniana, Trichosanthes lobate, Trichosanthes spp.*	383
Cucumis spp.	*Cucumis melo var. flexuosus, Cucumis hardwickii, Cucumis sagittatus, Cucumis sativus, Cucumis melo var. inodorus, Cucumis metuliferus, Cucumis melo var. utilissimus, Cucumis melo var. agrestis, Cucumis setosus, Cucumis melo, Cucumis melo var. conomon, Cucumis melo var. reticulatus, Cucumis trigonus, Cucumis hystrix, Cucumis melo subsp. melo, Cucumis vulgaris, Cucumis prophetarum, Cucumis rati, Cucumis callosus,, Cucumis javanicus, Cucumis maderaspatanus, Cucumis silentvalleyi, Cucumis muriculatus, Cucumis leiospermus, Cucumis spp.*	2373
Cucurbita species	*Cucurbita moschatus, C. argyrosperma, C.maxima, C. pepo, Cucurbita* sp.	282
Citrullus species	*Citrullus colocyhtis, Citrullus lanatus, Citrullus Sp, Citrullus Vulgaris Var Citrode .*	466
Onion and wild species	*Allium cepa, A. altaicum, A. auriculatum, A. clarkei, A. stracheyi. A. fistulosum, A. griffithianum, A. humile, A. oschaninii, A. albidum, A. pskemense, A. ramosum, A. tuberosum, A. ampeloprasum, A. orepprasum, A. porrum, A. sativum, A. senescens.*	1151
Cabbage	*B. oleracea var. capitata*	283
Cauliflower	*B. oleracea var. botrytis*	219
Broccoli	*B. oleracea var. italica*	24
Brassica species	*Brassica perkensis, Brassica oleracea var. compestris, Brassica rapa subsp. Chinensis, Brassica campestris var. rapa, Brassica oleracea var. caulorapa, Brassica campestris var. rapifera, Brassica juncea var. rugosa, Brassica oleracea var. gemmifera*	494
Carrot	*Daucus carota, Daucus carota var. sativa*	152

Crop	Botanical name	No. of accession in NGB
Radish	*Raphanus caudatus, R. sativus*	334
Beet root	*Beta vulgaris, Beta vulgaris var. bengalensis*	92
Spinach	*Spinacia oleracea, Spinacia sp*	163
Amaranthus species	*Amaranthus blitum, Amaranthus dubius, Amaranthus graecizans, Amaranthus leucocorpus, Amaranthus spinosu, Amaranthus tristis, Amaranthus gangeticus, Amaranthus tricolo, Amaranthus viridis*	765
Fenugreek	*Trigonella corniculata, T. foenum-graecum, T. caerulea*	1432
Leguminous vegetable	*Vicia faba, lablab var typicus, Vigna unguiculata subsp. Sesquipedalis, Pisum sativum subsp. hortense, Pisum sativum var. arvense,* Adzuki Bean	1016
	Total	29837



How rich we are in CWR ?

166 species of native cultivated plants and over 320 wild relatives (Zeven and de Wet, 1982)

Phytogeographical region	Species
Western Himalaya	105
Eastern Himalaya	38
North-eastern region	53
Gangetic plains	82
Indus plain (North-west plains)	42
Malabar/Western Peninsular region/Western Ghats	123
Deccan/Eastern Peninsular region/Eastern Ghats	101
Islands	32

Fig. 3. Distribution pattern of wild relatives of vegetable crops in different region in India

L. cylindrica, L. tuberosa, L. echinata, L. umbellata, Trichosanthes anguina, T. dioica, T. dicaeleosperma, T. khasiana, T. ovata, T. truncata, T. multiloba, T. anamalaeiensis, T. bracteata, T. cuspidata, T. nervifolia, T. perotteliana, T. himalensis, Momordica cochinchinensis, M. macrophylla, M. subangulata, M. cymbalaria, M. dioica, M. cymbalaria, M. denticulata, M. balasamina, Neoluffa sikkimensis and *Citrullus colocynthis.* In *Abelmoschus*, 11 species and two varieties, namely, *A. angulosus, A. tuberculatus, A. manihot, A. moschatus, A. ficulneus, A. esculentus, A. tetraphyllus* var. *tetraphyllus, A. tetraphyllus* var. *pungens, A. crinitus, A. caillei, A. enbeepeegearense* and *A. palianus* are occurring in India. Of these, only *A. esculentus* is cultivated and others are wild taxa.

Rich genetic diversity in root and tuber crops, namely, *Amorphophallus paeoniifolius, Manihot esculenta, Ipomoea batatas, Dioscorea alata, Dioscorea rotundata, Psophocarpus Tetragonolobus, Dioscorea esculenta, Dioscorea bulbifera var. sativa, Colocasia esculenta, Alocasia macrorrhiza, Xanthosoma sagittifolium* in terms of species and landraces is occurring in India. Besides these crops, there are several tubers of minor importance, namely, *Maranta arundinacea, Solenostemon rotundifolius, Moghania vestita, Canna edulis, Psophocarpus tetragonolobus* and *Pachyrrhizus erosus* are also found and used as food in some parts of western peninsular region. Genus *Allium* represents a major group and about 30 species are found in Indian region. The cultivated Alliums are - *Allium cepa* var. *cepa, A. cepa* var. *aggregatum, A. cepa* var. *viviparum, A. fistulosum, A. tuberosum, A. sativum, A. ampeloprasum* var. *porrum, A. schoenoprasum*, whereas *A. carolinianum, A. chinensis, A. consanguineum, A. humile, A. przewalskianum, A. stolczkii, A. stracheyi, A. victorialis* and *A. wallichii* are important wild species occurring in Himalayan region.

Besides being identifying donors form cultivated form, their wild allies called CWR does have valuable genes with immense value for crop improvement and adaptation to changing environmental conditions. Utilization of CWR has enjoyed a great success only in a few crops. For example, in potato, (*Solanum demissum*) provided resistance to late blight while in tomato >40 resistant genes have been derived from *S. peruviannum, Solanum pennellii* Correll var. *pennellii, Lycopersicon cheesmanii, L. pimpinellifolium* for traits such as increased soluble solid content, fruit color, 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 and 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. Many genes are still lies untapped in these genetic resources, presumably due to the lack of useful genetic information and genetic bottlenecks as well. A good piece of work has been done by ICAR-NBPGR on biosystematics, screening and genomics of *Abelmoschus, Cucumis, Vigna, Alliums, Trichosanthes, Chenopodium* and *Amaranthus.* New records such as *Moringa concanensis* (Lakshadweep) and rare and endangered species *Cucumis silentvalleyi* (Anaimalai Hills in TN), and *Piper ribesioides* from Middle Andaman have been recorded. Similarly, new species have been described in *Momordica sahyadrica (Western Ghats), Curcuma amada var. glabra (Kerala), Curcuma longa var. vanaharidra, A. enbeepeegearense* and *A. palianus* in okra.

Table 3: Traits specific donors of wild species of major vegetable crops

Crop/trait	Wild species as donors
Tomato	
High TSS	*S. chmielewskii* (10%), S. *cheesmanii* (15%),
High temperature	*S. chilense, S. cheesmanii, S. pimpinellifolium*
Low temperature	*S. hirsutum, S habrochaites, S chilense, S lycopersicoides*
Drought	*S. Lycopersicum* var. *Cerasiformae, S pennellii, S pimpinellifolium*
Salt tolerant	*S. cheesmani, S. pennelli, S pimpinellifolium, S peruvianum*
Fusarium wilt / rot	*S. pimpinellifolium,*
Late blight	*S. hirsutum*, S. *pimpinellifolium*, S. *Lycopersicum var. cerasiforme*
Early blight	*S. peruvianum* var. *dentatum*, S. *peruvianum*, *SL. hirsutum* f. *glabratum*
TLCV	*S. hirsutum* f. *typicum*, S. *pimpinellifolium* 'A 1921', S. *hirsutum* f. *glabratum*
TYLCV, CMV	*S. chilense*
Grey mold	*S.neorickii*
Fruit fly	S. galapagense
Leaf miner	S. *hirsutum, S. hirsutum* f. *glabratum,*
Fruit borer	*S. hirsutum* f. *glabratum*
White fly	*S. hirsutum* f. *glabratum*
Nematode	*S. peruvianum*
Flooding	*S Lycopersicum var. cerasiforme, S. juglandifolium, S. ochranthum*

Crop/trait	Wild species as donors
Brinjal	
Fusarium wilt	*S. incanum, S. indicum, S. khasianum, S. sysimbrifolium, S aethiopicum*
Bacterial wilt	*S. torvum, S. melongena var. insanum, S. nigrum, S. sisymbriifolium,S. integrifolium*
Phomopsis blight	*S. gilo, S. integrifolium, S. sisymbrifloium*
Little leaf	*S. gilo, S. integrifolium, S. sysimbrifolium, . torvum, S. khasianum*
Verticillium wilt	*S. torvum, S. sysimbrifolium*
Shoot and fruit borer	*S. khasianum, S. incanum, S. gilo, S. indicum S. sisymbriifolium, S. hispidum, S. aethiopicum, S. macrocarpon*
Heat and drought tolerance	*S. macrocarpon, S. incanum, S. gilo*
Nematode	*S. sisymbrifolium*
Male sterility	*S. virginianum, S. angulvi*
Mites	*S. macrocarpon, S. integrifolium, S. mammosum*
Chilli	
Anthracnose	*C. baccatum*
Phytophthora blight	*C chinense*
Cucumber mosaic virus	*C chinense, C. frutescens*
Leaf curl virus	*C chinense, C. frutescens*
Bacterial leaf spot	*C. chacoense*
Curly top virus	*C. annuum, C. frutescens, C chinense, C. chacoense*
Pepper mosaic virus	*C. baccatum, C chinense*
Okra	
YVMV	*A. crinitus, A. angulosus*
Powdery mildew	*A. tetraphyllus, A. angulosus, A. crinitus*
Cercospora blight	*A. crinitus, A. moschatus, A. angulosus, A. ficulneus*
Enation leaf curl virus	*A. crinitus, A. ficulneus, A. manihot*
Fruit borer	*A. tuberculatus, A. moschatus*
Mites	*A. angulosus*
Jassids	*A. moschatus, A. crinitus*
Late blight	*Sollanum demissum*
Potato Virus Y	*Sollanum chacoense*
Colorado potato beetle	*Solanum chacoense*
Aphid	*S. polyadenium, S. berthaultii*
Nematode	*S. vernii*
Cucumber	
Downey mildew, powdery mildew, Anthracnose	*C. sativus* var. *hardwickii*
Muskmelon	
Water melon mosaic virus	*Cucumis metuliferus*
***Brassica* spp.**	
Black rot	*Brassica carinata, B. juncea, B. nigra,*
Cytoplasmic male sterility	*Brassica napus* 'nap and pol', *B. oleracea 'Ms-cd1', Diplotaxis berthautii, Trachystoma ballii 'trachystoma'*
Drought tolerance	*Brassica carinata, Brassica juncea, Brassica tournefortii*
Downy mildew	*Brassica oleracea*
Diamond-back moth	*Brassica juncea, Brassica oleracea*
Resistance to pod shattering	*Brassica juncea, Brassica macrocarpa, Brassica tournefortii*
Cabbage aphid	*Brassica fruticulosa, B. spinescens,,B. cretica, B. incana, B. macrocarpa, B. villosa*
Onion	
Cytoplasmic Male sterility	*A. galanthum*
Stemphilium blight	*A. tuberosum*
Downy mildew	*A. royeli*
Lettuce	
Leaf spot	*Lactuca saligna*
Downy mildew	*L. saligna, L. serriola*

For the past few decades, there is a significant success in introducing different traits from wild species into cultivated crops for overcoming biotic/abiotic stresses. For example, introduction of late blight resistance from the wild potato *Solanum demissum* Lindl is the main landmark. The primary approach for crop improvement today remains recurrent selection among elite modern varieties. Plant breeders are continuously looking into wild species as sources of novel genes to widen the genetic base of crops (Cooper *et al*., 2001; Hodgkin and Hajjar, 2007; Moore, 2015)

Wild relatives of cultivated crops are the raw material for plant breeder. Recently the importance of CWR has been realized globally to breed climate resilient crop varieties to meet out the future food security. CWR's has many fold applications in crop improvement which include different traits such as biotic stresses (pest /

disease resistance, yield, quality, and male sterility) and abiotic stresses (heat, flood, cold and drought tolerance). To develop trait- specific genotypes, the CWRs have been utilized with varying degrees for significant traits. At present, most of the varieties (65%) released for commercial cultivation are either direct selection from germplasm or developed (20%) using trait specific germplasm as one of the parents in hybridization program. This highlights the worth of germplasm collection and conservation to enable their use in crop improvement programs.

Some of the important wild relatives of horticultural crops have successfully been utilized for the introgression of genes are *Solanum incanum, S. viarum, S. melongena* var. *insanum* for fusarium wilt, bacterial wilt resistance, and frost tolerance; *S. torvum S. sisymbrifolium* for verticillium wilt and *Meloidogyne incognita*; *S. gilo, S. integrifolium* for *M. incognita* race 1 and 2 and *S. khasianum* for shoot and fruit borer resistance in brinjal; *Allium ampeloprasum* for downy mildew in onion, *Pisum sativum* var. *arvense* for podwery mildew in pea. In brinjal, K61, K62 used for *Fusarium* wilt resistance; SM81, SM56, SM71, SM72, SM74, H8, Kopek for bacterial wilt resistance; MM392, MM450 for nematodes (*M. incognita* and *M. aremeriai*) and H165, H407, H408 for Shoot and fruit borer resistance. The species of *Solanum* complex such as *S. incanum, S. viarum, S. melongena* var. *insanum, S. khasianum* have provided genes for resistance to fusarium wilt, bacterial wilt, frost tolerance and fruit and shoot borer in brinjal.

Interspecific hybridization is an important tool which can be used to improve traits through chromosome manipulation in wild species that aid in their adaptability to different agricultural environments and compete with the cultivated forms. Inter-specific hybrids have been produced in several genera of Cucurbitaceae like *Cucumis* (Deakin *et al*. 1971; Chen *et al*. 1997), *Citrullus* (Valvilov 1925), *Luffa* (Singh 1991) and *Cucurbita* (Weeden & Robinson 1986).

The *Abelmoschus* is one of the major vegetable genera under family Malvaceae. *Abelmoschus* with 14 species reported so far (Misra *et al*., 2023), has two major species under cultivation viz., *A. esculentus* (L.) Moench (okra) and *A. caillei* (A.Chev.) J.M.C.Stevels (Guinean okra). In South Pacific Islands, Papua New Guinea, and eastern Indonesia, *A. manihot* (L.) Medik. is also popular as leafy vegetable (Prabawardani *et al*., 2016; Rubiang-Yalambing *et al*., 2016). Apart from the cultivated genepool, the wild *Abelmoschus* spp. has many desirable traits like perennation tendency, extended bearing, biotic and abiotic stress tolerance (Suma *et al*., 2023). Cultivated Okra is facing challenges of YVMV and ELCV, diseases are the two major ones causing significant yield losses, which require search for resistance in the wild related taxa and their incorporation into cultivated genome.

Though Pusa Sawani (a derivative of a cross between IC1542 and Pusa Makhmali) was the first ever YVMV resistant variety of okra to be released at national level in India, Parbhani Kranti, Arka Anamika and Arka Abhay were the ones released as a result of interspecific hybridization between *A. esculentus* and *A. manihot* for the former (Jambhale and Nerkar, 1986), and *A. manihot* subsp. *tetraphyllus* (Roxb. Ex Hornem.) Borss. Waalk. for the latter two (Dutta, 1991). Further, *A. manihot* was used for developing a variety Anjitha, by exploiting interspecific hybridization followed by mutation breeding by Kerala Agricultural University (KAU) for transferring YVMV resistance and tolerance to shoot and fruit borer. Susthira was another variety belonging to *A. caillei* reported as resistant to YVMV, released by KAU. Gangopadhyay *et al.* (2016) reported resistance to YVMV disease in accessions belonging to three wild species viz. *A. caillei, A. manihot* and *A. moschatus* Medik., while resistance to shoot and fruit borer and leaf hopper was found in all the three above besides *A. tuberculatus* Pal and Singh.

It was also been noted that *A. manihot* subsp. *tetraphyllus* is one of the most widely used species worldwide for transferring genes responsible for resistance or tolerance to YVMV, jassids, and fruit borer (Badiger and Yadav, 2019; Patel *et al*., 2021). Promising accessions of *A. moschatus* (IC141055), *A. tetraphyllus* (IC90476-1), and *A. caillei* (Sikkim) were also reported by Santhiya *et al.* (2022) under natural epiphytotic screening, where the above accessions demonstrated a very low prevalence of YVMV and no incidence of ELCV diseases. Singh *et al.* (2023a) revealed that *A. angulosus* accessions IC203833 and IC470751 were extremely resistant to YVMV disease under artificial screening conditions employing mass inoculation mediated by viruliferous whiteflies.

With the implementation of National Agriculture Innovation Project (NAIP) during 2009-13 by the Indian council of Agricultural Research (ICAR), the biosystematics and crossability studies among various *Abelmoschus* species caught momentum, which were further progressed under the ICAR-Extramural Project of the ICAR, Horticultural Sciences Division (2015-17) and later under the ICAR-Emeritus Scientist Programme (2018–2021) for transferring genes tolerant/ resistant to YVMV and ELCV diseases. The tolerant species (*A. pungens* var. *mizoramensis, A. enbeepeegeearensis, A. tetraphyllus*, and *A. angulosus* var. *grandiflorus, A. crinitus, A. ficulneus*) were also identified through the field screening of wild *Abelmoschus* species germplasm

(John *et al.*, 2013a). These species were then employed in a wide hybridization program to produce interspecific hybrids with the cultivated okra at ICAR-National Bureau of Plant Genetic Resources, Regional Station, Thrissur to find out crossability relationships among various species of Abelmoschus.

A total of 113 amphidiploids generated were extensively characterized for the important morphological characters by Suma *et al.* (2023). The promising amphidiploids identified are currently being advanced through back crossing and selfing. Among them, 13 selfed derivatives (involving crosses between *A. esculentus* and *A. pungens* var. *mizoramensis*, and a multi-cross combinations of *A. esculentus, A. angulosus* var. *grandiflorus*, *A. tetraphyllus* and *A. pungens* var. *mizoramensis*), one back cross derivative (involving *A. esculentus* and a multi-cross combination of *A. esculentus, A. angulosus* var. *grandiflorus*, and *A. pungens* var. *mizoramensis*) and nine open pollinated bulked amphidiploid derivatives (involving *A. esculentus* with *A. angulosus* var. *grandiflorus*, and *A. pungens* var. *mizoramensis*) exhibited field resistance in three locations namely Varanasi, Ludhiana and New Delhi (not published).

In addition, *A. manihot* and newly described species *A. odishae* are also being currently utilized in wide hybridization programmes. Venkataravanappa *et al.* (2022) also identified cultivated, wild as well as advanced lines resistant to both YVMV and ELCV diseases. Embryo rescue was employed for successful production of F_1 hybrid for crosses involving *A. esculentus* and *A. moschatus* subsp. *tuberosus* (Zaman and Parihar, 2023) and *A. esculentus* and *A. tetraphyllus* (Rattan and Kumar, 2020).

Besides employing the wild species for transferring genes tolerant to biotic stresses, crosses were attempted to exploit the ornamental potential of hybrids of the cross between *A. moschatus* and *A. sagittifolius* as reported by John *et al.* (2013a and 2013b). All the plants derived from both direct and reciprocal crosses were yielding plants with bright red flowers. The F_2 plants showed segregation for the flower colour with various shades ranging from pink, yellow, light red, dark red and with combinations of these colors, including contrasting dark veins on petals with lighter shades (Suma *et al.,* 2024).

In tomato, several wild species have been used as donors, for example, genus *Lycopercicon hirsutum* and *L. pimpinellifoium* for fungus resistance, *Lycopercicon chilense* and *Lycopercicon peruvianum* for virus resistance, *Lycopercicon chmielewskii* for fruit quality and *Lycopercicon cheesmanii* for tolerance to adverse environments. And, further, use of quality genes such as 'Rin' in tomato resulted into better table and nutritional quality of the crop. Genes from *L. chilense* and *L.pennellii* species have been used to increase drought and salinity tolerance (Rick and Chetelat 1995). The TMS line of cassava, derived from an initial cross with a wild relative, gives a 40% more yield (Nweke 2004), which may be because of wild genes conferring disease resistance in the cross.

In a recent study, pyramiding of three independent yield-promoting genomic regions introduced from *Solanum pennellii*, a green-fruited wild relative of tomato has led to the development of hybrids with 50% more yield over a commercial variety (Gur and Zamir 2004). Wild relative of crop plants, as a source of cytoplasmic male sterile genes, can also play an important role in developing F_1 hybrids in vegetable crops. Attempts were made at Indian Agricultural Research Institute, New Delhi, IIHR, Bangaluru, IIVR, Varanasi, PAU, Ludhiana and some other palces to utilize wild relatives of tomato e.g. *Solanum habrochaites* for developing varieties/hybrids resistant to tomato leaf curl virus, Heat tolerance, and all these traits together as Tomato leaf curl virus + Heat tolerance+ superior fruit quality traits, *Solanum chilense* for Tomato leaf curl virus and varieties /hybrids like Pusa Tomato hybrid-6, Arka Abhed, Kashi Aman, PVB-4,Pusa Cocktail Tomato, Pusa Prasanskrit, Pusa Cherry Tomato Hybrid-1 were developed, *Solanum peruvianum* is also being utilized to address the problem of Root-knot nematode.

In potatoes, resistance to late blight incorporated from wild species *Solanum demissum* and *S. stoloniferum* Schltdl. and Bche´is still effective in some areas. Presently, 40% of the total area covered by the most popular cultivars of potato in the United States has *S. demissum* in their ancestry (National Potato Council, 2003).

The anthracnose resistance genes from *C. baccatum* were introgressed in *C. annuum* gene pool through embryo rescue and resulted in anthracnose resistant *C. annuum* introgressed lines (Yoon *et al.*, 2006). Interspecific hybridization with *C. baccatum* var. *pendulum* has been used for the introgression of resistance gene(s) into cultivated chilli peppers (Kim *et al.,* 2010). Male sterile lines are developed through interspecific hybridzation between *C. chacoense* and *C. annuum* (Kumar et al., 2007). In onion, powdery mildew resistant cultivar was developed by introgressing resistance genes from wild onion species *A. roylei*.

This species is used as bridge species to introduce genes from *A. fistulosum* (welsch onion) into *A. cepa* genomes (Khrustaleva and Kik, 2000). Wild relatives of crop plants grow in natural habitat, hence require specific set of environmental conditions for characterization, evaluation and their multiplication. Due to genotype x environment interaction, characterization and evaluation of different crop species becomes difficult especially in perennial species. In view of this, *in situ* characterization during exploration and collection visit is a feasible option. There are National Active Germplasm Sites (NAGs) which preserve the germplasm of perennial, recalcitrant and vegetatively propagated crop species. The trait specific evaluation and multiplication of germplasm of vegetables and wild species could be done at national active germplasm site.

Interspecific crosses are widely used in cucurbits to transfer desirable characteristics from wild progenitors or related species to cultivated genotypes. Interspecific hybrids have been produced in *Cucurbita, Cucumis, Citrullus, and Luffa*. However, only interspecific hybridization of *Cucurbita* has been successfully utilized for crop improvement (Robinson and Decker-Walters, 1997). In order to transfer certain desirable characters of one cultivated species to another *Cucurbita lundelliana* Bailey has been used as a bridge species (Rhode, 1959). *Cucurbita moschata* was also used as a bridge to transfer disease resistance (powdery mildew and cucumber mosaic virus), good fruit quality and insect resistance from *C. martinezii* to *C. pepo* (Whitaker and Robinson, 1986).

For enhanced fruit quality, cultivar 'Tetsukabuto' was developed which is an interspecific hybrid between C. maxima cv. 'Delicious' and C. moschata cv. 'Kurokawa no. 2' (Robinson and Decker-Walters, 1997). *Citrullus mucosospermus*, a close relative of *C. lanatus*, is native to west Africa and has a modified fleshy mucilaginous seed coat that becomes paper-thin when dried. The thin seed coat makes it easier to de-hull the seed. In China, specific varieties of watermelon have been bred for edible seeds (Levi *et al.,* 2017). The edible-seed watermelons can grow on marginal land and are drought tolerant, with small thin leaves, thin vines, and a large number of branches. Wild species such as *C. amarus* and *C. mucosospermus*, are valuable sources of resistance to many diseases and are crossable with *C. lanatus*, with variable fertility (Dhillon *et al.,* 2017; Levi *et al.,* 2017).

There are some multi-resistant accessions that have been deeply studied, such as the *C. mucosospermus* PI 595203 (readily crossable to watermelon) that display recessive resistance to the three potyviruses, ZYMV, WMV, and PRSV, which are most damaging to this crop, and the *C. amarus* PI 244019 (MartínHernández and Picó, 2021). In *Cucumis*, an amphidiploid was reported from the cross of *C. anguria L. and C. dipsaceus* E. ex S. (Yadava *et al.,* 1986). The cross made between cucumber and *C. hystrix* Chakr. (2n = 24) was the first repeatable cross between a cultivated *Cucumis* species and a wild relative (Chen *et al.,* 1997), and represented a breakthrough in interspecific hybridization in *Cucumis*.

The crosses of melon and cucumber genotypes with *C. prophetarum* (2n=24), *C. hystrix* (2n=24), *C. muriculatus* (2n=24), *C. setosus* (2n=24), *C. indicus* (2n=20) and *C. silentvalleyii* (2n=24) were produced with varying degrees of success but fertile F_1 hybrid could not be recovered. However intra-specific crosses with wild/weedy forms both as maternal and paternal parents were highly successful and F_1, F_2 generations were advanced through selfing at Thrissur. Backcross progenies of respective cultivated melon with *C. melo* var. *agrestis* and *C. melo* var. *callosus* and cucumber with *C. sativus* var. *hardwickii* were also produced. Under field epiphytotic conditions lines resisting aphid infestation, fruit rot, anthracnose and downy mildew were selected. *C. melo* var. *callosus* has high drought tolerance, high shelf life and bacterial fruit rot resistance but all F_1 and F_2 plants produced bitter fruits.

The wild melon *C. melo* var. *agrestis* (IC 539841) identified for prolificacy, non-bitterness and high rainfall tolerance has contributed to prolificacy, reduced fruit size and non-cracking skin in snap melon, musk melon and oriental pickling melon genotypes. The non-bitter fruity scented *C. melo* var. *agrestis* (Kachiri, JJK/03-1) was also used in crosses with cultivated melon groups for broadening the genetic base. The cross derivatives are conserved in the MTS for further field screening and utilization by breeders.

Extensive efforts made at Central Horticultural Experiment Station (ICAR-IIHR), Bhubaneswar and ICAR-NBPGR Regional Station, Thrissur have led to the development of fertile hybrids among *Momordica dioica, M. cochinchinensis*, and *M. subangulata* subsp. *renigera* through backcross and ploidy manipulation. The inter-specific hybrid (*M. suboica*) developed between *M. dioica* and *M. subangulata* subsp. *renigera* through ploidy manipulation and hybridization represents an important step in inter-specific hybridization in this genus. Fertile backcross progenies were also produced from inter-specific hybrids (*M. subangulata* subsp. *renigera* × M. *dioica*; *M. dioica* × *M. cochinchinensis*) by backcrossing the F_1 with the female parent. Movement of genes responsible for adventitious root character from *M. subangulata* subsp. *renigera* to *M. dioica* (for improved propagation efficiency), extended cropping period from *M. cochinchinensis* to *M. dioica* (for off season availability) through hybridization have been made possible.

Recently a new synthetic species (*M. suboica*; 2n=56) has been developed by crossing natural tetraploid *M. subangulata* subsp. *renigera* (2n=56) with induced tetraploid *Momordica dioica* (2n=4x=56). *M. suboica*, an autoallo polyploid can be propagated easily through root cutting, set fruits naturally (>60% fruit set), has extended harvesting period and gives higher yield. Bharathi *et al.* (2010, 2011) obtained successful hybrids between *M. cochinchinensis* and *M. subangulata* subsp. *renigera* while Mondal *et al.* (2006) reported complete incompatibility between these two species.

Wild relatives of *Phaseolus* are currently being screened for resistances to web blight, rust, white mold, bean golden yellow mosaic, bruchids, and seed storage insects (Singh 2001; Gallepo 1988). Very few examples of wild relatives conferring genetic resistance to abiotic stresses in crops have reached to the stage of cultivar release although many wild relatives with potential have been described (Shannon 1997). In general, the crop wild relatives do not have high yield potential compare to improved crop varieties, so they are rarely used in crop improvement programs for increasing yield in modern cultivars.

The CMS system has been used in commercial F_1 hybrid seed production in *Brassica. oleracea* using an improved 'Ogura' cytoplasm (Pelletier *et al,* 1989). Alteration in the contents of quality traits have been observed in cauliflower cybrids introgression with ogura cytoplasm (Dey *et al.,* 2017). Other improved 'Ogura' cytoplasms'Ogura' cytoplasms are available in *B. oleracea* as well as in vegetable B. *rapa*.

The wild species of cucumbers *Cucumis hardwickii* and *C. callosus* have resistance to downy mildew and fruit fly, *Cucumis melo* var. *chito* for fusarium wilt. The lack of useful genetic information and fertility barriers, lots of genes present in wild species are still unused. Scientists, from all over the world have argued that breeders were not fully exploiting the full potential of CWR. New records of endangered species *Cucumis silentvalleyi* (Anaimalai Hills in TN), and *Piper ribesioides* from Middle Andaman have been recorded (Ahlawat and Pardeep, 2018). Similarly, new wild relatives have been described from westerm ghats *Momordica sahyadrica such as Curcuma amada* var. *glabra* (Kerala), *Curcuma longa* var. *vanaharidra, A. enbeepeegearense* and *A. palianus (Jharkhand)* in Okra. Therefore, there is an urgent need to develop a set of core collection in important vegetable crops having a large number of accessions so that the entire genetic diversity is captured and managed effectively.

FUTURE PROSPECTS

The global challenge of food security due to climate change highlights the importance of vegetable crop wild relatives (VCWRs) as a source of valuable traits which are lost during domestication. To conserve and utilize VCWRs effectively, national strategies for both *in situ* and *ex situ* conservation must be developed, including identifying priority taxa and establishing genetic reserves. GIS tools and gap analysis can aid in targeted germplasm collection, while studies on habitat ecology, breeding behavior, and seed storage will strengthen conservation efforts.

Engaging specialized scientists and forming dedicated research groups can enhance pre-breeding programs. Integrating modern technologies with conventional approaches will improve the identification and use of novel genes, contributing to climate-smart crop development and ensuring food and nutritional security.

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