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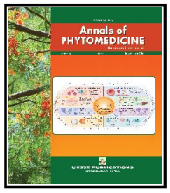

Review Article : Open Access

Harnessing the potential of wild relatives of Brassicaceae family for the crop improvement

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Abstract

The Brassicaceae family is essential for food security and human health because it comprises vital vegetables (cabbage, broccoli, and cauliflower) and oilseeds (mustard) that are high in vitamins, minerals, fibre, and health-promoting phytochemicals. These plants are essential oilseed crops that contribute greatly to the production of vegetable oil worldwide. The genetic diversity within cultivars has also decreased as a consequence of long-term selection of plants favouring yield attributes over many generations; as a result, these cultivars are more vulnerable to the effects of climate change as well as severity of biotic stress due to pests and diseases. By focusing on important characteristics like biotic and abiotic resistance or tolerance, enhanced nutritional quality, and utilizing the genetic variability found in its wild relatives within the Brassicaceae family. It is possible to solve the issue of food and nutritional security. This review discusses the commercially significant traits that have been found in the wild relatives of major and minor *Brassica* crops, the techniques used for introgression of traits into cultivars, and the challenges and potential benefits of using these wild relatives of *Brassica* crops for future crop improvement.

1. Introduction

The ongoing loss in biodiversity might have a detrimental effect on food and nutritional security. Natural variability provides resources to overcome challenges in food production, such as changes in the environment, pests, diseases, and limited land availability (Bélanger and Pilling, 2019). Traditional crop varieties can be improved and adapted to flourish in changing environments by understanding and conserving crop wild relatives, which contain a wealth of genetic variation (Dempewolf *et al.,* 2014; Eastwood *et al.,* 2022).Tolerance or resistance to biotic stresses like pest, diseases, and abiotic stressors like drought and salt are only a few examples of the desirable qualities that have lately been used in breeding programs to transfer to popular crops (Kilian *et al.,* 2021). Some of the most important crops and domesticated plants in the Brassicaceae family are members of the *Brassica* genus. The main crops and most economically important members of the *Brassica* family include turnips (*Brassica rapa* subsp. *rapa*), broccoli (*Brassica oleracea* var. *italica*), cabbage (*Brassica oleracea* var. *capitata*), mustard (*Brassica juncea* L. Czern.), and rapeseed (*Brassica napus* L.). A notable *Brassica* crop is oilseed rape, scientifically known as *B. napus,* which accounts for one-fifth of the world's edible oil production (Taylor *et al.,* 2018). *Xanthomonas campestris* pv. *campestris* (Xcc), the causative agent of black rot, is among the most important bacterial diseases impacting *Brassica* plants worldwide. There are nine different Xcc races, however the two most common and dangerous are races 1 and 4 (Tortosa *et al.,* 2018). The most common disease of Brassicaceae, soft rot, is caused by the highly pectinolytic bacteria *Pectobacterium carotovorum* (Pc) (formerly *Erwinia carotovora*) (Oskiera *et al.,* 2017). According to Saharan *et al*. (2016), the four species of *Alternaria* that are most commonly found in *Brassica* crops are: *Alternaria alternata, Alternaria brassicae, Alternaria brassicicola, and Alternaria raphani,* which are fungal diseases. The fungus *Sclerotinia sclerotiorum* (Ss) causes sclerotinia stem rot, a very dangerous disease. White blister rust disease in Brassicaceae is caused by *Albugo candida* (Ac), a biotrophic plant pathogen that is an oomycete infection (Cevik *et al.,* 2019). Insect pests known as aphids are a major problem for many crops across the world, especially those belonging to the *Brassica* family. *Lipaphis erysimi*, most often known as the mustard aphid or turnip aphid, is a notoriously damaging pest of *Brassica* plants, cutting yields by about half (Fening *et al.,* 2020). Lepidopteran diamondback moths, or *Plutella xylostella,* are the most destructive insect pests for *Brassica* crops. Similarly, the enormous white butterfly *Pieris brassicae*, sometimes known as the cabbage white butterfly, can do a lot of harm. Extreme heat, water shortages, and soil salt all contribute to drastically lower crop yields (Yadav *et al.,* 2020). In agriculture, several characteristics of these processes are required, including resilience to biotic diseases, ability to adapt or tolerate abiotic stresses, and improvement or enhancement of a genetic and functional attribute (Warwick, 2010). A decrease in genomic and local diversity has been seen as a consequence of domestication

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(Zhang *et al.,* 2017).The findings of CWR genomics provide credence to the notion of using crop wild relatives to enhance the genetic diversity of agricultural plants. Modern DNA sequencing techniques have made it possible to successfully sequence crop wild relatives, leading to their increased application in agricultural research and development (Brozynska *et al.,* 2016).

2. Brassicaceae family and its wild relatives

The Brassicaceae family of flowering plants has 3,709 species and 338 genera (Al-Shehbaz *et al.,* 2006; Warwick *et al.,* 2006). The mustard family or Cruciferae is another name for it. According to (Jaime *et al.,* 2018), mild-climate locations are ideal for growing *Brassica* crops. On roughly 40 million hectares, the most important crop in this genus is "rape or colza seed," which yields around 87 million tonnes of raw material, according to global data. "Cabbages," "cauliflowers," and "broccoli" are also widely cultivated. Species of the Brassiceae family exhibit a range of ploidy levels. 80% of these species fall between the n = 6 to n = 75 chromosomal count range (Warwick, 1993a). The herbaceous plants that make up this genus are thought to have their roots in the Mediterranean. Root vegetables (turnip, swede, rutabaga), stem vegetables (wasabi), leafy vegetables (pak choy, kale), spice crops (brown or black mustard), edible roots (radish), cooking oil (rapeseed) and cattle feed are common uses for *Brassica* crops (Rakow, 2004). The varied species of *B. oleracea* which encompasses kohlrabi, Brussels sprouts, cabbage, kale, broccoli, and cauliflower has long captivated the scientific community. Nevertheless, the evolutionary background of this species remains a mystery. Because it is possible to have such a wide variety of vegetables from just one species, *B. oleracea* is a great example of how artificial selection may work. The study of *B. oleracea* has long been plagued by two persistent problems the identification of the closest extant wild cousin and opposing ideas of domestication (Mabry *et al.,* 2021). It has been suggested that Chinese cabbage (*B. rapa* ssp. *pekinensis*) and other leafy vegetables may have originated in central China through a process of natural selection including hybridisation between turnip rape (*B. rapa* ssp. *oleifera)* and pak choi (*B. rapa* ssp. *chinensis),* as well as heading type (Li, 1981). The conventional wisdom holds that the six main species of *Brassica* may be systematically described using U's triangle (Nagaharu and Nagaharu, 1935). The natural allopolyploidization events in *Brassica* were described using three diploid species *(B. rapa, Brassica nigra,* and *B. oleracea*) and three derived allotetraploid species (*B. juncea*, *B. napus,* and *Brassica carinata*). This idea, which is called U's triangle, proved that polyploidization was crucial for the development of plant genomes. According to U's triangle, the diploid species *B. rapa* (AA, 2n = 2x = 20), *B. nigra* (BB, 2n = 2x = 16), and *B. oleracea* (CC, 2n = 2x = 18) gave rise to the three tetraploid species *B. juncea* (AABB genome, 2n = 4x = 36), *B. napus* (AACC, 2n = 4x = 38), and *B. carinata* (BBCC, 2n = 4x = 34) (Kim *et al.,* 2018).

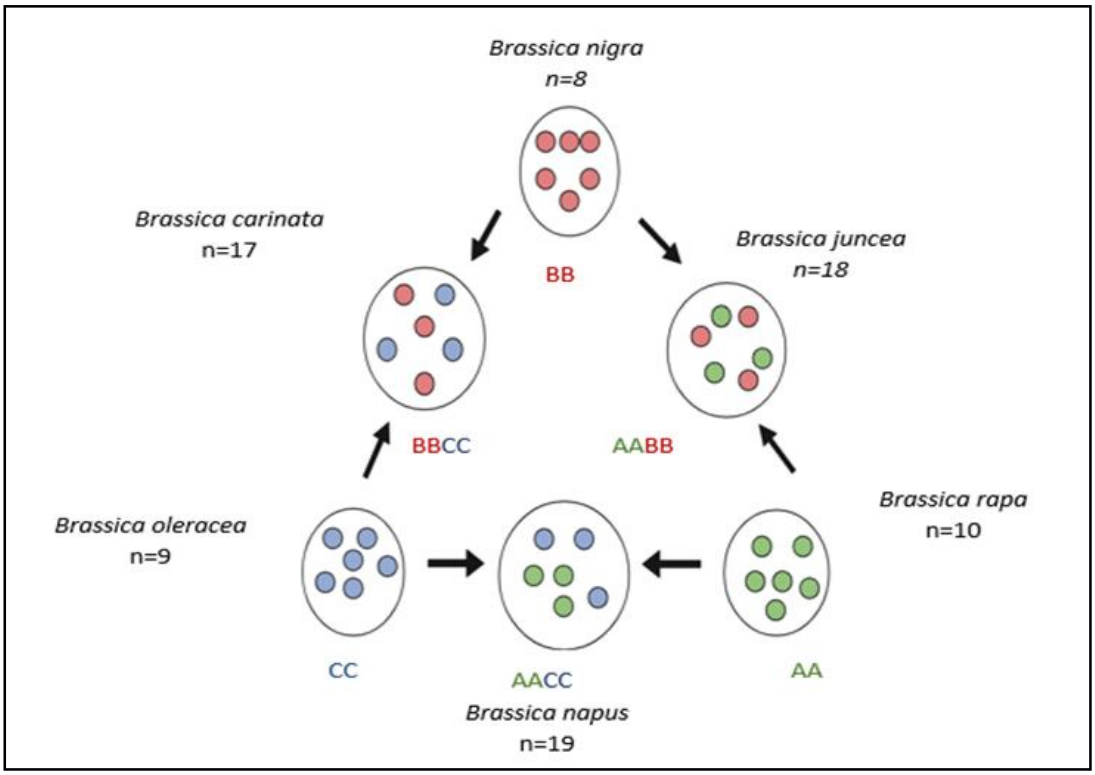

Figure 1: U Triangle showing evolutionary and genomic relationships in the genus *Brassica*.

3. Understanding wild relatives: A genetic source for breeding

Nevertheless, this category would include a vast array of species that might be either closely or distantly linked to the crop. Based on the findings of Kell *et al*. (2007), it appears that over 80% of the species present in the flora of Europe and the Mediterranean are species of socioeconomically relevant crop wild relatives. Crop related species include crop progenitors and other closely related species. These species can boost productivity, offer stability, and/or impart important traits like pest and disease resistance. The contribution of crop wild relatives is still growing due to the transfer of beneficial

genes that code for resistance to pests and illnesses, tolerance to abiotic stress, and higher nutritional value (Crinò *et al.,* 1993; Hodgkin and Hajjar, 2007), crops have been engineered to resist viruses, blight, powdery mildew, nematodes, and *Fusarium* by incorporating single gene controlled traits from crop wild relatives. This has been observed in rice, potatoes, wheat, and tomatoes, among others. The nutritional value of crops has been enhanced by the insertion of genes that boost the protein level in wheat and the vitamin C content in tomatoes. Using genes from wild *B. oleracea* domestic broccoli with high levels of anticancer compounds has been created (Hodgkin and Hajjar, 2007). By utilising novel breeding techniques like as introgressiomics, it is possible to insert genome fragments from largely wild crop relatives into the genetic makeup of crops, resulting in populations and plant materials that are extraordinarily diversified. At the outset of the introgressiomics program, there are five steps. First choosing the CWRs to use. Second using specific techniques to hybridise and backcross the crop with as many CWRs from different gene pools as possible. Third using genomic tools to create multiple introgression populations with introgressed fragments from one or more CWRs. Fourth creating databases with genomic and phenotypic data and repositories of the introgressed populations and materials and fifth putting the material into the breeding pipeline.

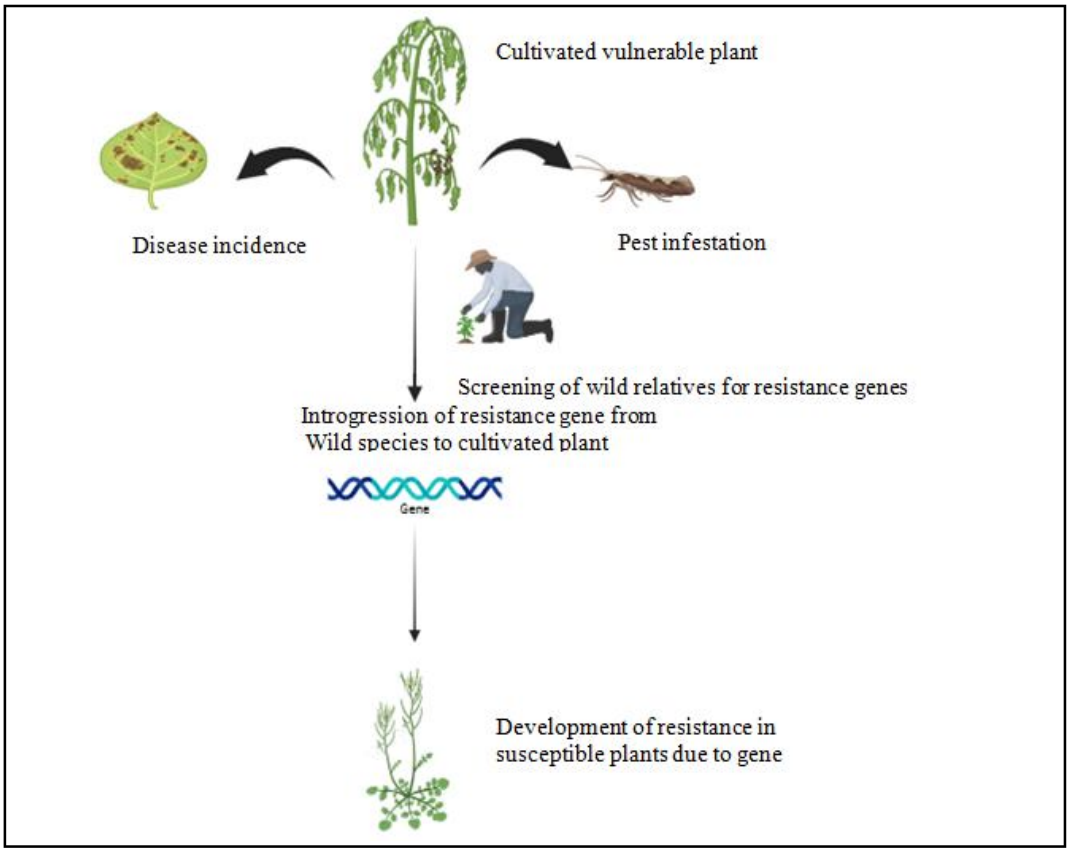

Figure 2: Wild relatives were utilized as donors to introgress resistance genes into cultivated varieties.

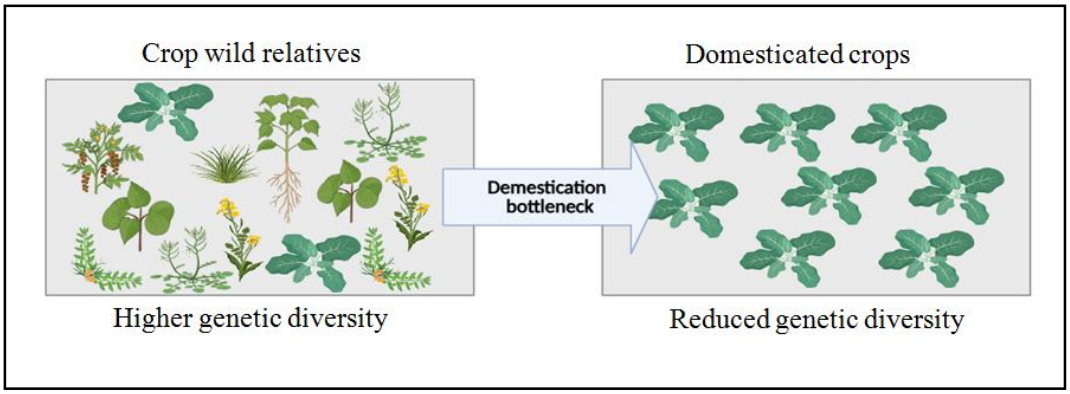

Figure 3: Crop wild relatives maintain higher level of genetic diversity than domesticated cultivars making them valuable reservoirs for crop improvement.

4. Comparison between genetic diversity in crop wild relatives and domesticated crops

Crop wild relatives still exhibit a high level of genetic diversity when contrasted with the domesticated population. The genetic diversity structure appears to be stronger in wild populations than in domesticated ones (Papa and Gepts, 2003). Because of first and subsequent domestication bottlenecks, crop wild relatives usually exhibit far greater genetic diversity than contemporary apex crops. Due to the thousands of years of natural selection, crop wild relatives have a significantly wider range of genetic variations than domesticated cultivars (Zhang *et al.,* 2017).

5. Key traits sourced from crop wild relatives of *Brassica* crops

5.1 Biotic stress resistance

5.1.1 Pest resistance

Damage to Brassicaceae plants is occurring all around the globe due to a wide variety of pests. One example of a pest is the rotting causing flying bug Diptera. Additionally, plants belonging to the Brassicaceae family are consumed by insects such as Lepidoptera, Coleoptera, and Hymenoptera. Pests that feed on the sap of Brassicaceae plants include Hemiptera and Thysanoptera, which attack these plants (Kumar and Singh, 2015). Brassica family must cope with a wide range of pests. The most troublesome pests include the diamondback moth, the cabbage looper, and the cabbage white. The diamondback moth has a narrow diet, exclusively eating members of the Brassicaceae family of plants. Just like the cabbage white butterfly, the diamondback moth is extremely picky about the plants it eats. It would not even touch anything that is not in the Brassicaceae family. A diamondback moth will cling to anything it eats. Unlike moth, cabbage looper, and cabbage white. It may cause crop losses of up to 90% and is considered the most damaging insect pest of *Brassica* crops worldwide (Charleston and Kfir, 2000; Malik *et al.,* 2020). According to research conducted by Kumar (2011), a great deal of resistance related traits may be found in wild and weedy crucifers. An important potential source of pest resistance genes in crop plants might be their wild counterparts (Kaur and Kumar, 2025).The *Brassica* pest *P. brassicae* is a major problem for cruciferous crop farmers in many countries. According to Kaur and Kumar (2025), cruciferous crops, which include the two most popular vegetables in India cabbages and cauliflower are negatively impacted. One of the most coveted goals in insect pest management is the development of insect resistant cultivars. This would provide farmers with a practical, economical, and ecologically sound way to control pests. To develop an insect resistant cultivar, it is necessary to first pinpoint the source (or sources) of resistance (Kaur and Kumar, 2025). A number of plant species, including *Crambe abyssinica*, *Diplotaxis muralis*, *D. tenuisiliqua*, *Erucastrum abyssinicum*, *Raphanus rugosum*, *Sinapis alba*, *Brassica barrelieri*, *Brassica fruticulosa*, and *Sinapis arvensis* . *B. fruticulosa* was the source of the seven most resistant accessions out of the nineteen total. All of the demographic variables that were considered were negatively affected by one *S. alba* accession (WS-09-98) due to its extremely high resistance level (Kaur and Kumar, 2025). According to Lamb (1980), the presence of trichomes on *S. alba* might be the cause of its resistance. Biochemical analysis of the hypothetical accessions revealed that high levels of total glucosinolates considerably impeded insect growth, in contrast to total phenols and flavonols, which had the reverse effect (Kaur and Kumar, 2025).The usual relationship between *Pieris rapae* and the isothiocyanates that are formed when glucosinolate is hydrolysed.

According to Verma *et al.* (2023), CWRs might potentially be a valuable source of genes for improving the stress resilience of Indian mustard. When screening weedy and wild allies for resistance to *L. erysimi*, *B. fruticulosa* and *Brassica montana* were identified as the most probable CWRs for this trait (Kumar *et al.,* 2011). Biochemical research suggests that elevated lectin concentrations may be associated with reduced aphid infestation in *B. fruticulosa* (Kumar *et al.,* 2011). Field assessments of cabbage root fly (*Delia radicum*) resistance in wild *Brassica* species and associated breeding lines were conducted in 1993, followed by assessments in 1996 in a combination of the field, laboratory and a glasshouse. It was discovered in the field in 1993 and confirmed in 1996 that *B. fruticulosa*, *Brassica incana*, *Brassica villosa*, and *Brassica spinescens* had high levels of antibiosis resistance, although two *B. oleracea* accessions and the susceptible control variety, ‘’Oliver,’’ were very sensitive (Ellis *et al.,* 1999). According to Ellis *et al.* (1999), while certain plants, such *Brassica macrocarpa* and *B. villosa*, and two F_1 lines that were created from a hybrid of *B. macrocarpa* and *B. oleracea*, showed some resistance, the bulk of plants, including *B. incana*, *B. fruticulosa*, and *B. spinescens*, were very resistant. Field tests carried out in 1993-1994, and again in 1996-1997, revealed that eight species of wild *Brassica* were significantly resistant to *D. radicum*, an antibiotic used to treat bacterial infections (Ellis *et al.,* 1999). Among these species, three that are part of the CC genome, *Brassica insularis*, *B. villosa*, and *B. macrocarpa*, exhibited extremely high levels of resistance.

Given that dual resistance to insect pests is advantageous for both developing resistant cultivars and reducing the demand for pesticides by producers, this is particularly noteworthy (Ellis *et al.,* 1999). *B. oleracea* crops, such as savoy cabbage, kale, and Brussels sprouts, are severely threatened by the phloem feeding cabbage whitefly (*Aleyrodes proletella*) (Pelgrom *et al.,* 2015). The resistance is most likely caused by trichomes in crop wild cousins *B. villosa and B. incana* accessions it is already showing up in plants that are six weeks old (Pelgrom *et al.,* 2015).

5.1.2 Disease resistance

Many *Brassica* genotypes and allies were tested in field and controlled settings for resistance to *Pseudocercosporella capsellae*, also known as white leaf spot disease. Genotypes from *B. fruticulosa*, *B. oleracea, B. napus, B. juncea*, and *B. carinata* showed the highest levels of resistance (Gunasinghe *et al.,* 2014). The generalist fungus *S. sclerotiorum* affects over 400 different plant species. Although there are reports of wild *Brassica* species that are quite resistant to the disease, sources of plant resistance usually only lead to partial control. It is unclear how aggressive *Sclerotinia subarctica* is in contrast to *S. sclerotiorum*, however reports of it on *Brassica* have also been documented (Taylor *et al.,* 2018). In leaf tests, *B. oleracea* and *B. incana* lines had the highest levels of resistance, whilst *B. incana* and *Brassica cretica* showed the highest levels of resistance in petiole testing. A *Brassica bourgeai* line exhibited both partial petiole and leaf resistance. Sources of resistance to *S. sclerotiorum* in wild *Brassica* species, including *B. cretica* and an isolate from the United Kingdom, might be used to develop resistant cultivars suitable for

cultivation in Europe (Taylor *et al.,* 2018). The potential lack of success in managing Sclerotinia stem rot *via* chemical and cultural approaches can be attributed to their lengthy lifespan and ability to infect a vast area (Kamal *et al.,* 2016; Singh *et al.,* 2020). The wild relatives of Brassicaceae, including *B. fruticulosa*, *Brassica bursa-pastoris*, *D. tenuisiliqua*, *Erucastrum gallicum*, and *Erucastrum cardaminoides*, have a high degree of resistance to stem rot pathogen infection (Chen *et al.,* 2007; Mei *et al.,* 2013). Resistance to Sclerotinia stem rot and other diseases is likely derived from *E. cardaminoides*, another wild cousin of *B. juncea* (Chandra *et al.,* 2004; Gomez-Campo *et al.,* 1999). Horizontal breeding may be the best way to introduce resistance to Alternaria blight, a polygenic trait, into farmed *Brassica* Unfortunately, resistant crossable germplasm is not present in mature *B. juncea*. Alternaria leaf blight resistance is high in several wild relatives of cruciferous plants. Some examples are: *Brassica desnottesii, Camelina sativa, Diplotaxis berthautii, Diplotaxis catholica, Diplotaxis cretacea, Diplotaxis erucoides*, and *E. gallicum* (Sharma *et al.,* 2002). According to Bhat *et al.* (2006), the Alternaria blight pathogen, *A. brassicae*, is strongly repelled by *D. erucoides*, a crop wild relative of *Brassica* because *Acinetobacter candida* continues to exhibit racial variation, the known genes that provide resistance to the disease are often rendered ineffective (Mehta *et al.,* 2023). White rust disease tolerance or resistance can be introduced through breeding programs with the help of wild cousins like *Brassica tournefortii* (Kumar, 2015).

This fungus known as black rot can severely damage *B. oleracea* crops. This disease gets into plants by hydathodes or cuts. A hallmark ''V''shaped chlorotic lesion along the leaf edges is formed as a result of its rapid multiplication and the production of abundant xanthan and extracellular polysaccharides, which obstruct the vascular system (Tonguç and Griffiths, 2004). Given the potential dangers of pesticide residue and environmental pollution, the most effective technique for preventing black rot disease is to breed Xcc resistant cultivars. Pesticides are worthless in this regard. Because Xcc occurs in nine distinct races, the most common of which are 1 and 4, it is difficult to find sources that are resistant to the virus (Fargier and Manceau, 2007; Vicente *et al.,* 2001). The inheritance pattern of resistance was examined in a research by Sheng *et al.* (2020) that tested 26 cauliflower and six related wild species for novel sources of resistance to *X. campestris* pv. *campestris race* 4 (Xcc4).The majority of the accessions that were evaluated were either susceptible or showed intermediate resistance, with the exception of the Boc4601 stable inbred line of cauliflower and the wild accessions PI435896, UNICT5168, and UNICT5169.Both UNICT5169 (*B. montana*) and PI435896 (*Brassica balearica*) showed the greatest resistance to Xcc4, with significantly reduced values for disease index (DI), area of the infected part (AIP), and proportion of the infected part to the total leaf area (PTL). This disease gets into plants by hydathodes or cuts. The organism produces xanthan and extracellular polysaccharides in huge quantities, which block the vascular system and cause the distinctive ''V''-shaped chlorotic lesions along the edges of the leaves to appear. It multiplies rapidly. Happstadius *et al.* (2003) and Ding *et al.* (2015) found that *B. incana* and *B. villosa* are resistant to *Verticillium longisporum*, *S. sclerotiorum,* and *Brevicoryne brassicae.* Reportedly, *B. macrocarpa* is extremely resistant to *Pyrenopeziza brassicae*, whereas *B. insularis* is quite resistant to *Leptosphaeria maculans*. (Bradburne *et al.,* 1999; Heaney *et al.,* 1987; Mithen *et al.,* 1987).

Table 1: Wild relatives of major *Brassica* crops which having resistance against biotic stress

Crop	Biotic stress	Wild relatives/species	References
Mustard	**Aphid (*L. erysimi)***	*B. fruticulosa* *B. montana*	Kumar *et al.,* 2011
	Sclerotinia stem rot	*B. fruticulosa* *B. bursa-pastoris* *D. tenuisiliqua* *E. gallicum* *E. cardaminoides*	Chen *et al.,* 2007
	Alternaria blight	*B. desnottesii* *Camelina sativa* *Diplotaxis berthautii* *D. catholica* *D. cretacea* *D. erucoides* *E. gallicum*	Sharma *et al.,* 2002
	White rust	*B. tournefortii*	Kumar, 2015
Cabbage	**Cabbage root fly *(D. radicum)***	*B. incana* *B. fruticulosa* *B. spinescens*	Ellis *et al.,* 1999
	Cabbage whitefly (*Aleyrodes proletella)*	*B. villosa* *B. incana* *B. montana*	Pelgrom *et al.,* 2015
	Sclerotinia stem rot	*B. cretica*	Taylor *et al.,* 2018
Cauliflower	**Black rot**	*B. montana*	Sheng *et al.,* 2020

Common	**Downy mildew**	*B. oleracea,* wild accessions	Greenhalgh and Mitchell, 1976
	Verticillium wilt	*B. incana*	Happstadius *et al.,* 2003
	Blackleg (*L. maculans*)	*B. insularis* *Brassica atlantica* *B. macrocarpa*	Mithen *et al.,* 1987
	Diamond-back moth	*B. juncea* *B. oleracea*	Suma *et al.,* 2025
	Cabbage aphid	*B. incanaB. villosa*	Ellis *et al.,* 2000
	Flea beetle (*Phyllotreta cruciferae*) and *Phyllotreta striolata*	*B. incana*	Bodnaryk, 1992

5.2 Abiotic stress tolerance

A further 0.4-2.6°C of global warming is possible until 2050, with the exact amount depending on various measures aimed at reducing greenhouse gas emissions (Smith *et al.,* 2020). Warming temperatures, more frequent and severe droughts, more pests and diseases, more frequent and severe weather events, and other unfavourable circumstances are only a few ways in which climate change could diminish crop yields. Optimal tolerances to biotic and abiotic stresses are often greater in wild relatives because of less rigorous selection for yield and yield related traits. One possible strategy to enhance the resilience of our modern crop cultivars is to breed elite crop types with wild related germplasm, with the goal of introducing genetic factors from these relatives that contribute to better environmental tolerances (Quezada-Martinez *et al.,* 2021). As a result of climate change, agricultural yields are declining throughout the world. Soil oxygen depletion, brought on by flooding, leads to denitrification and ionic toxicity. Also depending on the depth of the water, flooding might hinder gas exchange and photosynthesis, which in turn affects plant metabolism (Sasidharan *et al.,* 2018). Incorporating these traits of abiotic stress tolerance into high-yielding varieties of Indian mustard may be possible with the use of the genetic diversity seen in CWRs (Kashyap *et al.,* 2022).

5.2.1 Drought stress

Overall mustard yield is reduced because water stress affects pod setting during stem elongation and pod development. Drought stress impacts yield. Both Bhardwaj *et al.* (2015) and Wei *et al.* (2023) found that when Indian mustard is subjected to drought stress, many genes and transcription factors are controlled differentially. According to previous studies, *S. alba* is a drought tolerant wild mustard cousin of Indian mustard (Warwick, 1993a). The potential drought tolerance of wild and U-triangle *Brassica* species during germination and the early seedling stage was investigated in a recent research and it was shown that *B. fruticulosa* is drought tolerant. Compared to the control plants, *B. fruticulosa* exhibited a greater proline content when subjected to drought stress caused by polyethylene glycol (Kashyap *et al.,* 2023).

5.2.2 High temperature stress

B. juncea exhibited heat tolerance so, crop wild relatives might be a good place to start. *S. alba* possesses a number of stress resistant traits, one of which is heat stress tolerance. Protoplast fusion was used to construct hybrids of *B. juncea* and *Solanum alba*, with the goal of transferring the genes important for heat stress tolerance (Kumari *et al.,* 2018). According to a recent study by Kashyap *et al.* (2023), one of the wild allies of Indian mustard, *B. tournefortii* (Rawa), has heat stress endurance features. The germination rate increased by the greatest margin (38.46%) in *B. tournefortii* (Rawa) when heat stress was applied. The capacity of *B. tournefortii* (Rawa) to survive high temperatures during germination and other early stages of development is highlighted in this study (Kashyap *et al.,* 2023).

6. Utilising crop wild relatives for other important traits

B. juncea var. *foliosa*, which has the potential to be used for phytoremediation in soils polluted with thorium (Th) due to its tolerance of this metal (Zhou *et al.,* 2016). Plant metabolism and growth rates were affected by high Th concentrations, although *B. juncea* var. *foliosa* grew better at low Th concentrations. One such variety of *Brassica* vegetable is Chinese cabbage (*B. rapa* subsp. *pekinensis*), which has the ability to accumulate high amounts of heavy metals in its leaves without displaying any obvious symptoms. From an evolutionary point of view, breaking pods is a fantastic way to spread seeds. Unfortunatley, there is a risk of substantial seed loss while harvesting *Brassica* oilseed crops. In optimum conditions, this loss might reach 2-5%, but in less than perfect conditions, it can reach 20% or even 50% (Price *et al.,* 1996). A hybrid *B. rapa* spp. *pekinensis* is the product of crossing two varieties *of B. rapa* that do not get along pekinensis with internal leaves. This characteristic is indeed present in Pekinensis hybrids. The inner leaves of the hybrid *B. rapa* spp. *Pekinensis* are orange in colour. The study was conducted by YangJun *et al.* (2005). Anthocyanin formation is associated with freezing tolerance in *B. rapa* cultivars (Ahmed *et al.,* 2015).

7. Gene families linked to wild crops ability to withstand both biotic and abiotic stress

One component of plant genes that helps regulate gene expression is known as a W-box sequence. The NPR1 gene and genes associated to pathogenesis are examples of plant defence genes that include these W-box sequences. Plants can experience extreme stress in the face of adverse environmental conditions, pest infestations, or illnesses. Salicylic acid, jasmonic acid, and abscisic acid are among the compounds that plants can produce in response to stress. In addition to producing compounds that aid in stress management, plants have the ability to activate certain pathways that enhance their response to adverse environmental conditions (Fujita *et al.,* 2006). According to Kayum *et al.* (2015), several types of abiotic stress in *B. rapa* trigger responses from WRKY and Alfin like transcription factors. WRKY gene expression levels that were around 175, 32, 54, and 42 fold greater after cold stress compared to controls. It is possible to

overexpress or introgress the BrWRKY22 and BrWRKY44 genes into *B. rapa* vegetables in order to create lines that are resistant to cold temperatures. According to Kayum *et al.* (2015), the levels of BrWRKY51, 65, 98, and 104 were found to be approximately 85, 15, 18, and 38 fold higher than the control after drought stress treatment, respectively. On the other hand, BrWRKY17, 57, and 58 exhibited expression levels that were approximately 5, 2, and 3 fold higher under salt stress conditions. The expression of BrAL2, 3, 7, 9, 12, 13, 14, and 15 was shown to increase in response to all abiotic stimuli, including cold, salt, and dryness (Kayum *et al.,* 2015). All eight of the CBF/DREB1 genes respond to cold stress, and several of those genes also respond to drought, salt, and ABA treatment. According to Kayum *et al*. (2016), alfalfine like transcription factors in *B. oleracea* (BoAL1, 4, 5, 6, 7, 8, 9, 10, and 12) are caused by abiotic stresses such cold, salt, drought, and ABA. The osmotic stress sensitivity of BrMYB210, BrMYB137, BrMYB88, BrMYB154, and BrMYB222 was reported. When subjected to such stress, these BrMYB genes respond strongly. The AtMYB28-like BrMYB261, on the other hand, is insensitive to cold. Osmotic stress affects it greatly. The number of MYB genes is six. For example, BrMYB140, BrMYB172, BrMYB229, BrMYB208, BrMYB137, and BrMYB210. That are influenced by ABA therapy. When these BrMYB genes are treated with ABA, they become active. Activated when treated with auxin. Both treatments have different effects on the BrMYB genes. However, leaf auxin treatment resulted in down-regulation of BrMYB210, an ortholog of AtMYB96. Cold stress treatment caused two separate cabbage lines to express twelve BoCRGs differentially (Ahmed *et al.,* 2015). Of them, twelve were expected to be engaged in pathways that regulate cold, including BoCRG54, 56, 59, 62, 70, 72, and 99.

Table 2: Wild relatives of major *Brassica* crops that are resistance to abiotic stress and having other important traits

Crop	Abiotic stress	Wild relatives/species	References
Mustard	Drought stress	*S. alba*	Warwick, 1993b; Kashyap *et al.,* 2023
		B. fruticulosa	
	High temperature stress	*S. alba*	Kumari *et al.,* 2018; Kashyap *et al.,* 2023
		B. tournefortii	
	Resistance to pod shattering	*B. macrocarpa*	Mithen and Herron, 1991
		Brassica hilarionis	
Quality traits	Glucosinolates	Wild *B. oleracea* complex	Heaney *et al.,* 1987
	High glucoraphanin	*B. villosa*	Faulkner *et al.,* 1998
	High erucic acid (>45-50%)	*B. villosaB. incana*	Velasco *et al.,* 1998
		Brassica rupestris	
Breeding systems	Cytoplasmic male sterility	*Brassica oxyrrhina*	Prakash and Chopra, 1990

The effects of biotic stress on plant and vegetable harvests are devastating. In response to various forms of environmental stress, many genes alter their levels of activity. The BrWRKY4, BrWRKY65, BrWRKY72, BrWRKY97, BrWRKY133, and BrWRKY141 genes were significantly more active. When the plant became infected with *Fusarium oxysporum* f.sp. *conglutinans*, the BrWRKY genes were active at a rate of approximately 8, 6, 3, and 5 times higher than normal. In order to combat this infection, the BrWRKY genes were much more active (Kayum *et al.,* 2015). The BrWRKY141 in plants experiences a dramatic rise of 180 times when they are infected with *P. carotovorum* subsp. *carotovorum* (Kayum *et al.,* 2015). When a plant becomes infected with *F. oxysporum* f.sp. *conglutinans,* something similar happens: the levels of BrAL2, BrAL3, BrAL4, BrAL7, BrAL9, BrAL10, BrAL13, BrAL14, and BrAL15 in that plant also grow significantly. Additionally, when plants are stressed by either living or nonliving entities, the following genes are expressed: BrAL2, BrAL3, BrAL7, BrAL9, BrAL13, BrAL14, and BrAL15 (Kayum *et al.,* 2015). As per the findings of Ahmed *et al.* (2012b), three chitinase genes BrCLP1, BrCLP2, and BrCLP3 respond when *P. carotovorum* subsp. *carotovorum* is infected. The expression of the defensin like family protein (BrDLFP) was shown to rise significantly following Chinese cabbage infection with *P. carotovorum* subsp. *carotovorum* (Ahmed *et al.,* 2012). Two Alfin like genes, BoAL8 and BoAL12, were activated in *B. oleracea* when infected with *P. carotovorum* subsp. *carotovorum* (Kayum *et al.,* 2016).

8. Conventional to genomic approaches for trait introgression from crop wild relatives

Several species of *Brassica* have complicated partial barriers that make reproductive compatibility even more difficult. This is difficult because of problems that arise both before and after fertilisation, and because of the termination of hybrid embryos that are the result of crossings between different species. Recent developments in embryo rescue and vitro culture have given rise to several successful attempts to produce interspecific hybrids (Islam *et al.,* 2021; Pen *et al.,* 2018). Microspore embryogenesis is the transition of male gametes from their usual direction of development to either embryogenesis or callogenesis. In diploid plants, the pollen grains originate from microspores, which normally contain an uneven number of chromosomes. While there are a lot of factors that affect how well embryogenesis works, it is possible to develop mature plants from microspores under the right conditions. According to Berenguer *et al.* (2020) and Rodríguez-Sanz *et al.* (2014) the most effective stage of embryogenesis in *B. napus* occurs just before pollen mitosis, when the microspores are strongly vacuolated. Cis genesis refers to the process of crop genetic modification employing CWR genes in a way that avoids linkage drag by not utilising selectable markers from other species. According to Dempewolf *et al.* (2017) CWR may often be included into breeding operations through the use of cross first and choose first procedures.

Interspecific hexaploidy hybrid bridge approach to transfer Sclerotinia resistance into *B. napus*. This resistance is regulated by multiple loci found in a wild C-genome species, *B. incana*. (Mei *et al.,* 2020) Found that the BC1F8 line, by pyramiding three major QTLs, achieved around 35% resistance relative to the *B. napus* parent. The variety groups of *B. napus* and the spring type *B. napus* have both yielded many QTL for blackleg resistance (Huang *et al.,* 2016; Larkan *et al.,* 2016). While searching for resistance in subgenomes other than C, researchers discovered one gene resistance locus on linkage group B7 in *B. carinata* (Sharma *et al.,* 2016). This resistance was subsequently transferred into *B. oleracea* by embryo rescue (Sharma *et al.,* 2017). Somatic fusion between *B. oleracea* var. *capitata*, *B. oleracea* var. *botrytis*, and *B.oleracea* var. *capitata* resulted in 61.2%, 83.6%, and 33.2% of the hybrids produced, respectively, a resistance to the TuMV virus found in *Raphanus sativus* (Scholze *et al.,* 2010). Frequent use of distant hybridisation technologies has allowed for the introduction of superior genes from neighbouring wild species or other species into target crops through inbreeding. The vast genetic diversity within the Brassicaceae family provides strong evidence that remote hybridisation may be successful hybridisation. By generating myrosinase mutants, plants in the Brassicaceae family are able to ward against insect pests, including both generalist and specific insect pests. Glucosinolates are a kind of chemical that plants in the Brassicaceae family utilise for defence. This is what makes this family unique. There are more than 132 unique GSL structures in the Brassicales order. Despite their relative evolutionary youth, GSLs and cyanogenic glucosides have several commonalities (Agerbirk and Olsen, 2012). Biological stress may be caused by several insect pests, such as sucking and chewing bugs, which affect *Brassica* crops. Under typical conditions, plant cells contain glucosesinolates, which are stable molecules. Although, they are located in different areas of the cell, glucosenolates and myrosinase are enzymes that collaborate. Myrosinase converts glucosinolates into isothiocyanates, thiocyanates, and nitriles in response to insect attacks on plants. Myrosinase mutations in Brassicaceae species are the focus of current research. Because they produce glucosinolate compounds, which have a strong odour, these myrosinase mutants make plants more resistant to insects. Plants rely on glucosinolates and myrosinase as part of their defence mechanism against insect pests. According to Malik *et al.* (2025), this type of study is being conducted globally. The many methods utilised to create myrosinase, including as breeding, RNA interference (RNAi), ablation, and CRISPR-Ca12a technologies, have not prevented these plants from exhibiting antagonistic and synergistic effects on the growth and performance of various chewing and sucking insect pests of *Brassica* crops. According to Malik *et al.* (2025), new genomic technologies have the potential to enhance *Brassica* crops resistance to insect pests by precisely changing its myrosinase genes. One practical approach is to employ RNA interference to reduce the expression of the myrosinase gene, which is cloned from *Brassica parachinensis.* The growth and developmental characteristics of the Diamond Back Moth were reduced in transgenic plants of *B. parachinensis* that had myrosinase inhibited.

9. Challenges in utilising wild relatives for crop improvement

It may be challenging to transfer genes from CWRs to crops because of reproductive barriers between each species (Dempewolf *et al.,* 2017). The economic importance of Indian mustard, scientifically known as *B. juncea*, as an edible oil crop cannot be overstated. In spite of plant breeders producing a plethora of top *B. juncea* varieties with enhanced yield traits, studies on the introgression of stress resistance traits have lagged behind due to a shortage of resistant donors. The term ‘’crop wild relatives” describes the relatives of domesticated plants. They are underutilised because of a few undesirable genes that prevent them from bearing many offspring, which is why their domestication has been largely neglected (Verma *et al.,* 2023). More and more, people are realising that CWRs are vital for crop survival in the face of climate change. We can increase our chances of securing funding to safeguard CWRs if we can get the word out. Unfortunately, the lack of resources and qualified personnel is causing progress to be glacial. Gene banks also face challenges such as inaccurate accessions, a lack of complete characterisation data, and an under-representation of natural diversity. Methods such as systematic examination, genome based comparisons, and improved documentation are tackling these issues. Further obstacles to collaboration include dispersed research groups and material restrictions imposed by national laws. However, with better coordination and clearer job descriptions, collaboration may overcome these obstacles and go forward. When these problems are fixed, CWR can be used more efficiently in breeding programs (Dempewolf *et al.,* 2017). According to Singh *et al.* (2007), when domesticated and wild species are crossed extensively using the classical hybridisation method, the crossability barriers tend to be strong. It depends on how isolated the two parental species are from one another during reproduction. Reproductive isolation is typically higher when barriers begin to act earlier. So, even in closely related species, there are prefertilization barriers that prevent pollen from germinating or the pollen tube from growing past the stigma and style. On the other hand, when it comes to closely related species, post-fertilization obstacles are usually observed later in embryonic development (Singh *et al.,* 2007). For smaller crops, there is a dearth of data on phenotypic and genotype characterisation. For larger crops, there is plenty of data on cross compatibility between wild species and crops, which has helped in the search for new possible CWRs. Approximately, 70% of wild Brassicaceae did not have genetic sequence information available in public archives, and only 40% had recorded chromosomal numbers (Castillo-Lorenzo *et al.,* 2024).

10. Future perspective: Increasing the contribution of crop wild relatives

Despite the increased use of CWRs, their usefulness in improving crop yields has been underappreciated, especially in light of recent developments in molecular techniques, the abundance of wild accessions in gene banks and the ease with which different species can be crossed. Knowing how a CWR will interact with a crop will help breeders figure out how to bring in features from wild species into the cultivar. On the other hand, except from publications focusing on the genus *Brassica* (FitzJohn *et al.,* 2007). There is less evidence of successful sexual crosses between crops and CWRs belonging to the Brassicaceae family. It is critical to understand the compatibility of CWRs with Brassicaceae crops and to safeguard prospective CWRs so that they can be more easily accessible and preserved for future sustainable usage. In order to have enough data for future breeding programs, it is necessary to conduct substantial ex situ

conservation efforts (Castillo-Lorenzo *et al.,* 2024). Castillo-Lorenzo *et al.* (2025) choose wild relatives of Brassicaceae crops to be used in breeding programs. Some *B. oleracea* accessions drastically decreased their germination ability when exposed to high temperatures, which seemed to be stress symptoms. Their ability to withstand heat varied with their origin those from the south, who had likely adapted to warmer yearly average temperatures, had the highest levels of tolerance. Increased resilience, sustainability, and production would result from adding these heat-tolerant traits to commercial germplasms of *Brassica* species (Tiret *et al.,* 2025). Using Brassicaceae CWRs most effectively over the next decade will require expanded pangenomic sampling of wild taxa, objective phylogenetic prioritisation of under-represented species, and the creation of regional pre-breeding hubs that integrate genomic selection, doubled haploids, and embryo rescue. According to MacNish *et al*. (2025), with the use of open data, standardised phenotyping, and equitable access frameworks, this integrated approach can convert CWR alleles into *Brassica* cultivars that are climate resilient on a large scale. Abiotic and biotic stresses on crops have caused food prices to rise, which has disrupted the global food supply chain and worsened poverty and hunger. Modern molecular methods must be utilised in crop breeding if we are to achieve long term food security. These days, rapid genomic selection requires genomics-assisted breeding and high throughput phenomics. In order to enhance agricultural operations and control invasive species, this strategy is crucial for producing plant cultivars that are resistant to pests, diseases, and herbicides (Sabeem *et al.,* 2022).

11. Conclusion

To supplement the small genetic pool of elite cultivars, the Brassicaceae family relies on crop wild relatives as a genetic reservoir. This review has highlighted several instances where commercially important crops, such as *B. juncea* and *B. napus*, have been successfully improved by incorporating desirable features from wild species, such as *S. alba* and *B. carinata*. The oil's nutritional value and quality are both enhanced, and it is resistant to a wide range of biotic and abiotic challenges. Although, there were challenges with interspecific hybridisation and linkage drag in the past, modern genomics, molecular breeding, and state of the art biotechnological methods have made targeted and efficient gene transfer a reality. Smart and sustainable utilisation and management of this rich genetic variety is crucial for the development of climate resilient *Brassica* crops and for the long term food and nutritional security of a rising global population.

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Conflict of interest

The authors declare no conflicts of interest relevant to this article.

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