Genetic diversity and its association with heterosis in *Brassica rapa*

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Abstract

Diverse morphotypes of *Brassica rapa* comprising toria (99), brown sarson (22), yellow sarson (12, including 6 land races) and some toria introgression lines (26) besides six land races were evaluated for various morphophysiological traits. Diversity analysis (UPGMA) allowed delineation of test germplasm (159) into four distinct groups out of which two major groups comprising 59 and 96 lines each had high dissimilarity coefficient of 1.19. Three genotypes were included in group III with dissimilarity coefficient of 1.10 whereas group IV comprising one yellow sarson type land race (Bithari Mandi) appeared to be most distinct with a dissimilarity coefficient of 2.26. Group I included all morphotypes whereas majority of the toria genotypes (69) were associated with few accessions of brown sarson (9), yellow sarson (1) and introgressed lines (17) in group II. Based on clustering, inter-group and intra-group crosses were made and resultant hybrids evaluated for standard and better parent heterosis. Standard heterosis in the intra-group hybrids ranged from -5.4 to 102.0 per cent (average 31%) whereas estimates for the inter-group hybrids were -45.9 to 103.5 per cent (average 17%). Similarly, better parent heterosis ranged from -32.2 to 231.6 per cent (average 92%) for intra-group hybrids, and -44.8 to 82.6 per cent (average 0.1%) for inter-group hybrids. Intra-group hybrids showed higher heterosis than inter-group hybrids. Two intra-group hybrids showing high standard heterosis were EC 3390-101×PBT 37 (102%) and MBR 101×EC 513426 (67%). Promising inter-group hybrids were EC 3390-101×Sanya (104%), Candle×Sunbean (54%), EC 3390-102×Agena (52%), EC 3390-101×Sunbean (47%), IB 309×Bithari Mandi (37%), Debra×Chail Chowk Badi (32%) and EC 3390-102×Emmer (25%). Results indicated blurred intersubspecies boundries, a consequence of extensive inter sub-species hybridizations undertaken by *Brassica* breeders. Further, heterosis for yield appeared to have resulted largely from complementation of yield contributing traits in specific hybrid combinations involving agronomically superior parents rather than genetic or geographic diversity per se. Association of heterosis with diversity analysis based on DNA polymorphism will be discussed.

Key words: *Brassica rapa*, heterosis, diversity, gene pools

Introduction

Heterosis is a major breeding tool for improving productivity potential of crop plants and genetic diversity of parental lines is usually considered to be an important factor to maximize the chances of heterotic combinations. *Brassica rapa* is a cross pollinated crop owing to self incompatibility. The availability of CMS systems in this crop has now prompted efforts to develop F_1 hybrids. Although, prevalence of self-incompatibility is a limiting factor for exploiting CMS systems. Not many attempts have been made to assess genetic diversity of adequate number of germplasm lines and its association with performance of F_1 combinations. Present communication reports the outcome of a very elaborate study, involving 159 diverse morphotypes, to delineate germplasm on the basis of morphological diversity and polymorphism generated by molecular markers. Association of diversity patterns with heterosis was also attempted at a limited scale.

Material and Methods

Experimental material comprised 159 diverse morphotypes of *Brassica rapa* comprising toria (99), brown sarson (22), yellow sarson (12, including 6 land races), toria introgression line (26). All the brown sarson types were of exotic origin. Beside this, twenty hand bred F_1 combinations were also evaluated. The F_1 combinations were developed based on divergent clustering. Parental lines and the hybrids (along with commercial check variety, TLC 1) were raised separately as paired row in an augmented design at a row to row spacing of 30 cm and plant to plant spacing of 10-15cm. Standard agronomic practices were followed throughout the crop season. Data were recorded for ten random plants per genotype/F_1 and averaged for key morpho-physiological characteristics including yield and its components. Statistical analysis for morphological data and polymorphic data generated by RAPD primers was conducted using the software programme NTSYS pc version 2.02e (Rholf 1998). Clustering was done on the taxonomic distance matrix with the unweighted pair group method based Arithmetic average (UPGMA). Dendrograms were generated based on the genetic distance matrix. Heterosis was estimated as increase or decrease in the mean performance of hybrid(s) over commercial variety, TLC 1, expressed as per cent.

Results

Diverse morphotypes of *Brassica rapa* comprising toria (99), brown sarson (22), yellow sarson (12, including 6 land races) and toria germplasm carrying stable introgressions from a wild species *Enarthrocarpus lyratus* (26) were evaluated for for various morphological traits to understand diversity patterns. Cluster analysis divided test germplasm (159) into four groups (Table 1), two major groups each comprised 59 and 96 lines respectively, with dissimilarity coefficient of 1.19. Three and one genotype each were grouped into two small groups with dissimilarity coefficients of 1.10 and 2.26, respectively.

Group I carried 13 brown sarson, 9 yellow sarson, 9 introgressed and 28 toria lines. Majority of toria genotypes (69) were clubbed with small number of brown sarson (9), yellow sarson (1) and introgressed lines (17) in group II. Group III had three genotypes two from toria and one from yellow sarson. A yellow sarson land race Bathari Mandi appeared to be the most diverse.

Tabel 1: Germplasm grouping based on morphological parameters

Group	Germplasm Lines	Germplasm Type
I	5244, Agena, BAUR 9502, BXY, Candle, CH 1, Chail Chowk Badi, EC 3390-101, EC 513426, EC 513427, ECHO, IB 309, IB-648, Mandi 1, Mandi 2, Margon, MBR 101, MCT 96, Mitra, MYSEL 201, NAKO YELLOW, NDTC 9810, NDYR 17, NRCT 9813, PBT 101, PBT 37, PBT 47, PT 2-2002-26, QRT MK 3411, RADAYS, S 31-2, Sissue, SL 5-13, SL 5-15, SL 5-213, SL 244, SPAN, T 9, TH 68, TK 032, TKG 5, TL 15, TL 23, TL 28, TL 88-12, TL -88-9, TL 9001, TL 9001-85, TL 96-6, TL-88-29, TL-88-4, TLV 2019, Torch, TS 001	Toria (28) Introgressed lines (9) Brown sarson (13) Yellow sarson (9)
II	BAUST 1, BAUST 2003, BAUST 21, Debra, EC 102, Emmer, JMT 01, JMT 03, JMT 05, JMT 06, JMT 07, K 24-1, MOT 9901, NDT 2021, NDT-03-1, NDTC 9810, NPJ 951, NRCT 0102, OR 9804, PBT 11, PBT 221, PT 303, PT 2002-15, PT 9902, PTYS 2010, RCBC, RGN 107, Sanya, SLC-6, SL 5-13-2, SL 5-31-3-85, SL-27, SRT 1-1-2, Sunbean, Sunford, T 1437, TCN-03-7, TH 01-02, TH 9804, TH 9806, TH 9902, TK 02-3, TK 081, TK 9901, TL 2, TL 11, TL 13, TL 17, TL 25, TL 2001, TL 2012, TL 2013, TL 2014, TL 2015, TL 2016, TL 2017, TL 2018, TL 2020, TL 2022, TL 2023, TL 2032, TL 2033, TL 2034, TL 2036, TL 3, TL 30, TL 88-13, TL 88-14, TL 88-16, TL 88-17, TL 88-18, TL 88-31, TL 88-5, TL 9001-1, TL 9001-5, TL 9001-4, TL 9002, TL 9002-2, TL 9003, TL 95-5, TL-95-21, TL 95-22, TL 96, TL 96-19, TL 96-3, TL 9802, TL 99-2, TLC 1, TLC 3, Tobin, TWB 881, Tyko, VLT 1, VLT 2, YSIB 24	Toria (69) Introgressed lines (17) Brown sarson (9) Yellow sarson (1)
III	BAUST 4, OR (NO), PTYS 2005	Toria (2) Yellow sarson (1)
IV	Bathari Mandi	Yellow sarson (1)

Based on genetic diversity, intergroup and intragroup crosses weere made and resultant hybrids evaluated for better parent and standard heterosis. Standard heterosis in the intragroup hybrids ranged from -5.4 to 102.0 per cent (average 31 %), corresponding estimates for the intergroup hybrids were -45.9 to 103.5 per cent (average 17 %). Similarly, better parent heterosis ranged from -32.2 to 231.6 per cent (average 92 %) for intragroup hybrids and standard heterosis ranged from -44.8 to 82.6 per cent (average 0.1%) for intergroup hybrids. Intergroup hybrids showed higher heterosis as compared to intragroup hybrids (Table 3).

Diversity analysis based on polymorphism generated by 30 confirmed polymorphic RAPD primers allowed delineation of a sample germplasm (42), selected on the basis of morphological grouping, into four distinct groups (Table 2). The group III and IV were major groups each comprising 12 and 23 genotypes and related to each other with similarity coefficient of 0.72. Majority of exotic brown sarson lines (10) along with 2 toria lines were clubbed in group III. Group IV comprised brown sarson (6), yellow sarson (4), and toria lines (13). IB 309 appeared to be the most diverse and related to group II with similarity coefficient of 0.68. The group II represented 3 yellow sarson types, including two land races, 2 toria, and 1 brown sarson line.

Tabel 2: Germplasm grouping based on polymorphism generated by RAPD markers

Group	Germplasm Lines	Germplasm Type
I	IB 309	Brown sarson (1)
II	BXY, Bathari Mandi, Nako Yellow, PT 303, SL 6, YSIB 24	Toria (2) Yellow sarson (3)
III	Echo, EC 513426, EC 3390-102-1, EC 3390-101, EC 513427, EC 3390-102, IB 313, IB 1320, Mitra, PBT 37, Sanya, Tobin	Brown sarson (1) Toria (2) Brown sarson (10)
IV	Agena, BAUST 1, Chail Chowk Badi, Debra, EC 3390-102-2, Emmer, Mandi 1, OR (NO), PBT 101, PTYS 2010, PTYS 2005, Sunford, TL 15, TL 2014, TL 2016, TL 2018, TL 2022, TL 2034, TL 2036, TL 30, TL 88-18, TLC 1, Torch	Toria (13) Brown sarson (6) Yellow sarson (4)

Inter and intragroup combinations based on molecular diversity analysis revealed that standard heterosis in intragroup combinations ranged from -45.9 to 103.5 per cent (average 31.7 %), where as better parent heterosis ranged from -34.3 to 231.6 per cent (average 58.2 %). Standard heterosis in intergroup crosses ranged between -19.0 and 52.1 per cent (average 6.4 %) and better parent heterosis ranged from -44.8 to 57.7 per cent (average -7.7 %). Molecular data revealed intra group combinations were more heterotic as compared to intergroup combinations (Table 3).

Discussion

Morphological assessment allowed delineation of a fairly large and geographically diverse *B. rapa* germplasm into four broad groups. The grouping was largely inconsistent with ecotypic and/or geographic diversity. For further fine tuning the diversity patterns, a representative sample (42) from each morphological grouping was used for delineation based on polymorphism generated by molecular (RAPD) markers. Four groups could be formed. The grouping based on molecular markers appeared more consistent with available pedigree records. For example, group II comprised four yellow sarson types (all land races) and two toria types. Aside the toria genotypes Mitra and PBT 37, group III comprised ten exotic brown sarson accessions. Group IV, largest one, was a loose grouping. It included 13 toria, 6 brown sarson and 4 yellow sarson (including 2 land races). There was no perfect sympatny between diversity groups based on morphological and molecular analysis.

Molecular markers have been used in the past to assess genetic variation available in *B. rapa* (Das *et al*, 1999). Several combinations, showing high heterosis were identified (Table 3). However, the level of heterosis is likely to reduce significantly in large scale yield evaluation. Uniformly higher level of average heterosis in intragroup combinations than that observed in intergroup combinations was indicative of poor correlation between geographic/genetic diversity and hybrid performance.

Table 3. Heterosis patterns in intra- and inter-group crosses of *B. rapa*

Diversity assessment mode	Group Combination	Standard Heterosis		
		0-10%	10-30%	>30%
Morphological	I×I	Mitra×EC 513427	IB 648×SV 3333	MBR 101×EC 513426 EC 3390-101×PBT 37
	I×II	-	Mitra×Sunbean	Candle×Sunbean, EC 3390-10×Sunbean EC 3390-101×Sanya EC 3390-102×Agena EC 3390-102-1×Emmer
	I×IV	-	-	EC 3390-102×YSIB 24 IB 309×Bathari Mandi
	II×I	-	-	Debra×Chail Chowk Badi
Molecular	II×II	-	-	EC 3390-101×PBT 37
	III×III	Mitra×EC 513427	-	EC 3390-101×Sanya
	IV×IV	-	-	Debra×Chail Chowk Badi
	I×II	-	-	IB 309×Bathari Mandi
	I×IV	Bxy×Agena	-	
	III×II	-	-	EC 3390-102×YSIB 24
	III×IV	-	-	EC 3390-102-1×Emmer

Conclusions

Geographic/ecotypic/genetic diversity may not be used as a sole criterion for identifying the parents of a hybrid combination. This analysis can, at the best, be used to reduce the number of germplasm lines as candidates for evaluation in hybrid combinations.

References

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