

Review Paper:

Wild relatives: a treasure trove to improve crop plants to achieve sustainable crop production

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Abstract

Global food demand is expected to nearly double by 2050 due to an increase in the world's population. The green revolution has played a key role in the past century by increasing agricultural productivity worldwide, however, limited availability and continued depletion of natural resources such as arable land and water will continue to pose a serious challenge for global food security in the coming decades. High yielding varieties with proven tolerance to biotic and abiotic stresses, superior nutritional profiles and the ability to adapt to the changing environment are needed for continued agricultural sustainability. The narrow genetic base of modern cultivars is becoming a major bottleneck for crop improvement efforts and, therefore, the use of crop wild relatives (CWRs) is a promising approach to enhance genetic diversity of cultivated crops. They have great potential to combat future challenges and important source of the genes for breeding stress tolerant high yielding varieties as they have been evolving for thousands of years in adverse climatic conditions and possess a much higher degree of adaptability.

Plant breeders have utilised their genes to improve many cereals, grain legumes, oilseeds, fruits and vegetables through introgression and pre-breeding. The use of CWRs lags far behind its potential due to certain hindrances such as cross incompatibilities, infertility in the F1 and subsequent progeny, non-availability or poor conservation of CWRs, under-utilized and under-explored wild germplasm and the expression of desirable traits in cultivated genetic background. Therefore, CWRs has been utilized through advanced biotechnology and molecular breeding techniques.

Keywords: Wild relatives, crop production, sustainability, biodiversity.

Introduction

Crop wild relatives are wild plant that are closely related to crop species whose geographic origins can be traced to regions known as Vavilov Centers. They may be a wild ancestor of the domesticated plant, or another closely related taxon. Crop wild relatives (CWR) include the progenitors and wild or weedy relatives (primary gene pool) and

distantly related taxa, having potential for crop improvement (secondary and tertiary gene pools). Wild relatives have poor plant type, perennial and seed-shattering habit, long harvest period and low yielding. They are locally adapted and grow in diverse climatic conditions. Wild relatives are generally adapted to extreme environments.

Major efforts are underway to utilize them to develop climate resilient crops. Many of today's food crops bear no resemblance to their wild relatives. Domesticated crops have been substantially changed compared to their wild relatives including morphological, compositional and physiological modifications. These modifications made dramatic improvement in crop abundance, productivity and nutrition. Wild relatives possess tremendous genetic diversity. Important sources of 'new' genes are for wider adaptability, tolerance or resistance to disease, insect-pests, yield, quality attributes, sources of male sterility and abiotic traits. For centuries, crop wild relatives have provided farmers with the genetic material to improve the nutritional quality of crops, enhance productivity and provide cultivated varieties with resistance to pests and diseases.

Plant breeders utilize traits in CWR to improve crops. Climate change is predicted to bring about increased global temperature along with associated carbon dioxide (CO₂) increase, altered pattern of rainfall and salinity, emergence of new pest strains and diseases⁸⁶. These predicted climatic changes are expected to have fairly widespread impacts on agriculture for example, rice flowers show increased sterility at high temperatures, maize is very sensitive to drought at the time of flowering, wheat senescence starts earlier and faster under warmer conditions etc.⁴³.

To meet these challenges, plant breeders need all the genetic diversity available in the form of germplasm, landraces and wild or weedy forms. Some of the genetic diversity may be found in landraces, traditional/farmer's varieties that are still being cultivated by farmers around the world. The conservation of crop wild relatives has become even more critical during a period of climate change.

Increasing and evolving patterns of human food consumption, together with high rates of urbanization, pollution, unsustainable use of natural resources, spread of invasive species, displacement of local varieties and environmental changes are all threats to the world's rich and highly adapted plant genetic resources for food and agriculture (PGRFA). To prevent the loss of CWR and wild food plant diversity and to maximize their availability,

especially for crop improvement, there is an urgent need to ensure their appropriate conservation and sustainable use at the global, regional, national and local levels.

Harlan and de Wet’s genepool (GP) concept (1971):

Classify CWR species into primary, secondary and tertiary gene pools based on how easy it is to use them in breeding²⁴. Primary gene pool (GP1) consists of the taxa including cultivated, weedy and wild forms of a crop species. They are cross compatible and produce fertile hybrids. Secondary gene pool (GP2) includes all the taxa that will cross with the GP1- hybrids. These hybrids are usually sterile but with some fertility. Gene transfer is possible with some difficulties. Tertiary gene pool (GP3) consists of taxa that are distinctly related to the cultivated plants from which crossing is difficult and produces always non-viable embryos and sterile hybrids. Gene transfer is still possible with great difficulties due to strong barriers. Among them primary and secondary gene pools are the easiest to use in plant breeding²⁵.

Importance and Utilization of wild relatives in crop improvement:

Vavilov⁸⁹ first realized the importance of crop wild relatives in the early 20th century. CWRs have potential to contribute beneficial traits to crops or that are gathered for food or feed. CWRs retain high levels of genetic diversity compared to their domesticated descendants and a vital component of agricultural biodiversity (agrobiodiversity). A potential source of genes and alleles

for adapting crops is changing environmental conditions and human needs^{6,19}. CWRs determine the genetic relationship between the crop and its wild relatives. CWR were used in crop improvement in sugar cane in the first half of the 20th century. Their utility was recognized in breeding programs of major crops in the 1940s and 1950s⁶².

Recently significant advances have been made in molecular technologies and hybridization procedures available for breeding and cultivar development that allow for the incorporation of more distantly-related taxa. Farmers have used traditional breeding methods for millennia, wild maize (*Zea mexicana*) is routinely grown alongside maize to promote natural crossing and improve yields. Plant breeders have utilised these genes to improve many cereals, grain legumes, oilseeds, fruits and vegetables through two approaches i. e. gene introgression and pre-breeding³⁰.

Gene introgression: Introgression, also known as introgressive hybridization, is the movement of a gene (gene flow) from one species into the gene pool of another by the repeated backcrossing of an interspecific hybrid with one of its parent species. Introgression is an important source of genetic variation in natural populations and may contribute to adaptation. Introgressive hybridization has also been shown to be important in the evolution of domesticated crop species. Modern maize is postulated to have developed through introgressive hybridization between the primitive maize and wild grass, *Tripsacum*.

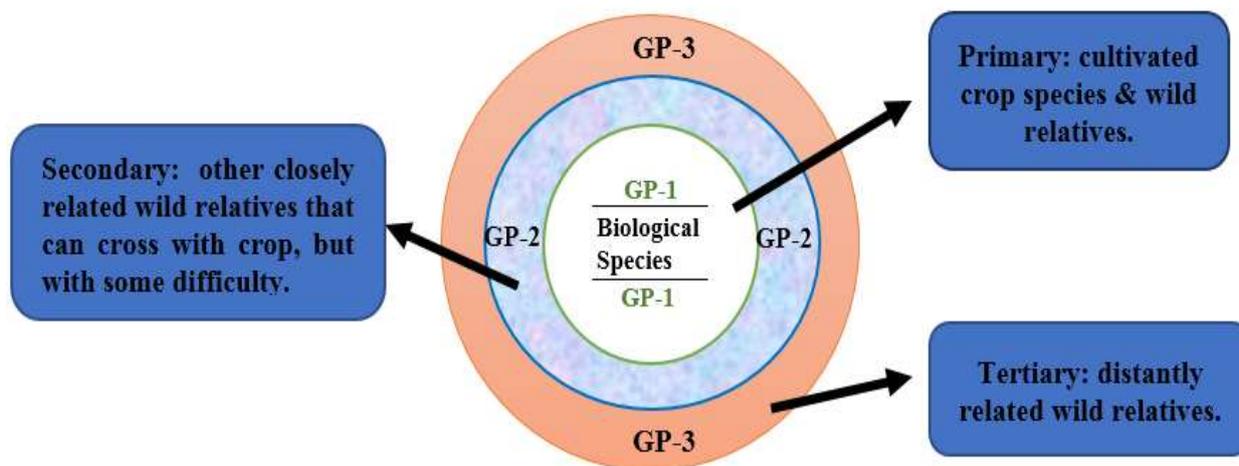


Table 1
Gene pool of some selected crops

Crop	GP1	GP2	GP3
Barley	<i>H.vulgare H.spontaneum</i>	<i>H.bulbosum</i>	<i>Hordeum spp.</i>
Wheat	<i>T.aestivum</i>	<i>Triticum spp., Aegilops, Secale, Thinopyrum</i>
Chickpea	<i>C.arietinum, C.reticulatum</i>	None	<i>C.bijugam, C.pinnatifidum</i>
Lentil	<i>L.culinaris</i>	None	<i>L.nigricans</i>
Sugarcane	<i>S.officinarum, S.barberi</i>	<i>Erianthus spp., Imperata spp.</i>	-----

Incompatibility barriers can be manifested in several ways: for example, poor pollen growth, embryo formation, hybrid viability and hybrid fertility can all inhibit use of wild relatives in hybridization programed^{1,15}. Embryo rescue, somatic hybridization, or protoplast fusion, has been successfully employed to make interspecific hybrids in many crops^{22,41}. Bridge crosses are other techniques that use an intermediary species, which is crossable with both parents, to indirectly transfer genes into the desired cultivated background⁹¹.

Pre-breeding: Breeders have also worked to recover some of the beneficial genetic diversity lost (or never included) during the domestication and crop improvement process by crossing cultivated varieties with wild species. Utilization of crop wild relatives (CWR) in crop improvement is much more difficult than breeding with domesticated varieties. Pre-breeding is an early phase of any breeding programme that utilizes wild germplasm and is also called as Developmental breeding or Germplasm enhancement.

This pre-breeding attempt to reset the genetic diversity of crops by reintroducing genetic variation has been left behind. Pre-breeding aims to isolate desired genetic traits (e.g. disease resistance) from unadapted material like CWR and introduce them into breeding lines that are more readily crossable with modern elite varieties. It broadens the elite gene pool by re-capturing lost beneficial genetic diversity that was not previously accessible either due to genetic incompatibilities or nonoverlapping geographic ranges^{10,14,60}.

Potential achievements of CWRs in crop improvement: The plant breeders have not fully exploited the potential of wild relatives as they depend on searching genes for beneficial traits associated with certain wild relatives rather than searching more generally for beneficial genes. Plant breeders prefer to use pre-breeding lines containing the desirable wild traits in domesticated genetic backgrounds. Major efforts have been concentrated primarily on use of

wild relatives in certain food crops such as wheat, rice, barley, tomato, soybean and mustard.

The use of wild relatives lags far behind its potential due to certain obstacles such as cross incompatibilities, infertility in the F₁ and subsequent progeny, under-utilized and under-explored wild germplasm, lack of faithful evaluation of data and the expression of desirable traits in cultivated genetic background. Accessibility of wild relatives resources to researchers and breeders is another important issue for crop improvement utilizing wild relatives. Many international collections such as International Center for Tropical Agriculture (CIAT), Crop Trust and Kew as well as National Gene Banks of respective countries, conserve a number of wild relatives (Table 2) and provide information on pre-breeding data, distribution and potentially useful traits.

Biotic stress resistance: Narrow genetic base has created genetic vulnerability of crop species to diseases and insect pest. Breeding for biotic stress resistance aims at maintaining productivity by reducing losses due to these insect pest. Resistant varieties offer the cheapest means of disease and insect control and mostly these resistant gene are found in wild relatives. It is estimated that wild relatives of cultivated crops conferred over 80% genes for the beneficial traits⁶¹. There are a number of examples of successful gene discovery and transfer of superior alleles from CWRs to domesticated crops despite a variety of difficulties in using CWRs. The CWRs along with their utilization traits have been summarized crop-group wise under following subheads:

Rice (*Oryza sativa*): Bacterial leaf blight has been one of the most widely distributed and detrimental rice disease worldwide. In 1990, the transfer of *Xa21* gene from wild rice (*O. longistaminata*) for resistance to bacterial blight in IR72 started the systematic use of wild rice gene pool. Wild rice, *O. rufipogon* has been used for blast resistant gene, *Pi33* introgression into rice variety IR64 which is the most used rice blast resistant variety⁷.

Table 2
World collections of wild relatives of important food crops

Crop	Wild relatives	Storage location
Rice	<i>Oryza rufipogon</i> , <i>O. officinalis</i> , <i>O. granulate</i>	Chinese Academy of agriculture Sciences, International Rice Research Institute
Wheat	<i>Triticum</i> , <i>Aegilops</i> , <i>Dasypyrum villosum</i>	The Wheat Genetics Resource Center
Barley	<i>Hordeum spontaneum</i> and other <i>Hordeum</i> wild species	International Barley Core Collection (300), USDA-ARS National Small Grains Collection
Soybean	<i>Glycine soja</i>	USDA Soybean Germplasm Collection, Chinese National Crop Genebank
Sorghum	23 wild sorghum species	International Crops Research Institute for the Semi-Arid Tropics
Tomato	Wild <i>Lycopersicon</i> and <i>Solanum</i> species	Tomato Genetics Resource Center
Potato	187 wild <i>Solanum</i> species	International Potato Center

Pi40 gene from *O. australiensis* conferred broad-pectrum durable resistance to blast. Other sources for blast resistant genes such as Xa23 (*O. rufipogon*); Xa27 (*O. minuta*); Xa29 (*O. officinalis*); Xa30, Xa38 (*O. nivara*); Xa34 (*O. brachyantha*) were reported by different scientist.^{16,103,104}

Sharma and Shastry incorporated grassy stunt virus resistant gene from *Oryza nivara* in most of the germplasm at International Rice Research Institute⁴⁰. Brown planthopper (Bph) resistance genes, Bph14 and Bph29 were introgressed from *O. officinalis* and *O. rufipogon* respectively^{72,83}.

Wheat (*Triticum aestivum*): Stem and leaf rust resistance were transferred from *Agropyron elongatum* and *Aegilops umbellulata* respectively. Leaf rust and stripe rust have been transferred from *T. monococcum* to bread wheat var. WL711 and one gene for leaf rust into PBW343 using marker assisted selection^{78,82}. *Ae. tauschii* has many leaf rust res. genes: *Lr21, Lr22a, Lr32, Lr37, Lr39, Lr41, Lr42* and *Lr43*. Among them *Lr34* provides durable resistance & presently used extensively in wheat improvement programme in India and worldwide. Resistance to Hessian fly in wheat derived from *Aegilops tauschii*¹⁰¹. *Aegilops tauschii* (D genome

progenitor) and *Triticum turgidum* ssp. *dicocoides* contribute for drought and salt tolerance also³⁸.

Maize (*Z. mays*): Teosinte (*Z. mays* ssp. *parviglumis* Itis and Doebley) and *Tripsacum* are two WRs that have been extensively characterized as donors of economically importance⁴⁵. Resistance genes were introduced against *Helminthosporium, Puccinia*, rootworm, drought and aluminum stress from *Tripsacum* and *Z. diploperennis* into cultivated maize³⁰. Blight and rootworm resistant genes were transferred from *Tripsacum dactyloides* into cultivated varieties⁶⁵.

Groundnut: Cultivated groundnut variety did not express resistance against groundnut tobacco armyworm (*Spodoptera litura*). *Arachis kempff* is a wild relative reported to be resistant to *S. litura* which is transferred through interspecific crosses into cultivated groundnut varieties.

Abiotic stress tolerance: Abiotic stresses are the primary source of yield losses as they reduce yield up to 20 per cent. Heat, drought and salinity are the main abiotic stresses.

Table 3
Improved traits in some important cereal crops for biotic and abiotic stresses using wild relatives

Crop	Wild Relative	Traits
Wheat ^{35,90,100}	<i>Triticum monococcum</i>	Heat tolerance Salt tolerance Powdery mildew resistance
Wheat ²³	<i>Agropyron elongatum</i>	Rust resistance
Rice ⁷	<i>Oryza rufipogon</i>	Blast resistance
Rice ⁵	<i>O. longistaminata</i>	Bacterial blight resistance, drought tolerance
Rice ⁷⁷	<i>O. glaberrima</i>	Weed competitiveness, drought tolerance and high yield
Barley ^{12,32,34}	<i>Hordeum spontaneum</i>	Severe salt and dehydration stress; aluminum tolerance; Fusarium resistance
Barley ^{20,79}	<i>H. bulbosum</i>	Resistance to powdery mildew and leaf rust
Maize ⁶⁵	<i>Tripsacum dactyloides</i>	Corn root-worm resistance

Table 4
Improved traits in legumes for abiotic and biotic stresses using wild relatives

Crop	Wild relative	Improved Traits
Soybean ⁶⁷	<i>Glycine soja</i>	Salt tolerance, Soybean cyst nematode resistance
Soybean ^{96,106}	<i>C. echinospermum, Cicer reticulatum</i>	drought tolerance and <i>Ascochyta</i> blight
Common bean ⁵³	<i>Arachis stenosperra</i>	Root-knot nematode resistance, drought tolerance
Peanut ^{2,47}	<i>A. duranensis, A. stenosperra</i>	Late leaf spot resistance
Peanut ⁴²	<i>Cajanus scarabaeoides</i>	Drought tolerance and Pod borer insect resistance
Pigeon Pea ⁸¹	<i>L. ervoides</i>	Anthracoze resistance

Table 5
Improved traits in vegetables for biotic and abiotic stresses using wild relatives

Vegetable crop	Wild species	Improved traits
Tomato ^{18,27,29,36,63,69,99,102}	<i>Solanum pimpinellifolium</i> <i>S.peruvianum</i> <i>S. pimpinellifolium</i> <i>S. chilense</i> , <i>S. habrochaites</i> <i>S. pimpinellifolium</i> <i>S. cheesmanii</i>	Bacterial wilt Bacterial spot Tomato leaf curl virus High lycopene content Salt tolerance
Brinjal ^{4,8,33,46,48}	<i>Solanum linnaeanum</i> <i>S. torvum</i> , <i>S.</i> <i>Sisymbriifolium</i> <i>S. indicum</i> , <i>S. violaceum</i> , <i>S. aethiopicum</i> , <i>S. incanum</i> <i>S. violaceum</i>	Verticillium wilt Powdery mildew Bacterial wilt Fruit and Shoot Borer Male sterility
Cucumber ^{11,57}	<i>Cucumis hystrix</i> <i>C. metuliferous</i>	Downy mildew Cucumber mosaic virus, Papaya ringspot virus,
Crucifer ⁶⁴	<i>Brassica tournefortii</i>	Cytoplasmic male sterility

Wild relatives those adapted to arid habitats are known to be rich in drought or salinity resistance attributes. IARI released 'BG1103' a drought and heat tolerance chickpea variety derived from *Cicer reticulatum* and is a leading cultivar (40% more yield) in Northern India. *Triticum dicoccoides* and *H. spontaneum* provide heat and drought tolerance in wheat and barley respectively⁵⁹.

Oryza rufipogon genes have been exploited for tolerance to high acidic-sulfate content soil in Vietnam⁵⁸. *O. longistaminata* genes for drought tolerance in cultivars of Philippines are allowing the spread of rice production to previously unusable lands⁵. In maize, Drought and Salinity tolerance genes were derived from Eastern gamagrass. Drought and heat tolerance in cotton were introgressed from *G. tomentosum*⁴⁶.

Higher productivity: At present, the yield reaches a plateau because the variability for yield in a crop species is exhausted almost. Wild relatives of cultivated species may provide yield genes for breaking yield plateau. Rice variety Dhanrasi, an example of improving yield potential and disease resistance is by introgressing gene (*Os11Gsk* and *Os12Mat*) from wild species (*Oryza rufipogon*)⁷¹. In chickpea, productivity enhancement related traits have been introgressed from *C. reticulatum*. *C. echinospermum* yield increased up to 39 per cent⁷⁴.

CMS or fertility restorers for use in producing hybrids: Genetic vulnerability arising due to wide spread use of a single CMS source can be overcome by using alternative CMS source. Wild relatives are the most common source of sterile cytoplasm.

In rice, male sterile cytoplasm was transferred from *O. spontanea* to nuclear genome of cultivated rice species. About 95% of the male sterile lines used in commercial rice hybrids were grown in China and other countries have WA type of cytoplasm⁹⁷. CMS based on using wild *Helianthus*

annuus and *H. petiolaris* has been used in high yielding commercial sunflower hybrids since 1972. Currently, 100% of sunflower production in the US and 60–70% of production worldwide is estimated to be from these hybrids. CMS and fertility restorer lines derived from *Pennisetum purpureum* Schum. were used in the first pearl millet grain hybrids and commercial forage hybrids²⁶.

In pigeonpea, six male sterile cytoplasm were reported by several scientists. These cytoplasm are such as A₁ cytoplasm from *C. sericeus*⁷³, A₂ cytoplasm from *C. scarabaeoides*⁷⁶, A₃ cytoplasm from *C. Volubilis*⁹⁵, A₄ cytoplasm from *C. Cajanifolius*⁵⁶, A₅ cytoplasm from *C. Cajan*⁵¹ and A₆ cytoplasm from *C. Lineatus*⁸⁰. ICPW 89 an Indian accession of *Cajanus scarabaeoides* (L.) Thouars, a wild relative of pigeonpea, was used to develop a CMS line ICPL 2039A.

Improvement in quality: In tomato, many classic examples of improved quality traits are from wild genes, from increased soluble solid content, fruit color and adaptation to harvesting. In wheat, cultivars having increased protein content were derived from *Triticum dicoccoides*²⁸.

Better grain quality synthetic hexaploid wheat cultivar Carmona⁷ (Spain) High protein and seed size breeding lines such as HPL 2, HPL 7, HPL 40 and HPL 51 were developed from pigeon pea wild relatives *C. sericeus*, *C. albicans* and *C. scarabaeoides*.

Enhanced Utilization of wild relatives through Advanced Biotechnology and Molecular Breeding: The present scenario of wild relatives shows that new emerging technologies of biotechnology enhance the utility of wild relatives in crop improvement e.g. transferring gene(s) of interest from wild to cultivated backgrounds with precision through advanced embryo rescue techniques, transgenic technologies, marker-assisted selection (MAS).

Table 6
Improvement in quality traits using wild relatives

Crop	Wild relative	Quality trait
Rice ⁹⁸	<i>O. glandiglumis</i>	Increased grain width and thickness.
Wheat ³⁷	<i>T. turgidum var.dicoccoides</i>	Grain protein content
Soybean ⁷⁵	<i>G. soja</i>	Protein content
Pigeonpea ⁶⁸	<i>C. scarabaeoides</i>	Protein content
Tomato ^{3,84}	<i>L. hirsutum</i> <i>L. pimpinellifolium</i>	Red color Fruit Size
Cotton ³⁷	<i>Gossypium thurberi</i> <i>G. raimondii</i>	Fibre length
Tobacco ⁵³	<i>Nicotiana debeneyi</i>	Leaf quality

Omics approaches: Omics technologies includes genomics, transcriptomics, proteomics and metabolomics have provided alternative opportunities for global analysis of regulatory genes, expressed proteins and metabolites regulating important traits in CWRs. High throughput next generation sequencing technology led to the discovery of single nucleotide polymorphisms (SNPs) and their association with important traits^{44,67,105}.

Combining the phenotypic data with genotypic data helps in identifying genes and discovering novel genomic regions underlying valuable agronomic traits in CWRs by association mapping. These omics approaches are particularly suitable for dissection of complex traits such as drought tolerance and pest resistance by characterizing CWRs under diverse treatments e.g. dehydrin genes in both wild barley (*H. spontaneum*) and wild tomato (*S. chilense* and *S. peruvianum*) and ABA/water stress/ripening induced (Asr) gene family members (Asr2 and Asr4) from wild Solanum species are known to be involved in drought tolerance²¹.

It is also feasible to transfer an appropriate metabolic pathway from CWRs into cultivated plant species to increase resistance against biotic stress e.g. terpenoid biosynthetic pathway in wild tomato to cultivated one⁹.

Genome modification: Genome modification technology used to transfer target genes to crop cultivars has been considered a revolutionary technique to produce transgenic crops with desired traits. Another approach is induced mutagenesis in existing genes rather than introduction of new genes. This includes cisgenesis, intragenesis, genome editing and RNA-dependent DNA methylation. Cisgenesis has been successfully used to confer late blight resistance in potatoes³¹ and scab resistance in apples⁹³ through transfer of single desired gene from native or cross compatible species. These approaches avoid linkage drag and achieve in less time compared with traditional breeding.

Threats to CWRs: CWRs are increasingly subject to a wide range of threats, some of which are anthropogenic i.e. they

are linked to human activities. Some of the key factors threatening the existence and diversity of CWR are:

- i. Unsustainable use of natural resources including over-exploitation and excessive use or extraction of wild plants for timber, fuel, feed etc.
- ii. Habitat conversion for agricultural production, industrial development or urban expansion.
- iii. Habitat destruction, degradation, homogenization and fragmentation.
- iv. Climate change, changes in agricultural practices and land use.
- v. Introduction of exotic species (other plants, animals or microorganisms) that compete with, hybridize with cause physical or biological damage to, or kill native species.
- vi. Natural calamities such as, floods, landslides and soil erosion.

FAO estimated that about 75% of the genetic diversity of agricultural crops has been lost in the last century due to the widespread abandonment of genetically diverse traditional crops in favour of genetically uniform modern crop varieties. Crop domestication and improvement can be described as a process of successive rounds of selection that ultimately results in the isolation of genetic diversity valuable to agriculture from ancestral wild species. These successive rounds of selection have resulted in the crops that feed the world today, but at the cost of reducing their genetic variation leaving them with less allelic diversity than their wild progenitors and other crop wild relatives (CWR)^{70, 92}.

This is often referred to as “domestication bottleneck”⁸⁵. The reduction in genetic diversity during domestication is exacerbated by the demand for high crop productivity and crop uniformity in the field and the marketplace.

Conservation of CWRs: A systematic, wise conservation and use of CWRs involves crop improvement, increasing food security, eliminating poverty and maintaining the environment⁸⁵. Crop wild relatives thrive in their natural habitats without human intervention. In fact, they are continuously evolving adaptive characteristics that enable

them to cope with changing environmental conditions. Therefore, they are a rich reservoir of novel traits and genes that can be used to develop crop varieties that are adapted to climate change. There is ample evidence of their successful use in crop improvement. Only 2–10% of global gene bank collections comprise CWR accessions and that these samples only represent a very small proportion of global CWR species⁵². Conservation strategies for CWRs often consider both *in situ* and *ex situ* conservation⁸⁷.

***In situ* conservation:** It involves the maintenance and recovery of populations of crop wild relative species in their natural surroundings and is necessary to ensure their continued evolution in the field including the natural exchange of genes with each other and their cultivated cousins. Conservation takes place in Protected Areas (PAs) known as natural park, biosphere reserve or gene sanctuary and the conservation can target either the populations themselves or the full ecosystems in which they occur. Biosphere Reserve in Jalisco, Mexico, which preserves the endemic maize relative to *Zea diploperennis*, Biosphere Reserve in Armenia, which helps to conserve a number of wild wheat relatives and other wild cereal species, Gene sanctuary in Meghalaya for Citrus etc. Biosphere reserves in India are Nanda Devi (UP), Sundarbans (WB), Gulf of Mannar (TN), Nilgiri (TN), Great Nicobar (A and N islands) etc.

***Ex situ* conservation:** *Ex situ* conservation of crop wild relatives which means protecting them outside of their natural habitats is essential both to prevent the loss of CWR genetic diversity and to facilitate the use of their diversity in crop breeding. Crop wild relatives are held *ex situ* in national crop diversity collections, international genebanks such as those of the CGIAR, the Millennium Seed Bank and the Svalbard Global Seed Vault. NBPGR houses the Indian National Genebank and maintains crop wild relatives in seed banks, field banks, as slow-growth cultures and as cryopreserved accessions (*in-vitro* genebanks). Examples of *in-vitro* genebanks are CIAT (cassava) and IITA, CIP (potato). Among these techniques, *Seed genebanks* predominates as the most practical *ex situ* conservation technique for many plant species.

Conclusion

Crop wild relatives support the genetic improvement of crops in multiple ways. To cope with problems arising from intensive modern agriculture and changing climate scenario, it is essential to utilize genetic diversity within crop wild gene pools. Intense pre-breeding to widen the genetic base of the crops coupled with priorities evaluation of major genes with marker system should be developed to further enhance the utilization of CWRs in breeding programme. Improved technologies especially genomics assisted breeding are facilitating the plant breeders to deal with the problem of linkage drag and incompatibility barriers while dealing with CWRs. Therefore, plant breeders have to work closely with genetic engineers to develop new cultivars.

Under the assumption that a vast reservoir of beneficial alleles for crop improvement exist in the wild gene pool, the continued development and implementation of strategies for the efficient utilization and conservation of these resources are underway.

References

- Andersson M.S. and Vicente, Gene flow between crops and their wild relatives, *Evol. Appl.*, **3**, 402–403 (2010)
- Burow M.D., Simpson C.E., Paterson A.H. and Starr J.L., Identification of peanut (*Arachis hypogaea* L.) RAPD markers diagnostic of root-knot nematode (*Meloidogyne arenaria* (Neal Chitwood) resistance, *Mol. Breed.*, **2**, 369–379 (1996)
- Bernacchi D., Beck-Bunn T., Eshed Z., Lopez J., Petiard V., Uhlig J., Zamir D. and Tanksley S., Advanced backcross OTL analysis in tomato and identification of QTL for traits of agronomic importance from *Lycopersicon hirsutum*, *Theor Appl Genet.*, **97**, 381–397 (1998)
- Behera T.K. and Singh G., Studies on resistance to shoot and fruit borer (*Leucinodes orbonalis*) and interspecific hybridization in eggplant, *Indian J. Hort.*, **59**, 62–66 (2002)
- Brar D., Broadening the gene pool and exploiting heterosis in cultivated rice, In Rice is life: Scientific perspectives for the 21st century, Toriyama K., Heong L. and Hardy B., eds., Proceedings of the World Rice Research Conference November, 2004, Tokyo and Tsukuba, Japan, 4–7 (2005)
- Biodiversity International, Crop wild relatives, Biodiversity International, Rome (2006)
- Ballini E., Berruyer R., Morel J.B., Lebrun M.H., Nottoghem J.L. and Tharreau D., Modern elite rice varieties of the ‘Green Revolution’ have retained a large introgression from wild rice around the Pi33 rice blast resistance locus, *New Phytologist*, **175**, 340–350 (2007)
- Bubici G. and Cirulli M., Screening and selection of eggplant and wild related species for resistance to *Leveillula taurica*, *Euphytica*, **164**, 339–45 (2008)
- Bleeker P.M., Mirabella R., Diergaarde P.J., VanDoorn A., Tissier A., Kant M.R. and Schuurink R.C., Improved herbivore resistance in cultivated tomato with the sesquiterpene biosynthetic pathway from a wild relative, *PNAS USA*, **109**, 20124–20129 (2012)
- Cooper H.D., Spillane C. and Hodgkin T., Broadening the genetic base of crop production, CAB International, Wallingford (2001)
- Chen J.F., Chen L.Z., Zhuang Y., Chen Y.G. and Zhou X.H., Cucumber breeding and genomics: Potential from research with *Cucumis hystris*, In Pitrat M., ed., Proceedings of the IX EUCARPIA meeting on genetics and breeding of Cucurbitaceae, INRA, Avignon, France, 95–100 (2009)
- Cai S., Wu D., Jabeen Z., Huang Y., Huang Y. and Zhang G., Genome wide association analysis of Aluminum tolerance in cultivated and Tibetan wild barley, *PLoS ONE*, **8**, 69776 (2013)

13. Dreisigacker S., Kishii M., Lage J., Warburton M., Calderini D. and Ortiz-Monasterio I., Use of synthetic hexaploid wheat to increase diversity for CIMMYT bread wheat improvement, *Aust. J. Agric. Res.*, **59**, 413–420 (2008)
14. Dwivedi S.L., Upadhyaya H.D., Stalker H.T., Blair M.W., Bertioli D.J., Nielen S. and Ortiz R., Enhancing crop gene pools with beneficial traits using wild relatives, *Plant Breed. Rev.*, **30**, 179–230 (2008)
15. Dempewolf H., Baute G., Anderson J., Kilian B., Smith C. and Guarino L., Past and future use of wild relatives in crop breeding, *Crop Science*, **57**, 1070–1082 (2017)
16. Ellur R.K., Khanna A., Bhowmick P.K., Vinod K., Nagarajan M. and Mondal K.K., Marker-aided incorporation of Xa38, a novel bacterial blight resistance gene, in PB1121 and comparison of its resistance spectrum with xa13+ Xa21, *Sci. Rep.*, **6**, 29188 (2016)
17. FAO, The State of the World's Plant Genetic Resources for Food and Agriculture, FAO, Rome (1998)
18. Fernandez-Ruiz V., Sanchez-Mata M.C., Camara M., Torija M.E., Rosello S. and Nuez, F., Lycopene as a bioactive compound in tomato fruits. Symposium on Dietary Phytochemicals and Human Health, The Phytochemical Soc. of Europe. Salamanca, 193–194 (2002)
19. FAO, Establishment of a global network for the in situ conservation of crop wild relatives: status and needs, FAO, Rome (2008)
20. Friedt W., Horsley R.D., Harvey B.L., Poulsen D.M.E., Lance R.C.M., Ceccarelli S., Grando S. and Capetini F., Barley breeding history, progress, objectives and technology, In Ullrich S.E., ed., Barley: production, improvement and uses, Oxford, UK, Wiley-Blackwell, 160–220 (2011)
21. Fischer I., Steige K.A., Stephan W. and Mboup M., Sequence evolution and expression regulation of stress- responsive genes in natural populations of wild tomato, *PLoS ONE*, **8**, e78182 (2013)
22. Glimelius K., Fahleson J., Landgren M., Sjodin C. and Sundberg E., Gene transfer via somatic hybridization in plants, *Trends Biotechnol.*, **9**, 24–30 (1991)
23. Gupta S.K., Charpe A., Koul S., Haque Q.M.R. and Prabhu K.V., Development and validation of SCAR markers co-segregating with an *Agropyron elongatum* derived leaf rust resistance gene *Lr24* in wheat, *Euphytica*, **150**, 233–240 (2006)
24. Harlan J.R. and de Wet J.M.J., Toward a rational classification of cultivated plants, *Taxon*, **20**, 509–517 (1971)
25. Harlan J.R., Genetic resources in wild relatives of crops, *Crop Sci.*, **16**, 329–333 (1976)
26. Hanna W.W., Characteristics and stability of a new cytoplasmic-nuclear male sterile source in pearl millet, *Crop Sci.*, **29**, 1457-1459 (1989)
27. Hanson P.M. et al, Diallel analysis of bacterial wilt resistance in tomato derived from different sources, *Plant Dis.*, **82**, 74–78 (1998)
28. Hoisington D., Khairallah M., Reeves T., Ribaut B., Skovmand S. and Warburton M., Plant genetic resources: what can they contribute toward increased crop productivity?, *PNAS*, **96**, 5937-5943 (1999)
29. Hanson P.M., Bernacchi D., Green S., Tanksley S.D., Muniyappa V., Padmaja A.S., Chen H.M., Kuo G., Fang D. and Chen J.T., Mapping a wild tomato introgression associated with Tomato yellow leaf curl virus resistance in a cultivated tomato line, *J. Am. Soc. Hort. Sci.*, **125**, 15–20 (2000)
30. Hajjar R. and Hodgkin T., The use of wild relatives in crop improvement: a survey of developments over the last 20 years, *Euphytica*, **156**, 1–13 (2007)
31. Haverkort A.J., Struik P.C., Visser R.G.F. and Jacobsen E., Applied biotechnology to combat late blight in potato caused by *Phytophthora infestans*, *Potato Res.*, **52**, 249–264 (2009)
32. Huang Y., Millett B.P., Beaubien K.A., Dahl S.K., Steffenson B.J., Smith K.P. and Muehlbauer G.J., Haplotype diversity and population structure in cultivated and wild barley evaluated for *Fusarium* head blight responses, *Theor. Appl. Genet.*, **126**, 619–636 (2013)
33. Isshiki S. and Kawajiri N., Effect of cytoplasm of *Solanum violaceum* Ort, On fertility of eggplants (*Solanum melongena* L.), *Sci. Hort.*, **93**, 9–18 (2002)
34. James V.A., Neibaur I. and Altpeter F., Stress inducible expression of the DREB1A transcription factor from xeric, *Hordeum spontaneum* L. in turf and forage grass (*Paspalum notatum* Flugge) enhances abiotic stress tolerance, *Transgenic Res.*, **17**, 93–104 (2008)
35. James R.A., Blake C., Byrt C.S. and Munns R., Major genes for Na⁺ exclusion, *Nax1* and *Nax2* (wheat HKT1; 4 and HKT1;5), decrease Na⁺ accumulation in bread wheat leaves under saline and waterlogged conditions, *J. Exp. Bot.*, **62**, 2939–47 (2011)
36. Kasrawi M.A., Inheritance of resistance to tomato yellow leaf curl virus (TYLCV) in *Lycopersicon pimpinellifolium*, *Plant Dis.*, **73**, 435–437 (1989)
37. Kunert A., Naz A.A., Dedeck O., Pillen K. and Leon J., AB-QTL analysis in winter wheat: I. Synthetic hexaploid wheat (*T. turgidum* ssp. *dicoccoides* x *T. tauschii*) as a source of favourable alleles for milling and backing quality traits, *Theor. Appl. Genet.*, **115**, 683- 695 (2007)
38. Krugman T., Peleg Z., Quansah L., Chagué V., Korol A.B., Nevo E., Saranga Y., Fait A., Chalhoub B. and Fahima T., Alteration in expression of hormone-related genes in wild emmer wheat roots associated with drought adaptation mechanisms, *Funct. Integr. Genom.*, **11**, 565–583 (2011)
39. Kaur V., Role of crop wild relatives in crop improvement under changing climatic conditions, *Crop Improvement for Sustainability*, 13-35 (2018)
40. Leung H., Hettel G.P. and Cantrell R.P., International Rice Research Institute: Roles and challenges as we enter the genomics era, *Trends Plant Sci.*, **7**, 139-142 (2002)

41. Liu J., Xu X. and Deng X., Intergeneric somatic hybridization and its application to crop genetic improvement, *Plant Cell Tissue Organ Cult.*, **82**, 19–44 (2005)
42. Leal-Bertioli S.C., José A.C., Alves-Freitas D.M., Moretzsohn M.C., Guimarães P.M., Nielen S., Vidigal B.S., Pereira R.W., Pike J. and Fávero A.P., Identification of candidate genome regions controlling disease resistance in *Arachis*, *BMC Plant Biol.*, **9**, 112 (2009)
43. Lobell D.B., Sibley A. and Ivan Ortiz-Monasterio J., Extreme heat effects on wheat senescence in India, *Nature Climate Change*, **2**, 186–189 (2012)
44. Li Y.H., Zhou G.Y., Ma J.X., Jiang W.K., Jin L.G., Zhang Z.H. and Qiu L.J., *De novo* assembly of soybean wild relatives for pan-genome analysis of diversity and agronomic traits, *Nature Biotechnol.*, **32**, 1045–1052 (2014)
45. Li F., Fan G., Lu C., Xiao G., Zou C. and Kohel R.J., Genome sequence of cultivated Upland cotton (*G. hirsutum* TM-1) provides insights into genome evolution, *Nat. Biotechnol.*, **33**, 524–530 (2015)
46. Liu J., Zheng Z.S., Zhou X.H., Feng C. and Zhuang Y., Improving the resistance of eggplant (*Solanum melongena*) to *Verticillium* wilt using wild species *Solanum linnaeanum*, *Euphytica*, **201**, 463–469 (2015)
47. Leal-Bertioli S.C., Moretzsohn M.C., Roberts P.A., Ballén-Taborda C., Borba T.C., Valdisser P.A., Vianello, R.P., Araújo A.C.G., Guimarães P.M. and Bertioli D.J., Genetic mapping of resistance to *Meloidogyne arenaria* in *Arachis stenosperma*: A new source of nematode resistance for peanut, *G3: Genes Genomes Genetics*, **6**, 377–390 (2016)
48. Mian I.H., Ali M. and Akhter R., Grafting on *Solanum* rootstocks to control root-knot of tomato and bacterial wilt of eggplant, *Bull. Inst. Trop. Agric., Kyushu. Univ.*, **18**, 41–47 (1995)
49. Miller T.E., Iqbal N., Reader S.M., Mahmood A., Cant K.A. and King I.P., A cytogenetic approach to the improvement of aluminum tolerance in wheat, *New Phytol*, **137**, 93–98 (1997)
50. Matsuoka Y., Vigouroux Y., Goodman M.M., Sanchez J., Buckler E. and Doebley J., A single domestication for maize shown by multilocus microsatellite genotyping, *Proc. Natl. Acad. Sci.*, **99**, 6080–6084 (2002)
51. Mallikarjuna N. and Saxena K.B., A new cytoplasmic-nuclear male sterility system derived from cultivated pigeonpea cytoplasm, *Euphytica*, **142**, 143-148 (2005)
52. Maxted N. and Kell S.P., Establishment of a global network for the *in situ* conservation of crop wild relatives: Status and needs, Commission on Genetic Resources for Food and Agriculture, FAO, Rome (2009)
53. Mkwaila W. et al, Identification of QTL for agronomic traits and resistance to white mold in wild and landrace germplasm of common bean, *Plant Breed*, **130**, 665–672 (2011)
54. Maxted N., Magos Brehm J. and Kell S., Resource book for preparation of national conservation plans for crop wild relatives and landraces, Section Context 1.5 (2013)
55. Mammadov J., Wild relatives of maize, rice, cotton and soybean: treasure troves for tolerance to biotic and abiotic stresses, *Frontiers in Plant Science*, **9**, doi: 10.3389/fpls.2018.00886 (2018)
56. Mallikarjuna N., Saxena K.B. and Jadhav D.R., Cajanus, In Kole C., ed., Wild crop relatives: Genomics and breeding resources, Legume Crops and Forages, Springer-Verlag, Berlin, Heidelberg, 21-33 (2011)
57. Norton J.D. and Granberry D.M., Characteristics of progeny from interspecific cross of *Cucumis melo* L. with *C. metuliferus* E. Mey, *J. Amer. Soc. Hort. Sci.*, **105**, 174–180 (1980)
58. Nguyen B.D., Brar D.S., Bui B.C., Nguyen T.V., Pham L.N. and Nguyen H.T., Identification and mapping of the QTL for aluminum tolerance introgressed from the new source, *O. rufipogon* Griff., into indica rice (*O. sativa* L.), *Theor. Appl. Genet.*, **106**, 583–593 (2003)
59. Nevo E. and Chen G., Drought and salt tolerance in wild relatives for wheat and barley improvement, *Plant, Cell and Environment*, **33**, 670-685 (2010)
60. Ogonnaya F.C., Abdalla O., Mujeeb-Kazi A., Kazi A.G., Xu S.S. and Gosman N., Synthetic hexaploids : Harnessing species of the primary gene pool for wheat improvement, *Plant Breed. Rev.*, **37**, 53-122 (2013)
61. Prescott-Allen C. and Prescott-Allen R., The first resource: Wild species in the North American economy, Yale Univ. Press, New Haven, CT (1986)
62. Plucknett D., Smith N., Williams J. and Murthi A.N., Gene Bank and the World's Food. Princeton University Press, Princeton, NJ (1986)
63. Pilowsky M. and Cohen S., Tolerance to tomato yellow leaf curl virus derived from *Lycopersicon peruvianum*, *Plant Dis.*, **74**, 248–250 (1990)
64. Pradhan A.K., Mukhopadhyay A. and Pental D., Identification of the putative cytoplasmic donor of a CMS system in *Brassica juncea*, *Plant Breed.*, **106**, 204–208 (1991)
65. Prischmann D.A., Dashiell K.E., Schneider D.J. and Eubanks M.W., Evaluating *Tripsacum*-introgressed maize germplasm after infestation with western corn rootworms (Coleoptera: Chrysomelidae), *J. Appl. Entomol.*, **133**, 10–20 (2009)
66. Porch T., Beaver J., Debouck D., Jackson S., Kelly J. and Dempewolf H., Use of wild relatives and closely related species to adapt common bean to climate change, *Agronomy*, **3**, 433–461 (2013)
67. Qi X., Li M.W., Xie M., Liu X., Ni M., Shao G., Song C., Yim A.K.Y., Tao Y. and Wong F.L., Identification of a novel salt tolerance gene in wild soybean by whole-genome sequencing, *Nat. Commun.*, **5**, 4340 (2014)
68. Reddy L.J., Green J.M., Singh U., Bisen S.S. and Jambunathan R., Seed protein studies on *Cajanus cajan*, *Atylos* spp. and some hybrid derivatives, In Seed Protein Improvement in Cereals and Grain Legumes, Proceedings of an International Symposium Jointly Organized by IAEA and FAO in Cooperation with GSF Neuherberg, 105-117 (1979)

69. Rick C.M., Germplasm resources in the wild tomato species, In EI-Bollagy A.S. and Pearson A.R., eds., Symposium Tomato Production in Arid Land, Cario, 7 (1986)
70. Ross-Ibarra J., Morrell P.L. and Gaut B.S., Plant domestication, a unique opportunity to identify the genetic basis of adaptation, Proc. Natl. Acad. Sci., **104**, 8641–8648 (2007)
71. Ram T., Majumdar N.D., Krishnaveni D. and Ansari M.M., Rice variety Dhanrashi, an example of improving yield potential and disease resistance by introgression gene(s) from wild species (*Oryza rufipogon*), *Curr Sci*, **92**, 987-992 (2007)
72. Ram T., Deen R., Gautam S., Ramesh K., Rao Y. and Brar D., Identification of new genes for brown planthopper resistance in rice introgressed from *O. glaberrima* and *O. minuta*, *Rice Genet. Newsl.*, **25**, 67–69 (2010)
73. Saxena K.B., Singh L., Kumar R.V. and Rao A.N., Development CMS System in pigeonpea at ICRISAT Asia Center. Proc. Working Group on CMS in Pigeonpea, ICRISAT, Patancheru, A.P., India, 32-50 (1996)
74. Singh K.B. and Ocampo B., Explanation of wild Cicer species for yield improvement in Chickpea, *Theor Appl Genet.*, **95**, 418-423 (1997)
75. Sebolt A., Shoemaker R. and Diers B., Analysis of a quantitative trait locus allele from wild soybean that increases seed protein concentration in soybean, *Cell Biol Mol Genet.*, **40**, 1438-1444 (2000)
76. Saxena K.B. and Kumar R.V., Development of a cytoplasmic-nuclear male sterility system in pigeonpea using *C. scarabaeoides* (L), *Thouars. Ind. J. Genet.*, **63**, 225-229 (2003)
77. Sarla N. and Mallikarjuna Swamy B.P., *Oryza glaberrima*: A Source for the Improvement of *Oryza sativa*, *Current Sci.*, **89**, 955–963 (2005)
78. Singh K., Chhuneja P., Ghai M., Kaur S., Goel R.K., Bains N.S., Keller B. and Dhaliwal H.S., Molecular mapping of leaf and stripe rust resistance genes, In Buck et al, eds., T. monoocum and their transfer to hexaploid wheat, Wheat production in stressed environment, Springer publication, 779-786 (2007)
79. Schmalenbach I., Korber N. and Pillen K., Selecting a set of wild barley introgression lines and verification of QTL effects for resistance to powdery mildew and leaf rust, *Theor Appl Genet.*, **117**, 1093-1106 (2008)
80. Saxena K.B., Sultana R., Mallikarjuna N., Saxena R.K., Kumar R.V., Sawargaonkar S.L. and Varshney R.K., Male sterility systems in pigeonpea and their role in enhancing yield, *Plant Breed.*, **129**, 125-134 (2010)
81. Saxena R.K., Cui X., Thakur V., Walter B., Close T.J. and Varshney R.K., Single feature polymorphisms (SFPS) for drought tolerance in pigeonpea (*Cajanus* spp.), *Funct. Integr. Genom.*, **11**, 651–657 (2011)
82. Sohail Q., Inoue T., Tanaka H., Eltayeb A.E., Matsuoka Y. and Tsujimoto H., Applicability of *Aegilops tauschii* drought tolerance traits to breeding of hexaploid wheat, *Breed. Sci.*, **61**, 347-357 (2011)
83. Sarao P.S., Sahi G.K., Neelam K., Mangat G.S., Patra B.C. and Singh K., Donors for resistance to brown planthopper *Nilaparvata lugens* (stal) from wild rice species, *Rice Sci.*, **23**, 219–224 (2016)
84. Tanksley S., Grandillo S., Fulton T.M., Zamir D., Eshed Y., Petiard V., Lopez J. and Beck-Bunn T., Advanced backcross QTL analysis in a cross between an elite processing line of tomato and its wild relative *L. pimpinellifolium*, *Theor Appl Genet.*, **92**, 213-224 (1996)
85. Tanksley S.D. and Mc Couch S.R., Seed banks and molecular maps: Unlocking genetic potential from the wild, *Science*, **277**, 1063–1066 (1997)
86. Tester M. and Langridge P., Breeding technologies to increase crop production in a changing world, *Science*, **327**, 818–822 (2010)
87. Taylor N.G., Kell S.P., Holubec V., Parra-Quijano M., Chobot K. and Maxted N., A systematic conservation strategy for crop wild relatives in the Czech Republic (PDF), *Diversity and Distributions*, **23**, 448–462 (2017)
88. Tullu A., Bett K., Banniza S., Vail S. and Vandenberg A., Widening the genetic base of cultivated lentil through hybridization of *Lens culinaris* “Eston” and *L. ervoides* accession IG72815, *Can. J. Plant Sci.*, **93**, 1037–1047 (2013)
89. Vavilov N.I., Studies in the origin of cultivated plants, Institute of Applied Botany and Plant Breeding, Leningrad (1926)
90. Vierling R.A. and Nguyen H.T., Heat-shock protein gene expression in diploid wheat genotypes differing in thermal tolerance, *Crop Sci.*, **32**, 370–377 (1992)
91. Van de Wiel C., Schaart J., Niks R. and Visser R., Traditional plant breeding methods, Rep. 338, Wageningen UR Plant Breeding, Wageningen, the Netherlands (2010)
92. Van Heerwaarden J., Doebley J., Briggs W.H., Glaubitz J.C., Goodman M.M., de Jesus Sanchez Gonzalez J. and Ross-Ibarra J., Genetic signals of origin, spread and introgression in a large sample of maize landraces, Proc. Natl. Acad. Sci., **108**, 1088–1092 (2011)
93. Vanblaere T., Szadkowski I., Schaart J., Schouten H., Flachowsky H., Broggin G.A.L. and Gessler C., The development of a cisgenic apple plant, *J. Biotechnol.*, **154**, 304-311 (2011)
94. Vikas V.K., Stem and leaf rust resistance in wild relatives of wheat with D genome (*Aegilops* spp.), *Genetic Resources and Crop Evolution*, **61**, 861–874 (2014)
95. Wanjari K.B., Patil A.N., Manapure P., Manjaya J.G. and Manish P., Cytoplasmic male sterility in pigeonpea with cytoplasm from *Cajanus volubilis*, *Ann. Plant Physiol.*, **13**, 170-174 (1999)
96. Winter S.M., Shelp B.J., Anderson T.R., Welacky T.W. and Rajcan I., QTL associated with horizontal resistance to soybean cyst nematode in *Glycine soja* PI464925B, *Theor. Appl. Genet.*, **114**, 461–472 (2007)
97. Yuan L.P., Advantages and constraints to use of hybrid rice varieties, In Wilson K.J., ed., Proc Int Workshop on Apomixis in Rice, The Rockefeller foundation New York and China National Centre for Biotechnology Development, Beijing, China, 1-4 (1993)

98. Yoon D.B., Kang K.H., Kim H.J., Ju H.G., Kwon S.J., Suh J.P., Jeong O.Y. and Ahn S.N., Mapping quantitative trait loci for yield components and morphological traits in an advanced backcross population between *Oryza grandiglumis* and the *O. sativa japonica* cultivar, *Theor Appl Genet.*, **112**, 1052-1062 (2006)
99. Yang W. and Francis D.M., Genetics and breeding for resistance to bacterial diseases in tomato: prospects for marker-assisted selection, In Razdan M.K. and Mattoo A.K., eds., *Genetic Improvement of Solanaceous Crops*, **2**, 379-419 (2007)
100. Yao G., Zhang J., Yang M.L., Xu H., Jiang Y., Xiong L., Zhang C., Zhang Z., Ma Z. and Sorrells M.E., Genetic mapping of two powdery mildew resistance genes in einkorn (*Triticum monococcum* L.) accessions, *Theor. Appl. Genet.*, **114**, 351-358 (2007)
101. Yumurtaci A., Utilization of wild relatives of wheat, barley, maize and oat in developing abiotic and biotic stress tolerant new varieties, *Emir. J. Food Agric.*, **27**, 1-23 (2015)
102. Zamir D., Michelson I.E., Zakay Y., Navot N., Zeidan M., Sarfatti M., Eshed Y., Harel E., Pleban T., van Oss H., Kedar N., Rabinowitch H.D. and Czosnek H., Mapping and introgression of a Tomato yellow leaf curl virus tolerance gene, *Ty-1*. *Theor. Appl. Genet.*, **88**, 141-146 (1994)
103. Zhang Q., Wang C., Zhao K., Zhao Y., Caslana V. and Zhu X., The effectiveness of advanced rice lines with new resistance gene *Xa23* to rice bacterial blight, *Rice Genet. Newslett.*, **18**, 71-72 (2001)
104. Zhang F. and Xie J., Genes and QTLs resistant to biotic and abiotic stresses from wild rice and their applications in cultivar improvements, *Rice-Germplasm, Genetics and Improvement*, Doi: 10.5772/56825, 59-78 (2014)
105. Zhou Z.K., Jiang Y., Wang Z., Gou Z.H., Lyu J., Li W.Y. and Tian Z.X., Resequencing 302 wild and cultivated accessions identifies genes related to domestication and improvement in soybean, *Nature Biotechnol.*, **33**, 408-414 (2015)
106. Zhang H., Li C., Davis E.L., Wang J., Griffin J.D., Kofsky J. and Song B.H., Genome-wide association study of resistance to soybean Cyst nematode (*Heterodera glycines*) HG type 2.5.7 in wild soybean (*Glycine soja*), *Front. Plant Sci.*, **7**, 1214 (2016).

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