Harnessing Genetic Resources for Brassica juncea Improvement: Exploiting Wild Relatives and Landraces

Abstract

Around the world, the importance of Indian mustard (Brassica juncea) is especially recognized in South and Southeast Asia, where it is grown for oil and its leafy vegetable. Even though breeding is important, it is limited by the fact that today's B. juncea varieties have a narrow genetic base that results from using only a few selected features for many years. Lacking different kinds of genes means the crop does not adjust well and is more inclined to be affected by various stresses. With the help of genomics, molecular breeding and wild relative crops, new developments make it possible to increase the variety of genetics and boost key agronomic characteristics. It summarizes views on domestication, the wide range of forms and genes in B. juncea and new developments in hybrid breeding, QTL analysis and using markers for breeding in recent years. We draw attention to the role wild relatives could play in giving foods improved resistance to stress, diseases and better nutrients. Additional approaches involve combining molecular techniques, various pan-genomic resources and new phenotyping tools to develop high-performing B. juncea plants that perform well in a wide range of climates. For this reason, making use of underutilized germplasm will give mustard producers and farmers steady success in the future and in times of change.

Keywords: Wild relatives; Landraces; Molecular Breeding; Introgression; QTL mapping; Marker-assisted selection; Genomic diversity; Crop Improvement

INTRODUCTION

Mustard is highly valued crop in South and Southeast Asia, particularly for edible oil and leafy vegetables from Brassica juncea; an important species in the mustard family. However, there is a poor variability within the gene pool of cultivated types of B. juncea – one of the reasons for a relatively low yield in comparison with other oilseed crops (Istaitieh et al., 2024; Kang et al., 2021). This has also led to the crop having a narrow genetic variation, and thereby easily attacked by pests and diseases, due to historical domestication with a focus on certain attributes (Flint-Garcia et al., 2023; Banga & Banga, 2016). It is not known, how far there is genetic differentiate between different forms and cultivated types of B. juncea; there is no concrete classification (Saad et al., 2021). From the descriptions made by various workers morphologically and Agronomically, the crop can be grouped into the following types. Based on the analysis of the agronomic practices and yield of the various types of B. juncea in India, it had been identified that the cultivation, crop toria in India is limited to northeast region only in the dry temperate zone (Borah et al., 2020; Pokharia et al., 2024). Few other low varieties of toria are also cultivated in the normal and late sown cases which should not come under toria type. Thus, we see that toria and sarson types only share a degree of overlap in northwestern and central part of the country. It is proposed to subdivide the rape-mustard/engine horse 2 into the types corresponding to the primitive types of sarson. Raya is a low variety of B. juncea commonly associated with weedage and has been mainly grown in the rainfed area (Inturrisi et al., 2022). Tatsai is also a primitive 'hon kai tsiang' vegetable and it looks like some of the primitive vegetable forms in China (Hossain et al., 2023). In its endeavour to look for the B. juncea wild and weedy types, the studies undertaken in India had tried to differentiate between the two types. These types could have the potentiality to be genetically related to the forms existent in the Oriental region from where they have originated but there is very limited information available on the genetic diversification of the modern cultivars of B. juncea from their wild progenitor (Singh et al., 2021). In more detail, the respondents' views were obtained based on Hossain et al.'s (2023) survey.

Nevertheless, the ancestry of the domesticated B. juncea is not clear but it is postulated that it evolved from the Oriental region (Al-Yasi & Al-Qthanin, 2024; Kang et al., 2021). Such subtypes are still occurring in the Oriental region which closely resemble the weedy and wild variant of B. juncea (Cheng et al., 2023). The cultivated types have acquired the local names with change in the eco-geographic regions, for instance, Indian farmers have chosen with types that have better adaptation and preferable traits than wild types (Kundu et al., 2024; Vasisth et al., 2023). There are very limited local races of toria that are cultivated in East and Northeastern part of the country. This crop has been attributed to humans movements and thought to be neolithic since the spread is from eastern Europe to China (Pokharia et al., 2024). It has been pointed out how the historical continuity of the cultivation of toria has been supported by the 'Aryan' movements (Xie et al., 2023). The effects of migrations in the cultivation of this crop by humans might have been felt as against to the time before migrations. At later periods Mustard entered Southern, Western and Central India and local varieties have been developed which are distinct from the toria types and from each other (Liu et al., 2024). Much fewer attempts to enhance the sarson and raya types of B. juncea in the cultivated gene pool have been made in comparison to the toria types (Banga & Banga, 2016).

Brassica juncea, belonging to the family mustard plant belongs to the category of pulse that contains rich nutrients. It is mostly used for its edible oil and the leafy vegetables in South and South East Asian region. It is also well known for number of cytotypes and assortment of forms like sarson, toria, raya, tatsai etc. The high degree of its genetic variation could be utilized to bring out a wide range of B. juncea which possess farmers required traits (Saad et al., 2021). Variety is the wild and weedy species that can be used to develop genes of resistance to biotic and abiotic stresses (Subramanian et al., 2023). Now let us see the development of cultivated types of B. juncea from its primitive type before discussing the existence of wild relatives. According to Flint-Garcia et al. (2023). Eigenbrass is one species of the mustard plant family, which is loaded with nutrients that are dietary in nature. It is cultivated mostly for edible oil and green supplements in South and southeast Asia. It is also famous for a number of cytotypes and variation of forms like sarson, toria, raya, tatsai, etc. Due to high gene polymorphism, it becomes easier to work on this species and develop new B. juncea with desired traits by the farmers (Kang et al., 2021; Shorinola et al., 2024). Wild and weedy species are considered as genes resource for biotic and abiotic stress resistance (Saad et al., 2021; Subramanian et al., 2023). It is now time to consider how the cultivated types of B. juncea developed from the primitive type before we discuss the chance with wild relatives we have in particular consideration (Liu et al., 2024).

Brassica juncea is essential for food security and sustainable farming in countries around Asia and beyond. Even so, the limited genetic background and unexploited diversity point out the need to make better use of wild relatives, landraces and advanced genome technology. By using genetic reservoirs with modern methods and markers, we have the prospect to boost yield, improve resistance to stress and enhance nutritional content. The purpose of this review is to gather recent improvements in B. juncea and outline a plan for its growth under new agricultural and climatic conditions going forward.

2. Potential of genetic resources in the improvement of Brassica juncea.

The genetic resource available are the breeding materials that form the basis of genetic improvement process. In the present centuary, a huge breeding progress has been achieved during the utilisation of genetic variability from wild cruciferae relatives and landraces(Ali et al. , 2022). An example in this regard is the transfer of the Rfo gene for resistance to turnip mosaic virus from one of the wild relatives, B. oleracea into I. mustard. Different genetic stocks differentiation has enhanced the movement of preferred genes from one species of Brassica to the other. These are aneuploid stocks for each chromosome of B. rapa and identify B. juncea chromosome or chromosomal segments in B. rapa through substitution lines to establish the genetic linkage of a particular trait with B. juncea chromosome. In addition to the research work conducted about the B. juncea-B. of napus addition lines has led to the exchange of a number of desirable quality genes from B. napus into B. juncea through wide hybridization. B. juncea-B. oleracea monosomic addition lines are now being developed from these populations and these will be used to map alien chromosomes and transfer genes of interest from B. oleracea into B. juncea. While these classical breeding techniques are very useful in interspecific gene transfer, more extensive use can now be made of the new molecular marker technology to determine the transfer of specific genes and their consequences with respect to linkage drag. A new avenue for enhancing B. juncea and other Brassica plants has emerged with the use of genetic stocks and molecular maker along with genomics. Fraga et al. , 2022 This approach is expected to enhance the rates of plant breeding for crop improvement by enhancing the efficiency of selection for the target traits and also enable pyramid of genes to develop improved germplasm.

3. Wild Relatives of Brassica juncea

The analysis of genetic and adaptive variation in wild relatives of B. juncea improves its assortment and prospects. Drawing the peculiarities of their distribution and with reference to the processes that have driven their development we will be able to reveal important findings that are going to contribute to the improved understanding of genetic differentiation and adaptation. Such a detailed investigation will significant to the following research and conservation processes but also will set the stage for the creation of improved Brassica juncea varieties that will fit the needs of humanity and also the environment (Yang et al. , 2020).

Particular focus has been given in the evaluation of a subset of Brassica juncea landraces at a research station with emphasis on morphological and yield characters like days to flowering, maturity period, plant height, leaf area and yield. This comprehensive description has offered insights about a diverse morphological and phenological variation that exists in the landrace accessions brought together in this study. The evaluation has revealed genetic variability in these seven fundamental agronomic traits as a result of the Brassica juncea plant responding to the variation in the climatic conditions within its production zones (Li et al. , 2023). Moreover, extended molecular study employing microsatellite markers has been undertaken to study the worldwide distribution and dynamics of genetic variability in B. juncea. These valuable data may significantly contribute to the further identification of specific gene sets and peculiar allelic patterns which can be potentially targeted in the following focused breeding programs with desirable parental lines. This integration of the present deep phenotypic and genotypic data will help the breeder to formulate the right strategies in the breeding of Brassica juncea cultivars for higher agronomic yield and stress tolerance (Saad et al. , 2021)(Zhang et al. , 2022)

A total of 19 B. juncea landraces have been collected from different sources in Asia; however, India and China are the major contribution sources. These landraces were developed either through partnership or through the use of non-regulated germplasm materials to prevent repetition of the acquisition. These landrace accessions may be used to provide valuable historical perspective to the adaptation and genetic variation of B. juncea especially useful to create dryland mustard variety suited to Western Canadian production environment. Landraces with desirable like water use efficiency, drought tolerance and pest resistance can therefore be systematically incorporated into breeding programmes to generate elite mustard genotypes that are well adapted to the harsh environment in the region (Gerard et al. , 2022). Defining the high-risk areas and designing efficient strategies of collection and conservation are also the essential steps towards the preservation of BJ landraces' genetic stock. With respect to maize, these landraces valuable for farmers suffering from the process of contamination and possible disappearance due to the degradation of traditional farming technologies. The Brassica juncea varieties as a result of early domestication or seed dispersal are present all across the globe and possess appreciable genotypic variability and phenotypic plasticity specific to the area making it an excellent gene pool for enhancing the domesticated crop (Singh et al. , 2021). To obtain the maximum number of diverse genotypes, targeted surveys and collection campaigns have been done in the major producing area of Brassica juncea in India and followed by China. Such work has entailed sourcing germplasm from local farmers, agricultural research stations and gene banks with the aim of developing a collection of spring and winter BJ landrace populations. The collected landraces are then systematically described, tested and preserved in gene banks in order to sustain sequenced generations and to remain useful in future plant breeding activities (Banga & Banga, 2016).

Among the 48 Brassica juncea landraces studied, there is genetic variation for acid soil tolerance because of reduced Al uptake and organic acid release. They also show variability in phosphorus acquisition efficiency and it has been postulated that efficient genotypes will have higher yield under conditions of low phosphorus availability. These landraces, which have been under natural and traditional selection, consist of numerous adaptive traits making them well adapted to perform well in various agroclimatic environments, further resulting to the formation of ecotypes (Makhadmeh et al . , 2022).

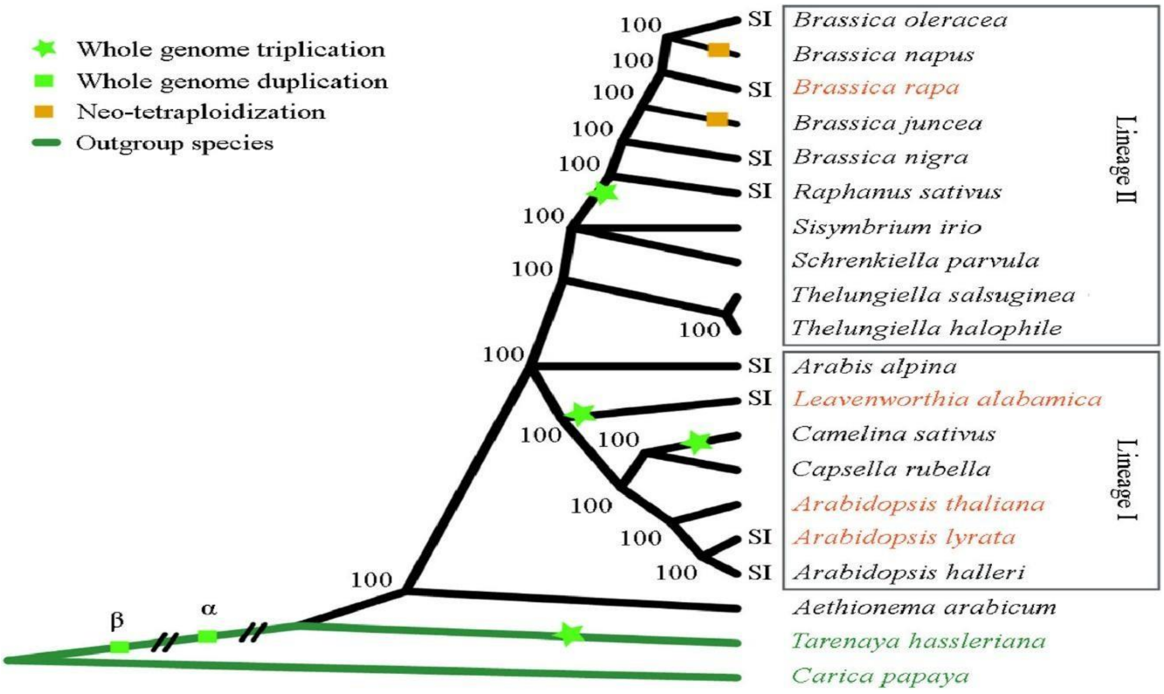

Figure 1. Phylogenetic tree showing the evolutionary relationships among Brassica species, highlighting the genomic origins of B. juncea as an amphidiploid (AABB) derived from B. rapa (AA) and B. nigra (BB). Source: Cui et al. (2020).

4. Utilization of Wild Relatives for enhancing Brassica juncea.

Breeding from related wild Juncea species aide in realizing the germline vigour that has enhanced the crop Brassica agronomics. This approach provides researchers an opportunity to identify novel genes, gene interactions, and interactions of genetic variance to breed improved and more tolerant B. Juncea varieties. This approach increases the gene base, which helps develop high yielding, disease tolerant and more responsive genes to varying ecological system. The utilization of the available broad genetic base of wild relatives is such a prospect for the Brassica juncea improvement and sustainable agriculture in the future (Subramanian et al. , 2023) .

Thus, means of introgression of desirable traits using genes from the wild relatives is considered a valid technology to bring an enhancement in the quality of Brassica juncea commonly known as Indian mustard. Through introgression of useful traits from related wild relatives, biologists and Plant breeders can improve on the genetical profile and productivity of cultivated Brassica juncea. This practice makes it possible to pass desirable characters such as disease inhibition, abiotic stress, higher production and enhanced nutritional content. According to the literature review conducted Kang et al. [2021]. Incorporation of wild relatives increases the genetic stock, thus increasing the gene pool, and resilience. Introgression is the process of hybridization between cultivated B. juncea and the wild relatives and then selection with backcrossing to find out the desirable traits along with reduced undesirable traits (Zhang et al. , 2022).

Wild relatives of Brassicaceae family hold large amount of exotic genetic variation that can be used by the breeders to improve the existing Indian mustard through the development of new BJ accessions with better opportunities for improved yield and adaptability factors. From the wild relatives it is also important to introduce desirable characters to combat challenges arising from climate change to enhance Brassica juncea to have a better protection against new pests, diseases and other unfavourable conditions. Additionally, this approach holds a great prospect to improve nutritional quality of Brassica juncea using genes from wild relatives (Xie et al. , 2023). In general, use of wild relatives for the purpose of genetic introgression to the extent of improving the agronomic performance, stress tolerance and nutritional quality of B. juncea is an essential practice in such crops, making a substantial contribution towards sustainable agriculture.

The major concern is to enhance disease tolerance in the variety of Brassica juncea. Long-term and high yielding and resistance soil and pest and pathogens cultivars increase production, protection in sustainable agriculture by decreasing chemicals. To improve on the various diseases that attack this plant the researcher applied genetic engineering, trait selection and classical breeding from Brassica juncea. Qualifying interactions of plants with pests increases the chances of unraveling resistance traits. The growing of disease resistant varieties leads to sustainable agriculture and environment. Moreover, due to international cooperation, the world will see the development of Brassica juncea high yielding, disease tolerant varieties which will boost the grower’s mustard business in the future (Subramanian et al. , 2023).

The use of genetic resources from wild relatives and landraces has received much attention in the past couple of years to improve the abiotic stress tolerance in Brassica juncea. These genetic resource pools are capable of harbouring great potential to enhance the adaptive mechanisms of Brassica juncea to cope up with unfavourable environment stress factors. Exploiting this genetic resource, it is possible to establish new approaches for enhancing the abiotic stress tolerance in B. juncea that will help in sustainable agriculture and stability, sustainability and productivity of the crop. Shi et al ., (2024)

The development and use of these genetic resources includes a combination of conventional plant breeding practices and approaches to the molecular and genomic knowledge and state-of-the-art phenotyping resources. As described in this article of Rajpal et al. (2023), this multi-disciplinary approach is expected to create a paradigm shift in plant breeding programs leading to rapid development of high yielding, climate resistant, and nutrition enhanced Brassica juncea varieties. Assessment, documentation and effective management of the genetic resources present in wild relatives and landraces are key steps noticed in this process of realizing the complete value of the above prospect on sustainable intensification and diversification of the plant production systems. Capacity building and knowledge sharing in the context of international cooperation also has a measureable contribution to meeting the current climate change, land degradation, water and food insecurity challenges enhanced by Brassica juncea genetic potentiality, according to Almeida et al. , 2024.

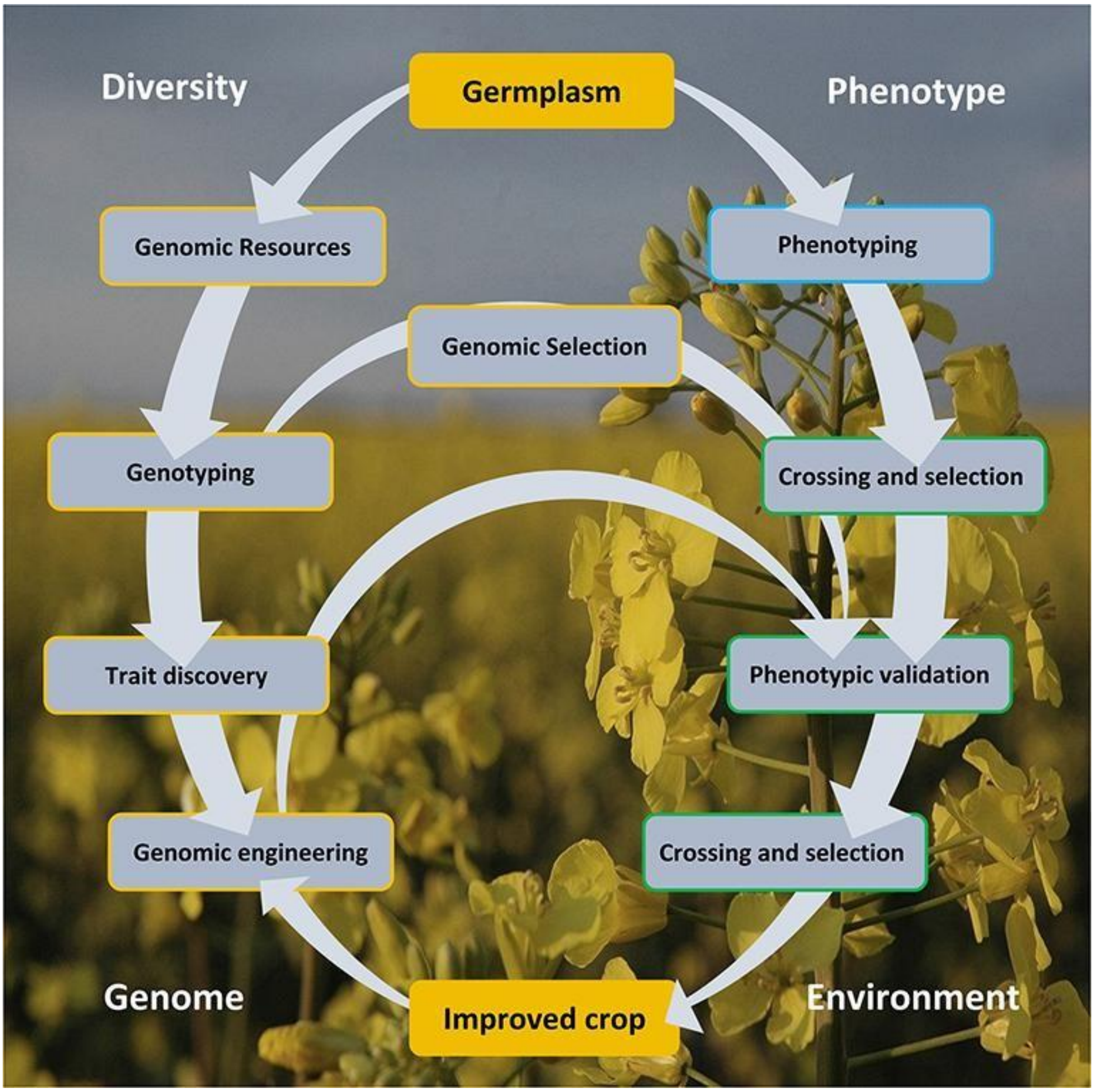

Figure 2. Schematic diagram illustrating traditional and molecular breeding strategies employed to harness genetic resources, including introgression from wild relatives and landraces, for the improvement of Brassica juncea. Source: Saad et al. (2021).

5. Using in Brassica juncea Genetic Enhancement

Apostol et al. said that landraces were earlier incorporated into breeding programs for crop improvement because they contain diverse gene pools and are well adapted to their growing environments. While modern breeding programs are characterized by high-input large scale farming systems, landraces have only gone through small scale and low input necessary for the farming practices in the developing world. Hence, landraces are seen as beneficial gene reserves for crops such as Brassica juncea , that are cultivated in the developing countries. However, there has been little systematic breed-ing of landrace varieties and much of this material is currently under threat of genetic erosion due to social and economic transformation of rural societies. This shows there is a dire need of collecting and characterizing B. juncea landraces before they are eradicated. Particularly, collection missions in the countries with the high concentration of native landraces or meeting immigrant communities preserving traditional farming practices can be useful in this regard (Ramírez-Villegas et al. , 2022).

6. 1. Use of the Landraces to Increase Yield

Geraghty also revealed that the use of the genetic resources of specific crops including the landraces has played an important role in enhancing yield traits such as yield potential in the process of B. juncea breeding. Hybrid mustard variety has made remarkable success in India as a result of adopting natural and induced variability in the local mustard landraces. The experiences from inheritance studies and breeding programs employing broad genetic base have brought useful information on the genetic regulation of yield components; this information has been used in transferring these traits into CMS lines. This has seen breeders concentrate in the creation of high yielding pure line varieties as seen in the improved variety namely Varuna with a yield that is 15-20% higher than the existing cultivars. This century old example shows how much contribution of Land races is towards the improvement of yield performance of present Brassica juncea varieties (Vasisth et al. , 2023).

6. 2. Improving Nutritional Value – How and Why of Using Landraces

Some of the varieties of B. juncea which have been used in developing higher quality of mustard are the land races. For example, an endemic variety ‘Pharsi Rai’ has high calcium, and iron and low glucosinolates. This variety was then crossbreed with high erucic acid rapeseed to produce a genotype WR49-43 with high oleic acid, higher erucic acid and low glucosinolates enhancing the oxidative stability and nutraceutical value of the oil(Istaitieh et al. , 2024). Likewise, an Indian mustard line CS52-3 obtained by crossing a Polish yellow sarson to a new B. juncea line has high oil yield (42. 8%) with favorable fatty acid composition (69-73% oleic acid, 1-2% erucic acid), and thereby suitable for the pharmaceutical and edible industries (Sawicka et al. , 2020).

This reveals that landraces could be a useful source of genetic diversity that could be used to improve on the nutritional quality of B. juncea further. Certain landraces of Indian mustard are bright yellow in colour because of the carotenoids which gives colour to stem, flowers as well as siliquae. Srilakshmi and Padmaja identified a yellow sarson landrace with high carotenoid content of 10 mg per 100 grams of oil as compared to other Indian type (3- 4mg/ 100 grams of oil). Singh et al. , 2022) Paria, Horticultural Research Station, NAU investigated the morphological characters, oil yield and quality of 15 accessions of yellow sarson and observed that there exists a high genetic variability in this crop.

These accessions contained carotenoids in the 6–15 mg/100 g of oil range. They also found out few high yielding (10–12 q/ha) accessions having oil contents of 42–45%. This was according to Momeni et al. , 2024.

6. Molecular Mapping and QTL Estimation in Jute Plant [Brassica juncea]

The last set of phenotyping trials carried on the Sclerotinia resistant RILs used a method described by Garg et al., 2010 which involved fungal culture of an aggressive isolate of SC-1 on petri plates to check resistance under controlled environement. In this study researcher used degree of plant damage, diseases symptom severity, and final plant yield as measures of resistance (McLoughlin et al. , 2018). The final set of RILs used was tested at CCS Haryana Agricultural University in Hisar, Haryana, India using four replications of the best and worst RILs for disease resistance coming from each parent lines. (Shehrawat, 2021). Phenotyping for slow bolting stress was conducted by performing an experiment in controlled environment at University of Agriculture, Faisalabad, Pakistan. The conditions were optimum for accurate measurement of the number of days from the planting of seed to the formation of ring around the apex and premature termination of the RIL (Naveed et al. , 2024).

Aphid resistance, many different sources of resistance were introduced into a susceptible line. Using NIAW 1461 seeds, the first two resistant populations that were developed were IT91K-377 and IT91K-100 and seeds of these populations were employed to create specific resistant RILs (Ewing et al. , 2024). Enumerating complete host genetic resources of mustard aphid, fungal pathogens and Sclerotinia sclerotiorum Garg et al. (2008) listed insect-resistant and slow bolting and Sclerotinia sclerotiorum resistant varieties. They also recognized a group of genotypes across these sources that were earlier chosen for a repeated analysis at another time (Clark et al. , 2024).

It is therefore important to construct genetic linkage maps using different molecular markers so as to successfully perform QTL analysis in B. juncea. At the beginning, RAPD protocol was applied to detect dominant markers in F1 generations; in to tal, B. juncea was genotyped using up to 1000 RAPD markers. Such markers were employed to develop a BCDH mapping population to highlight the possibility of transferring blackleg resistance genes from and B. juncea canola quality line to the seed production gene pool. However, the RAPD markers were less reproducible and not amenable for inter laboratory comparison and therefore other methods such as the simple sequence repeats were considered. Additional 1000 potential SSR markers for B. juncea are from B. rapa using in silico approach, and 95 SSR markers are under-utilization to show the transfer of sulfur efficiency genes from wild germplasm to cultivated B. juncea. SSR markers have offered some benefits over RAPDs and has over time been standardised but to create a high-density and cheap marker system, a SNP array specific to B. juncea using illumina sequencing has recently been developed. Chen et al. , Wang et al. , & (Wang et al. , 2024)

Hence, the knowledge of the genetic map and the QTL map is pivotal to the marker-assisted breeding in B. juncea improvement. First, screening was performed using markers already available from related species of Brassica, and subsequently, markers more accurate to the specific traits were developed. Different molecular markers including RFLPs, AFLPs, and microsatellites have been used in map development as well as in QTL analysis. Ronne et al. , 2024) Linking QTLs with higher density maps with gene oriented markers can support MAS. Finally, breeders could decide to have major QTLs and/or to pyramid several QTLs depending on the nature and architecture of target traits and cost of a marker-based approach. (Chizk et al. 2032)

7. Application of Marker-Assisted Selection for the Improvement of Brassica juncea.

That is why it can be said that marker-assisted selection is one of the most important tools in present day plant breeding. This brings ability to create efficient genetic map strains in order to harness the diverse genetic markers in Brassica juncea. This development makes it possible to improve the yield and market value of B. juncea varieties that breeders would prefer to develop. Through the application of this technique, breeders can manipulate the genetic map of this plant species and accordingly attend to the needs of the ever-evolving agriculture industry (Park et al. , 2024).

Derived markers are an invaluable implementation that facilitates and accelerates the process of transferring favourable genes from wild forms of crops to their cultivated counterparts. This technique has also been vigorously practiced contributing towards enhancement of productivity, disease resistance and agriculture sustainability. The success here is to select and transfer favourable genes for drought tolerance, disease control, and improved nutritional characters into elite varieties. Since there is an increased genetic pool it helps the breeders to come up with crops that are immune to environmental factors and changing pests.

This is witnessed through Yield and Stress-tolerant varieties which produced to meet the global yields, reduced inputs and minimal harm to the environment. In as much as there has been development in genomic technologies, it has been seen that marker assisted introgression is still opening up to even more possibilities in plant breeding. In the words of Montesinos-López et al. , 2023 , breeding for natural diversity of wild relatives can be a game changer in bringing out valuable traits to generate high performance, sustainable and resilient crops for the future.

Genomic selection, therefore, has dramatically changed crop improvement so far by allowing breeder to select for favorable traits as has not been seen before. Through this ground breaking technique advanced strains of crops with improved resistance and yield as well as nutritional worth have been produced. MAS proves to be an excellent breeders Facility to help breeders understanding the genetic potential of crops better and to take the process of crop improvement to new heights (Kundu et al. , 2024).

8. Molecular Techniques for Enhancing Brassica juncea Line.

It is possible to resequence specific lines or genotypes of B. juncea along with its wild relatives to the reference genome with benefits arising from a provisional identification of the genome. It can thus reduce the time and costs of discerning trait-associated variant(s), diagnosing the trait, and back-crossing the trait into elite line. The specified and nonspecified germlines can also be profiled via whole-genome sequencing technologies for genetic modification such as doubled haploid production to avoid linkage drag, and controlling for targeted trait expression (Wojcik et al. , 2023)

With the help of sequenced B. juncea genome, the identification of genes and traits important for this crop is going to be easier and more accurate. Thus, existing data of related species genetics such as Arabidopsis enables breeders to accelerate the search for wanted genes in the Brassica juncea and integrate them to enhance gene variety. Even though there could be limited interest in sequencing what can be regarded as a 'minor' crop such as B. juncea, reference genome serves as an indispensable starting point for speeding up the breeding programs and enhancing exploration of this essential crop's potential with reduced costs due to the progress in sequencing technologies (Shorinola et al. , 2024).

Advanced generation modification for improving Brassica juncea needs a group of genetic tools and expertise such as bioinformatics, comparative genomics and gene targeting. Marker-assisted selection can be helped by the processes of genetic mapping and physical map with gene-based markers. Using cytogenetic resources in conjunction with genomic techniques may offer a foundation for elucidating gene function, expression of genes, and the regulation of genes involved in transforming complex traits (Petroli et al . , 2023). B. juncea as made some genetic improvement due to domestication bottleneck therefore has limited ability to meet the demand in the industry. Gene targeting, insertional gene disruption as well as the in planta gene modification to change the gene expression and composition of plant. However, these methods needs higher transformation efficiency and more information of the B. juncea genome to get preferable genetic alteration. Here L., Y., T., and C., & E.(Liu et al. , 2024)

Al though a number of traditional plant breeding studies have been reported on Brassica juncea , very little molecular breeding efforts have fructified in terms of improved cultivars. The construction of saturated genetic linkage maps is important to dissect the genetic basis of complex quantitative traits and for the molecular improvement of this species(Patra, 2020). Previous linkage maps have been constructed with restricted links because high-throughput sequences can now allow linkage maps with single nucleotide polymorphism markers. Such complex advanced linkage maps will enable comparative genomic studies, the assessment of conserved gene blocks and utilization of information from other related species of the genus Brassica to enhance desirable traits in B. juncea. It will also be important to build a pan-genome from the different B. juncea genotypes for precision breeding because we will be able to relate specific genotypes to certain traits (Park et al. , 2024).

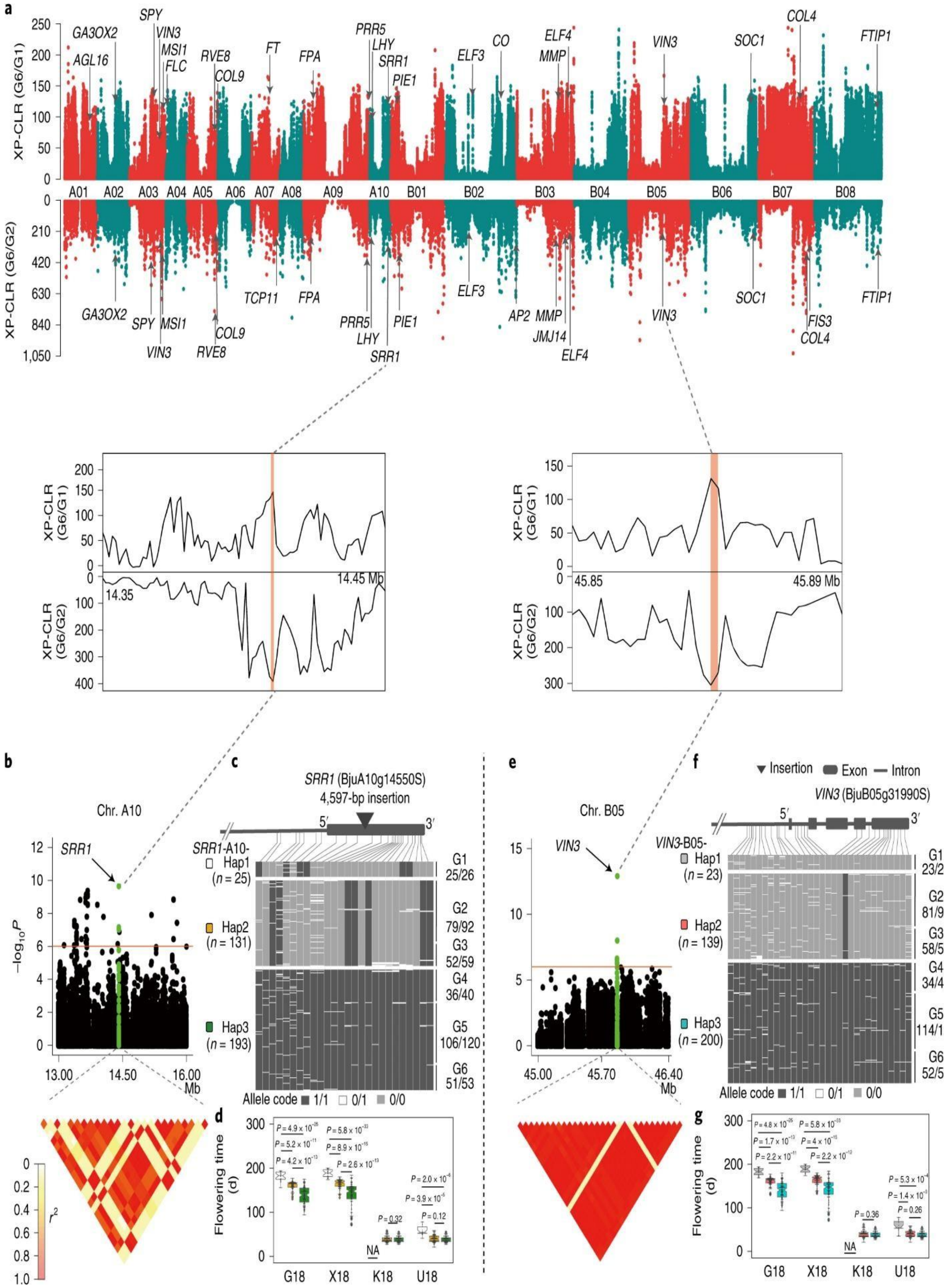

Figure 3. Genome-wide association analysis and domestication signals in Brassica juncea, showing selective sweeps, key flowering-time genes (e.g., SRR1, VIN3), haplotype structure, and flowering time associations across chromosomes. “Source: Kang et al. (2021).”

9. Future Prospects and Challenges

The major challenge in the short-term is to identify suitably the mechanisms that will facilitate links and reallocation processes in order to reveal the genetic improvement as developmentally stable and localized cultivars fit for the poor farming communities. One of the mistakes made in the past is in selectively identifying superior traits that are present in the elite germplasm, to be used in breeding efforts with the landraces, only to find that the actual change is hard to transpire, or introduce to the desirable traits of the landraces without eradicating beneficial and important traits altogether. A better strategy would be to develop enhancements for particular target environments and develop intermediate strategies to train local farmers regularly about the necessity of utilization and to enable them to put into practice breeding goals which they had previously not planned. Yet, this must be supported by a well coordinated capacity development process in relation to human capital development, development of community seed banks among others, and development of appropriate policy framework. This will assist to prevent the promotion of marginal solutions or the sell out of such innovations by multinational companies later.

Brassica juncea is believed to have undergone the first domestication in Western Asia then underwent secondary gene fixation in the regions of India and China and also Eastern Europe for seed production. As a result, there exists a large pool of diverse germplasm which is capable of withstanding various biotic and abiotic pressures and can efficiently suit human end uses. However, as compared to B. rapa, another relatively minor crop has not received the same level of investment in germplasm resources, characterization of diversity and systematic exploitation as has been invested in the better known and better documented B. oleracea. It is therefore expected that something done in the other member species of Brassica through genomics, genetics, and resourcing could be effectively utilized to overcome the challenges facing sustainable production and plant utilization in B. juncea. Closely related with this aspect is to determine how many genes and alleles there are for the major crops and model plant species currently available and examine if any of them could be implemented to enhance B. juncea through transgenic or participatory breeding techniques.

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