
REVIEW ARTICLE

Heterosis Breeding in Oilseed Brassicas: An Indian Perspective

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ABSTRACT

Rapeseed- mustard is the second most important oil seed crop in India. To cope up with the increasing population, the yield potential of this oil seed crop needs to be improved. Heterosis breeding is suggested as a strategy to break the yield barrier in these predominately self-pollinated crops. Considerable hybrid vigour for seed yield has been reported by many researchers. Several CMS-FR systems, the most reliable method of pollination control, have been developed and rectified in Brassica oil seed crop. Apart from the mori CMS system, the recently developed eru and ber systems are stable and with almost no adverse effect in B. juncea backgrounds. Now the efforts need to be directed towards developing rapeseed- mustard hybrids with superior yield potential. A few glimpses of the significant research findings from the past few decades in hybrid breeding of rapeseed- mustard in an Indian context have been reviewed in this article.

Key words: Heterosis breeding, Oilseed Brassicas, Pollination control systems, CMS system, Hybrid

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INTRODUCTION

Brassicas are the second most important oilseed crop in the world after soybean. China, India, Canada, Japan and Germany are the major rapeseed-mustard growing countries. It is the second most important oilseed crop in India, next to soybean. India is one of the largest rapeseed-mustard growing country occupying first position in area and third position in production. Four oleiferous *Brassica* species viz., *Brassica juncea*, *B. napus*, *B. rapa* and *B. carinata*, commonly called rapeseed-mustard, are cultivated in about 6.07 million ha area and producing 7.92 million tons in India during 2016-17 (www.nfsm.gov.in). Out of these, Indian mustard (*B. juncea*) contributes more than 80 per cent to the total rapeseed-mustard production of the country. *B. juncea* has an enormous cultivation potential in semi-arid areas as it is known to be more drought tolerant and shattering resistant than *B. napus* and *B. rapa* [1]. However, the production and productivity of rapeseed- mustard in India is almost static during the last decade and productivity is hovering between 1 to 1.2 t/ha, which is much below the world's average of 1.9 t/ha. Cultivar development in mustard has been mostly undertaken by breeding methodologies for self-fertilized crops. Efforts in past were directed towards development of pureline varieties, which do not mobilizes sufficient genetic variations. Heterosis breeding has been suggested as one of the most effective means to break the yield barrier. Oilseed *Brassica* species are well suited for hybrid breeding because of their natural biological characteristics and higher heterotic response.

Heterosis in *Brassica* was first reported by Singh and Mehta in 1954 [2]; however, its commercial utilization has been demonstrated only during the past two decades. Fu and Yang [3] divided the progress of rapeseed-mustard hybrid breeding into three periods viz., the exploration period (1940-1967), the preparation period (1968-1984) and the utilization period. Heterosis was recognized during the exploration period. During the preparation period different CMS systems have been developed. In the utilization period first CMS hybrid Qinyou No.2 of *B. napus* has been released. Utilization of biotechnological tools to rapeseed-mustard breeding has also been started in this period. Rapeseed – mustard hybrid breeding programmes in India was started in 1989 when Indian Council of Agriculture Research (ICAR) started a special project on “promotion of research and development efforts on Hybrids

in selected crops" [4]. The present review summarizes salient past research findings and developments and attempts to prioritize the future research needs in heterosis breeding of Brassicas in India.

REQUIREMENTS FOR COMMERCIAL EXPLOITATION OF HETEROSIS

There are three main requirements for hybrid breeding: 1. Extent of outcrossing 2. Standard heterosis 3. Pollination control systems

Extent of outcrossing

Among rapeseed-mustard, *B. juncea* and *B. napus* are predominantly self-pollinating but *B. campestris* (now known as *B. rapa*) ecotypes except yellow sarson are cross-pollinated [5]. In Indian mustard outcrossing varied from 7.6 to 22% [6] whereas, in *B. napus* it is reported up to 21% [7]. Insect pollination by honey bees has observed as an important mechanism of outcrossing in *B. juncea* [8]

Heterosis

In many crops, such as maize, pearl millet, sorghum, cotton, rice etc. hybrid vigour has been commercially exploited. After the report of heterosis in Brassica by Singh and Mehta [2], various studies were carried out to estimate the heterosis for seed yield. The results indicated significant level of heterosis like 13 to 91% in *B. juncea* [9], 25 to 110% in *B. campestris* [10] and 10 to 72% in *B. napus* [11]. In India, different workers reported heterosis in Indian mustard for yield traits to the extent of 67.71% [12], 44.80% [10] and 80.97% [13] in the F_1 crosses. Most of these studies reported heterosis over better parent (heterobeltiosis). Singh *et al.* [14] evaluated 72 *B. juncea* hybrids, of which 13 displayed highly significant sca effect, heterobeltios>15% and higher per se performance for seed yield. Up to 43% mid-parent heterosis for seed yield was reported after the evaluation of *B. napus* hybrids under nutrient poor conditions. This suggested the existence of a strong heterotic effect on nutrient uptake efficiency [15]. Besides seed yield, hybrid vigour has also been observed for other characters such as water absorption & esterase enzyme activity during seed germination [16], total biomass [17] and yield components [18].

It has been demonstrated by many researchers that the use of resynthesized brassicas as one of the parents in hybrid development led to much higher level of heterosis. Szala *et al.* (2019) [19] used semi – resynthesized *B. napus* lines as a parent for developing hybrid cultivars and found high heterosis effect for seed yield (4.56% to 90.17% heterobeltiosis) in the F_1 hybrids. A population of new type *B. juncea* was developed by Wei *et al.* [20] by combining the A^r subgenome from *B. rapa* and the B^c subgenome from *B. carinata* and observed a considerable potential for heterosis in inter-subgenomic hybrids between new-type *B. juncea* lines and traditional *B. juncea* accessions. It was found that the level of mid parent heterosis in hybrid of the inbred lines derived from *B. napus* × *B. oleracea* cross was twice greater than the level of heterosis found for the hybrids of inbred lines derived from spring × spring or winter × spring *B. napus* crosses [21].

Development of heterotic gene pool is an important approach in improving the level of heterosis in rapeseed-mustard hybrids [22]. Lefort-Buson *et al.* [23] conducted a study to investigate the relationship between heterosis and geographic distance in cultivars of *B. napus*. They established three groups of F_1 hybrids, i.e., the European group (E X E), the Asiatic group (A X A) and the mixed group (A X E), and observed that heterosis in the E X A group was higher than the E X E or A X A group. It was also observed that if the parents had originated from different geographic areas or had separate evolution over a long time or well adaptability to target areas, the heterosis would be better. Similar results were also reported in *B. juncea* by Jain *et al.* [24]. Different methods are available for selection of parents for their utilization in hybrid breeding. If small number of germplasm is available, it is possible to check the individual hybrid performance to select parents. Otherwise diallel /factorial crosses can be used to identify the better parental combinations. If large number of germplasm is available, considering the geographic origin of genotypes or polymorphism for molecular markers or using D^2 statistic, it is possible to determine the best parental combinations [25].

Pollination control systems

Commercial exploitation of heterosis is possible in brassicas with the availability of standard heterosis and efficient hybrid seed production systems such as self-incompatibility and male sterility systems. Sporophytic self-incompatibility (SI) and different male sterility systems such as genetic male sterility (GMS), cytoplasmic genetic male sterility- fertility restoration (CMS-FR) and genetically engineered male sterility systems are available in brassicas. Efforts were also made to identify gametocides which imparts male sterility [26]. Among these, CMS-FR is the most effective pollination control mechanism for the production of hybrid seed in many crop plants including *B. juncea* [27].

Genetic male sterility

Different genetic male sterility sources are available in *B. juncea* [28], *B. campestris* v. brown sarson [29], *B. campestris* v. yellow sarson [30] and *B. campestris* v. toria [31]. Most of them are spontaneous in origin

and exhibit monogenic inheritance. Use of genetic male sterility for hybrid seed production is not economically viable because rouging of fertile plants from the male sterile line plot require additional labour. Till now, any linked seedling markers or pleiotropic effect of the male sterility gene has not been reported for the easy identification of male fertile plants before the initiation of flowering [32].

Genetically engineered male sterility

A *B. napus* GMS called barnase/barstar system has been developed by engineering the chimeric ribonuclease gene which was characterized by its extreme cell specificity in the tapetal cells of immature anthers. The gene product destroys the tapetal cell layer, prevents pollen formation and results in male sterility [33]. It is also possible to restore fertility in genetically engineered male sterile plants by crossing with male plants that were transformed with a chimeric tapetal cell-specific ribonuclease inhibitor gene. The chimeric ribonuclease gene was linked to the phosphinothricin resistance gene, which act as dominant marker for sterility trait [33]. Similar system was developed in *B. juncea* by Jagannath and coworkers in 2002 [34].

Cytoplasmic male sterility-fertility restoration (CMS-FR) system

CMS-FR system has been identified as most potential method for hybrid seed production in brassicas. The male sterility inducing cytoplasm was first discovered in Japanese radish (*Raphanus sativus* L.) by Ogura in 1968 [35]. Later several male sterility systems, both autoplasmic and alloplasmic, have been developed in oilseed brassicas. Autoplasmic CMS are the result of mitochondrial genome mutations in a cultivated species while alloplasmic systems are produced through repeated backcrossing by transferring the nuclear background of a cultivated species into the cytoplasm of a wild species. The different autoplasmic and alloplasmic CMS systems reported in rapeseed-mustard [36] are given in table 1 and table 2.

Table 1: Autoplasmic CMS Systems reported in *Brassica* spp.

Code	Species	Restoration Status	Reference
Shiga-Thompson(nap) System	<i>B. napus</i>	Available	37 & 38
Polima (pol) system	<i>B. napus</i>	Available	39
Mokopo/ Korean system	<i>B. napus</i>	Available	40
MS-4 System	<i>B. juncea</i>	Available	28
Jun System	<i>B. juncea</i>	Available	41
Line-14/campestris System	<i>B. campestris</i>	Available	42
681A	<i>B. napus</i>	Available	43
hau	<i>B. juncea</i> <i>B. napus</i>	Available	44 & 45

Table 2: Alloplasmic CMS Systems reported in *Brassica* spp.

Cytoplasm donor	Code	Technique used	Restoration status	Species	References
<i>Raphanus sativus</i>	ogu	Inter specific cross, Protoplast fusion	Available	<i>B. napus</i> <i>B. juncea</i>	46 & 47
<i>Diplofaxis siifolia</i>	sif	Intergeneric cross	Not available	<i>B. juncea</i>	48
<i>B. tournefortii</i>	tour	?	Unstable, genotype specific partial restoration	<i>B. napus</i> <i>B. juncea</i>	49 & 50
<i>B. oxyrrhina</i>	oxy	Interspecific cross, protoplast fusion	Not available	<i>B. juncea</i>	51
<i>Trychystoma ballii</i>	trachy	Protoplast fusion	Incomplete	<i>B. juncea</i>	52
<i>Moricandia arvensis</i>	mori	Protoplast fusion	Available	<i>B. juncea</i>	53 & 54
<i>D. sietiana</i>	sie	Intergeneric cross	Not available	<i>B. juncea</i>	55
<i>D. catholica</i>	cath	Intergeneric cross	Available	<i>B. juncea</i>	55
<i>Enarthrocarpus lyratus</i>	lyr	Intergeneric cross	Available	<i>B. juncea</i> <i>B. napus</i>	56 & 57
<i>Erucstrum canariense</i>	can	Intergeneric cross	Available	<i>B. juncea</i> <i>B. napus</i>	58 & 59
Synthetic <i>B. napus</i> SN-706	126-1	Interspecific cross	Available	<i>B. juncea</i>	60
<i>D. eruroides</i>	Eru	Intergeneric cross	Available	<i>B. juncea</i>	61 & 62
<i>D. berthautii</i>	ber	Intergeneric cross	Available	<i>B. juncea</i>	61 & 63
<i>Isatis indigotica</i>	Inap CMS	Protoplast fusion	Not available	<i>B. napus</i>	64

Among all these CMS systems reported, the commercially exploited systems for hybrid production are *tour*, *ogu*, *polima*, 126-1 and *mori*. In case of alloplasmic CMS, floral deformities, absence of nectaries,

chlorosis etc. are common drawbacks, however this can be rectified through somatic hybridization. The major limitation in alloplasmic CMS system is the absence of fertility restoring genotypes among euplasmic germplasm and the restorer gene need to be introgressed from the corresponding alien species itself. Among the different sterile cytoplasms *Moricandia arvensis* (*mori*), *Diplotaxis eruroides* (*eru*) & *Diplotaxis berthautii* (*ber*) cytoplasms are proved to be stable and with almost no adverse effects in *B. juncea* backgrounds [65, 66].

Chemical hybridizing agents

In rapeseed-mustard, a few reports on chemically induced male sterility are available. A study by Banga and Labana (1984) [8] showed that spraying 0.25% ethrel, twice before the emergence of the first flowering shoot, induced 90% male sterility in Indian mustard. Guan *et al.* (1990) [67] investigated the extent of male sterility induction in *B. napus* by 17 chemical male gametocides, of which three gametocides; MG1, MG2 and MG3 induced 60-80% male sterility when the gametocides were sprayed at the bud stage. *B. napus* hybrid Shuza No.2 produced by spraying MG1 was released in China. But the major limitations of this system are incomplete male sterility (could be affected by environmental factors and/or the differential developmental stage of pollens), reduced female fertility and environmental hazard imposed by usage of gametocides [68].

Diversification of cytoplasmic male sterility-fertility restoration (CMS-FR) systems

For a sustainable hybrid breeding programme diversification of CMS-FR system is required. Exploitation of a single cytoplasm may lead to disease and insect-pests epidemics [69]. This is evident from past experiences with maize and pearl millet crops. In maize the extensive use of Texas cytoplasm lead to the southern leaf blight epidemics caused by *Bipolaris maydis* race T in USA [70]. In India the pearl millet hybrids based on Tift 23A₁ cytoplasm succumbed to downy mildew infection in 1970's [71]. This has led to discovery of diverse cytoplasms in different crop plants such as maize (CMS-T, CMS-C & CMS-S), pearl millet (A₁, A₂, A₃, A₄ & A₅), sorghum (A1, A2, A3, A4, A5, A6, 9E and KS) and rice (BT- CMS, HL- CMS, WA- CMS, LD- CMS and CW- CMS) etc. (72, 73, 74, 75, 76, 77). Similarly, in brassicas different alloplasmic and autoplasmic cytotsterility sources were identified (table 2.1 and 2.2).

In case of alloplasmic CMS system development of restorer lines, which restore fertility in their respective sterile cytoplasms, is also important for diversification of the CMS-FR systems. Fertility restorers for different cytoplasm in brassicas are not available in natural polulations, thus, need to be derived from their respective cytoplasm donors. The fertility restorers for different cytoplasm like *mori*, *ogura*, *cath*, *lyr*, *nap*, *pol* etc. are now available. Furthermore, a *B. juncea* line carrying fertility restorer (*Rf*) gene from *Moricandia arvensis*, restores fertility in *Diplotaxis catholica*, *Diplotaxis eruroides* and *Diplotaxis berthautii* cytoplasms and the fertility restoration is under gametophytic control [78, 62, 63]. In gametophytic fertility restoration system only *Rf* gene-carrying pollen is functional and F₁ hybrid plants produce 50% fertile and 50% sterile pollens [78]. This provides a great opportunity to diversify the cytotsterility sources without investing in looking for the fertility restorer gene.

Rapeseed-Mustard Hybrids Released In India

Availability of effective means of hybrid seed production led to the development of six commercial hybrids in India through All India Coordinated Research Project on Rapeseed-mustard [79] as given below:

Name of hybrid	Developing institution	Year	CMS source
<i>B. juncea</i>			
NRCHB-506	NRCRM, Bharatpur	2008	mori
DMH-1	DUSC, Delhi	2008	126-1
PAC-432	Advanta, India	2010	ogu
PAC-437	Advanta, India	2011	ogu
44S01	Pioneer	2012	ogu
<i>B. napus</i>			
PGSH-51	PAU, Ludhiana	1996	tour

However, the level of yield gain achieved from these hybrids is marginal. As a result, the adoption rates of these hybrids are very less in the country as compared to pure line varieties [4]. Recently, a genetically modified mustard hybrid Dhara Mustard Hybrid 11 (DMH 11) was developed by Professor Deepak Pental and his team, Delhi University. It contains the bar, barnase and barstar gene system and claims to yield 25-30% more than the best standard Varuna in the country. But its commercial release is delayed due to the conflicting results from field trials and safety evaluations [80, 81]

Effects of genetic backgrounds on fertility restoration

Identification of heterotic combinations and then converting them to CMS and restorer lines are important steps in hybrid breeding programmes [14]. For diversification of restorer lines stability of fertility restoration in hybrids developed from A and R lines having different nuclear backgrounds is important. The fertility restoration was governed by two genes in *tournefortii* (*tour*) cytoplasmic male sterility (CMS) system in rapeseed (*B.napus*). The fertility restoration showed different segregation patterns such as 12:3:1 or 9:3:4 depending upon female parent genotypes and/or modified expression of the restorer gene(s) in different genetic backgrounds [82]. Vinu and coworkers [83] studied the effect of nuclear background on fertility restoration in *B. juncea* using *mori*, *eru* and *ber* cytoplasm and a common fertility restorer line. 108 single cross hybrids, 36 hybrids in each cytoplasm were evaluated and found that the per cent pollen fertility in hybrids was influenced by the genetic backgrounds of parents. However, this effect was not consistent for any nuclear background of parents.

Application of molecular markers in heterosis breeding

Currently molecular markers are considered as highly effective tools for genetic analyses and have applications in all areas of plant breeding. They have been used for predicting the heterosis and tagging or mapping of male sterility/fertility associated genes and heterotic loci. In Brassica many researchers used different molecular markers for assessing genetic diversity and to predict the heterosis from the genetic distance estimates. Becker and Engqvist [84] indicated the usefulness of RAPD-based genetic distance estimates to predict heterosis for leaf dry matter production in *B. napus*. Plieske and Struss [85] by using SSR markers suggested that they provide a reliable and effective means for predicting heterosis in Brassica. Shen *et al.* [86] found a positive association between hybrid seed yield and genetic distance estimated from AFLP in *B. napus*. In rapeseed, as well as in other species, a positive correlation has been found between genetic distances determined by molecular markers and heterosis [87]. A study on Ethiopian mustard (*B. carinata* A. Braun) conducted by Teklewold and Becker (2006) [88] compared the phenotypic distance and molecular distance to predict the heterosis and F₁ performance. Parental distances estimated from phenotypic traits better predicted heterosis, F₁ performance and GCA than distances estimated from RAPD markers. However, correlation between phenotypic and molecular distances was observed to be low. Diers *et al.* [89] using RFLP markers and Riaz *et al.* (2001) [90] using sequence-related amplified polymorphism (SRAP) in *B. napus* reported a strong association of heterosis with marker heterozygosity and recommended their use for predicting heterosis. In contrast to above observations, Knaak and Ecke [91], Girke *et al.* [92] and Yu *et al.* [93] in *B. napus* and Jain *et al.* [24] in *B. juncea* reported a low association of DNA markers with heterosis. Qian *et al.* [94, 95] in their studies, involving parents from different ecotypes, reported low correlation between parental genetic distance and hybrid performance. Similarly no significant association was found between genetic distance and hybrid performance in *B. juncea* after studying the relationship of parental distances estimated from phenotypic traits and SSR markers [96].

Ashutosh and co-workers [97] tested the utility of repetitive sequence based Polymerase Chain Reaction (rep-PCR) technique for distinguishing different CMS lines of *B. juncea*; and also identified a Sequence Characterized Amplified Region (SCAR) marker capable of distinguishing CMS *catholica* from other lines. Cleaved Amplified Polymorphic Sequence (CAPS) markers for the plastid gene *psbB* have identified for *D. berthautii* [63] & *D. eruroides* [62] cytoplasm, which could be useful for quick identification of these CMS lines. Ashuthosh *et al.* (2007) [98] used BC₁F₁ population and identified two AFLP and one SCAR markers linked to the male fertility restorer gene, derived from *Moricandia arvensis* in *B. juncea* nuclear background, with a map distance ranging from 0.6 to 2.9cM. Both the AFLP & SCAR markers are located on one side of the *Rf* locus. Being the dominant markers application of these markers in MAS is limited because they could not differentiate heterozygous and homozygous dominant plants in the breeding populations. This *Rf* gene from *M. arvensis* can restore the fertility of *D. berthautii* & *D. eruroides* CMS systems as well. Recently Bisht *et al.* [99] identified 13 SSRs and one STS marker flanking the *Rf* gene and confirmed its location on A09 linkage group of *B. juncea*. The two closest flanking markers reported, BjESSR06 and BjEST01 were at 0.6 and 1.4 cM apart from the *Rf* locus and can be used for marker assisted selection (MAS). Since the SSR markers are codominant and reproducible in nature they are capable of differentiating the dominant homozygous plants from the heterozygous plants, thus, highly suitable for converting maintainers into restorers through backcross breeding. Wei and coworkers [100] identified restorer lines for hau CMS in *B. napus* by extensive test crossing and mapped the restorer gene *Rfh* to a 94 kb candidate region on chromosome A03.

Advances in genomic studies can lead to better understanding of the molecular mechanisms of heterosis. Transcriptome analysis of interspecific hybrid between *B. napus* and *B. rapa* revealed the coexistence of multiple gene actions in the hybrid and delivered a list of candidate genes and pathways for heterosis

[101]. Genetic analysis of heterosis in rapeseed at the QTL level detected a total of 33 QTLs for four traits and concluded that epistasis together with all levels of dominance from partial to overdominance is responsible for the expression of heterosis in rapeseed [102].

EPILOGUE

Few hybrids released in India are not adopted in a large scale because of their marginal yield improvement over the ruling pureline varieties. Many improved pollination control systems such as *mori*, *eru*, *ber* etc. are available which aid the large scale hybrid seed production. Currently the main challenge in Brassica hybrid breeding is the identification of superior heterotic combinations. Advances in molecular genetics and genomic studies are leading to the better understanding of the molecular mechanisms of heterosis and identification of heterotic QTLs. This may open a way forward to screen a large number of parental combinations to identify commercially viable heterotic combinations in cost effective manner within a short period of time.

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