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Evaluation of the breeding value of the spring oilseed rape (*Brassica napus* L.) inbred lines based on a multi-trait analysis

Jan Bocianowski*, Kamila Nowosad[1], Henryk Bujak[1], Tadeusz Luczkiewicz[2] and Dariusz Piesik[3]

Department of Mathematical and Statistical Methods, Poznañ University of Life Sciences, Wojska Polskiego 28, 60-637 Poznañ, Poland; [1]Department of Genetics, Plant Breeding and Seed Production, Wroclaw University of Environmental and Life Sciences, Grunwaldzki 24A, 53-363 Wroclaw, Poland; [2]Department of Genetics and Plant Breeding, Poznañ University of Life Sciences, Dojazd 11, 60-632 Poznañ, Poland; [3]Department of Entomology and Molecular Phytopathology, UTP University of Science and Technology, 20 Kordeckiego, 85-225 Bydgoszcz, Poland

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Abstract

Oilseed rape (*Brassica napus* L.) is the most important oilseed crop after soybean worldwide, especially in the countries with moderate climate. The aim of the present study was to assess the genetic crossing potential of eight inbred lines of the spring oilseed rape (*B. napus* L.) based on the indices of associative combinatory value. The main trait for calculation of multidimensional indices of genetic potential was the seed yield per plant. Obtained results showed that the selection index can enable the choice of the most valuable lines to be practically used in heterotic breeding of the oilseed rape.

Key words: General combining ability, hybrids, multidimensional indices, seed yield

Introduction

Owing to their high yield potential, hybrids are used throughout the world for increasing the productivity of spring oilseed rape. In a breeding programme, it is very important to know the combining abilities of the inbred lines that are used as parents in the process of acquisition of hybrids (Grant and Beversdorf 1985; Brandle and McVetty 1989). Plant breeders can take advantage from such information on combining ability while attempting to develop high-yielding lines and hybrids. Therefore, the knowledge of combining ability is essential for selection of suitable parents for hybridization and for identification of promising hybrids obtained in a breeding programme. With respect to agronomic traits, the breeding value of inbred lines can be estimated based on their progeny, which is developed through different crossing systems. The diallel method of genetic analysis has widely been applied to asses the combining ability of parents in hybrids (Miller et al. 1980; Kadkol et al. 1984; Sherrif et al. 1985). The analysis of the diallel cross by the method proposed by Griffing (1956), which partitions the total genetic variation into general combining ability (GCA) of the parents and specific combining ability (SCA) of the crosses, has commonly been employed. The GCA is the average performance of a particular inbred in a series of hybrid combinations, whereas SCA refers to the performance of a combination of specific inbreds in a particular cross.

The assessment of parent components is a very important stage in the breeding procedure and it is carried out based on different experiments with hybrids (Fabrizius et al. 1998; Bocianowski et al. 2011; Kozak et al. 2011; Liersch et al. 2013). Considering the simultaneous occurrence of positive and negative effects of the general combining ability, an unequivocal estimate of inbred line may be difficult to reach. A solution to this problem can be found through application of the multidimensional index which defines the genetic potential for crossing. The index, related to genetic correlations, heritability and regression coefficients enables selection of the best possible genotypes. The aim of the present investigation was to assess the genetic crossing potential of some inbred

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*Corresponding author's e-mail: jboc@up.poznan.pl

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lines of the spring oilseed rape (*Brassica napus* L.) based on the indices of associative combinatory value.

Materials and methods

As plant material for the preliminary experiment, we used 30 inbred lines of the spring oilseed rape (*B. napus* L.). The inbred lines, obtained from Strzelce Plant Breeding Station, Experimental Station in Borowo, represented wide genetic diversity of the major traits of this species useful in the breeding programmes in Poland. On the basis of field and glasshouse experiments conducted in 2009 and 2010, we selected eight lines. In 2010 and 2011, full diallel cross was performed among the eight chosen inbred lines [type I according to Griffings (1956)] in a glasshouse of the Department of Genetics and Plant Breeding, Poznañ Agriculture University (currently Poznañ University of Life Sciences). The F_1 hybrids were evaluated during 2012 and 2013 in the field of the experimental station of Poznan Agriculture University in Dlon. The field experiments, comprising 64 genotypes (eight parental lines and 56 hybrids), were established in a partially balanced square design (Cochran and Cox 1957) with four replications. In each experiment, there were 256 one-row plots, 1-meter long, with row-to-row distance of 0.5 m. During the vegetative period and after harvesting, the following quantitative traits were measured on 15 plants from each plot. The observations were taken on the diameter of the root neck (DRN), plant height (PH), number of branches per plant (NB), distance to the first branch (DFB), number of pods per plant (NP), number of seeds per plant (NS), 1000-seed weight (TSW), number of seeds per pod (NSP) and seed yield per plant (SY). Based on the data, analyses of variance were computed for all the traits as well as the effects of the general combining ability (GCA) were assessed for both the years. The relationships between pertinent traits were estimated with the use of the Pearson correlation coefficients on the basis of the means for the genotypes. The multidimensional indices which define the genetic crossing potential for the general combining ability (Y_i) were estimated using a maximum-likelihood approach according to the formula as follows (Bujak et al. 2004):

$$Y_i = \hat{g}_0 + \sum_{k=1}^{m} b_k \hat{g}_k ,$$

where: $\hat{g}_0$ represents the assessment of the general combining ability of the basic trait, $\hat{g}_k$ –assessment of the general combining ability of the *k*-th integrated trait, b_k –regression coefficient for the *k*-th integrated trait. The index for a line can be treated as a super-trait represented by the general combining ability for the expression of many traits.

The main trait for calculation of multidimensional indices of genetic potential was the seed yield per plant. The multidimensional indices were estimated based on two sets of data: (1) for all traits recorded in the experiment – Y_i^{all} , and (2) for the traits pertaining to the yield structure (NP, NS, SY, TSW, NSP) – Y_i^{yield} .

Results

Because genotype × environment interaction was statistically significant ($P<0.001$) for all observed traits, the statistical analyses was done separately for studied years. Analysis of variance showed significant differences between the genotypes for most of the evaluated traits, except NS in 2012 and NB in 2013 (Table 1). In the first year of study, significant differences between the general combining ability for all traits were observed, whereas in 2013 no significant diversity was detected in the GCA effects for NB and NP (Table 1). Statistically significant diversity of the SCA effects was recorded for PH and DFB in both the years, and for DRN, NB and TSW in 2012. Significant diversification with respect to reciprocal cross's was observed in DRN, NB and DFB in 2012, and in the case of DFB and NP in 2013.

In order to assess the genetic potential of crossing Y_i^{all} and Y_i^{yield} , the GCA effects have been calculated for particular trait for 2012 and 2013 (Table 2). Despite lack of statistically significant variability among the effects of the general combining ability for NB and NP in 2013, the GCA effects for particular lines have been estimated (Table 2). In the first year of research, 40 combining ability effects different from zero were recorded (Table 2). For PH, all the lines were characterized by GCA values significantly different than zero, whereas for DFB and NS, only three lines had their GCA values significantly differing from zero. Two lines in 2012 are worth noting. These are Li4 and Li58, for which eight out of the nine analyzed traits, statistically significant GCA effects other than zero were obtained. In the case of line Li4, the insignificantly different from zero was the GCA effect for TSW, and for line Li58 it was DRN. The fewest significantly non-zero values of the general combining ability were recorded for Li19, only for PH

Table 1. Mean squares from variance analysis (ANOVA) for general (GCA) and specific (SCA) combining ability as well as reciprocal crosses for F_1 hybrids in 2012 and 2013

Source of variation	df	Year	DRN	PH	NB	DFB	NP	NS	SY	TSW	NSP
Blocks	31	2012	0.05	110.7	2.96	63.66	1833.49	159525.8	7.37	0.49	7.84
		2013	0.11	262.21	3.33	61.82	2772.67	216936	14.58	0.82	6.52
Genotypes	63	2012	0.08***	261.84***	4.43***	85.83***	2269.69*	117977	6.27*	1.02***	6.45*
		2013	0.15**	214.17***	3.2	54.41***	2693.96*	287019.7**	17.95*	1.25*	7.92**
GCA	7	2012	0.28***	1590.52***	14.99***	325.59***	4734.79**	338856.5**	20.36***	5.02***	16.43**
		2013	0.55***	463.43***	6.49	132.61***	3030.03	720237.6***	41.97**	3.13**	26.00***
SCA	28	2012	0.05***	140.22***	3.41***	52.14**	2149.05	124721.3	6.03	0.59**	4.95
		2013	0.08	227.89***	3.08	55.35***	2409.49	225771	14.49	0.98	6.08
Reciprocal crosses	28	2012	0.05***	40.06	3.00***	62.68***	1809.73	56159.1	2.97	0.36	5.68
		2013	0.1	148.14	2.38	37.97*	3070.37*	255405	16.37	1.13	6.68
Residual	161	2012	0.02	34.74	1.02	26.71	1517.37	89195.6	3.96	0.28	4.51
		2013	0.09	96.13	3.47	22.67	1819.31	175416	11.33	0.83	4.88

* $P<0.05$; ** $P<0.01$; *** $P<0.001$

DRN = The diameter of the root neck, PH = Plant height, NB = Number of branches per plant, DFB = Distance to the first branch, NP = Number of pods per plant, NS = Number of seeds per plant, TSW = 1000-seed weight, NSP = Number of seeds per pod and SY = Seed yield per plant

and NB. In the second year, only 24 general combining ability effects were significantly differing from zero (Table 2). The trait which was characterized by the smallest number of GCA effects and significantly deviating from zero was NB, only for line Li62. For DFB, six significantly different than zero GCA effects were acquired, the highest number in 2013. The line distinguishable in 2013 was Li62 showing seven significant GCA effects for PH and TSW. The least promising number of lines in respect of the general combining ability of some traits were Li19, Li32 and Li49; merely one significant GCA effect each, for PH, DFB and NSP, respectively. The repeatability of the GCA effects significance in two years of investigation were inconspicuous. It was characteristic of line Li19 for PH, line Li4 for DRN, DFB, NP, NS and SY, line Li43 for DRN, line Li51 for PH, DFB, SY and NSP, line Li58 for DFB and TSW, and the line Li62 for DRN. Additionally, line Li62 deserves particular attention as its GCA effect for NP was negative in 2012 and had a positive value in 2013.

Table 2 also presents correlation coefficients between the respective multi-dimensional indices of crossing potential and the GCA values for particular trait(s). Table 3 provides multi-dimensional indices of crossing potential estimated on the basis of all traits analyzed in the experiment (Y_i^{all}) and based exclusively on the yield structure traits (Y_i^{yield}). In the first year of study, among the eight lines under analysis, two i.e., Li58 and Li32 can be distinguished, namely, which had the highest values of the Y_i^{all} and Y_i^{yield} indices are worth recommending for further development of experimental hybrids (Table 2). When considering the studied lines in the context of negative versus positive values of the Y_i^{all} and Y_i^{yield} indices, one should have observed full congruence of the results (Table 3, Fig. 1). In the research, the relationships between particular traits and the pertinent indices of the genetic

Table 2. General combining ability (GCA) effects of eight lines for the studied traits in 2012 and 2013

Line	Year	DRN	PH	NB	DFB	NP	NS	SY	TSW	NSP
Li4	2012	0.14**	4.79**	0.73**	–3.72**	–13.22**	–108.00**	-0.67**	0.04	-0.65*
	2013	0.20***	1.94**	0.44	–1.69**	–11.37**	–118.7*	-0.97*	-0.42***	-0.42
Li19	2012	0.02	3.81***	0.67***	–0.26	–1.55	3.3	0.01	0.05	0.21
	2013	0.03	2.99**	0.42	0.28	4.08	59.6	0.34	-0.14	0.01
Li32	2012	0.01**	3.66***	–0.02	1.11	12.40*	81.9*	0.68**	0.34***	0.35
	2013	0.04	–0.16	0.15	–1.45*	3.62	36.9	0.38	0.18	-0.16
Li43	2012	–0.05**	–6.41***	–0.53***	–0.50	–1.29	–46.1	-0.41	-0.30***	-0.53*
	2013	0.09*	0.08	–0.28	1.24*	–2.38	–94.3	-0.69	0.03	-0.50
Li49	2012	–0.07***	–4.16***	–0.73***	1.00	6.84	69.1	0.32	-0.08	0.46
	2013	–0.04	–0.45	–0.26	0.13	1.63	90.1	0.68	0.07	0.92**
Li51	2012	0.00	–6.02***	0.27*	–2.94***	–3.96	–71.4	-0.50*	-0.24***	-0.78**
	2013	–0.05	–6.25***	0.14	–2.00**	–9.05	–119.1*	-0.98*	-0.21	-0.80**
Li58	2012	0.03	6.75***	–0.38**	4.27**	10.85*	112.1**	1.00***	0.49***	0.69*
	2013	0.01	2.25	–0.12	1.32*	0.89	–59.7	-0.31	0.36**	-0.25
Li62	2012	–0.09***	–2.41**	–0.01	1.03	–10.06*	–40.9	-0.43	-0.31***	0.25
	2013	–0.11**	-0.40	–0.50*	2.17**	12.58*	205.3***	1.55***	0.12	1.20***
b_k^{yield}	2012					0.92**	0.98***	0.99***	0.84**	0.84**
	2013					0.95**	0.97***	0.99***	0.59	0.92**
b_k^{all}	2012	0.14	0.70	–0.25	0.77*	0.83*	0.91**	0.97**	0.93**	0.81*
	2013	-0.40	0.35	–0.55	0.67	0.96**	0.96**	0.98***	0.59	0.91**

*P<0.05;**P<0.01;***P<0.001; Li = Line

crossing potential have also been defined. Between all yield structure traits and the index, significant values of the correlation coefficients have been observed. Significant values of the correlation coefficients were observed between all yield structure traits and the Y_i^{yield} index (Table 2). On the other hand, the Y_i^{all} index has been found significantly correlated only with traits of the yield structure and with DFB (Table 2). In 2013 the most valuable line identified was Li62 ($Y_{Li62}^{all} = 5.79$, $Y_{Li62}^{yield} = 5.89$). Line Li49 was also distinguishable ($Y_{Li49}^{all} = 2.63$, $Y_{Li49}^{yield} = 2.85$) (Table 3). It was only for line Li58 that divergence of the marks of the Y_{Li58}^{all} and Y_{Li58}^{yield} index values was recorded (Table 3, Fig. 1). Both indices Y_i^{all} and Y_i^{yield} were significantly correlated with NP, NS, SY and NSP.

Table 3. Multidimensional indices estimated for all traits recorded in the experiment Y_i^{all} and for the traits of the yield structure Y_i^{yield}

Lines	Year			
	2012		2013	
	Y_i^{yield}	Y_i^{all}	Y_i^{yield}	Y_i^{all}
Li 4	–2.23	–1.63	–4.37	–3.96
Li 19	0.14	0.60	0.75	1.41
Li 32	2.52	2.95	1.22	1.11
Li 43	–1.51	–2.30	–2.16	–2.21
Li 49	1.19	0.60	2.85	2.63
Li 51	–1.91	–2.62	–4.11	–5.09
Li 58	3.38	4.34	–0.07	0.32
Li 62	–1.57	–1.94	5.89	5.79

Discussion

The magnitude of the heterotic effect will define the success of a hybrid breeding programme (Boeven et al. 2016; Zhao et al. 2015). Hybrid breeding promises the boost in yield and stability. The single most important element in implementing hybrid breeding is

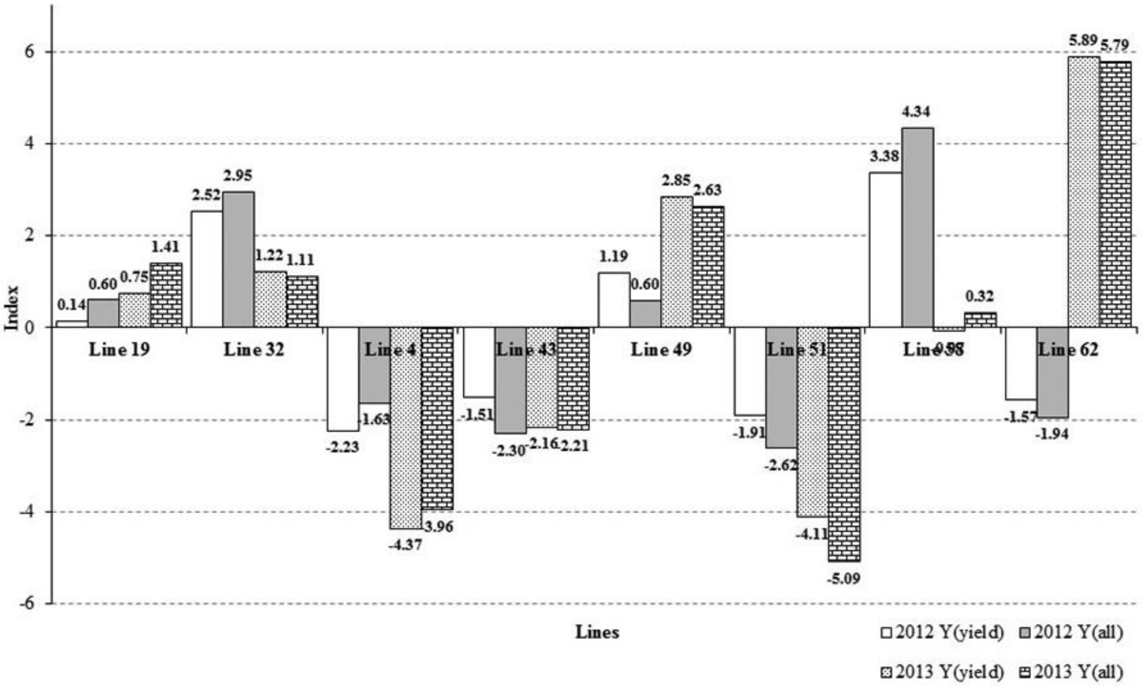

Fig. 1. Multi-dimensional indices estimated for all traits analyzed in the experiment (Y_i^{all}) and for the yield structure traits (Y_i^{yield}) for the two years

Table 4. Correlation coefficients for the analyzed traits studied for 2012 (above diagonal) and 2013 (below diagonal)

Trait	DRN	PH	NB	DFB	NP	NS	SY	TSW	NSP
DRN	1	0.57**	0.41**	-0.40**	0.30*	0.29*	0.37**	0.49**	0.01
PH	0.41**	1	0.43**	0.34**	0.37**	0.53***	0.59***	0.73***	0.40**
NB	0.49**	0.37**	1	-0.22	0.27*	0.15	0.14	0.12	-0.14
DFB	-0.21	0.35**	-0.20	1	0.18	0.38**	0.35**	0.25*	0.47**
NP	0.15	0.48**	0.42**	0.19	1	0.83***	0.83***	0.44**	-0.02
NS	0.08	0.41**	0.23	0.24	0.88***	1	0.98***	0.59***	0.48**
SY	0.08	0.40**	0.23	0.22	0.88***	0.995***	1	0.70***	0.44**
TSW	0.01	0.41**	0.09	0.29*	0.65***	0.63***	0.67***	1	0.38**
NSP	-0.07	0.34**	-0.10	0.38**	0.52***	0.79***	0.78***	0.60***	1

* $P<0.05$; ** $P<0.01$; *** $P<0.001$

the recognition of a high-yielding heterotic pattern (Zhao et al. 2015). For considerations of commercialization, the important criterion is the improved yield of hybrids from the best commercial pure line variety (Liersch et al. 2016; Nowosad et al. 2016). A survey of the literature revealed that high magnitude of heterosis has been recorded by a large number of researchers in rapeseed under a range of test conditions (Bommarco et al. 2012; Girke et al. 2012). The traits studied in the present experiment were, to a great extent, correlated with one another. Statistically significant correlation coefficients were observed in the first year of investigations (Table 4).

In all cases, the highest values of correlations were obtained for those lines, which were characterized by the greatest number of GCA effects significantly different from zero. And thus, the best lines in the context of the highest and values are not randomly distinguished: they are not designated based on 2–3 significant GCA effects. The knowledge of quantitative genetic parameters is crucial in allocating resources for different steps of multistage selection programmes of the spring oilseed rape (*B. napus* L.). The selection index can enable the choice of the most valuable lines to be practically used in heterotic breeding of the oilseed rape.

Authors' contribution

Conceptualization of research (JB, KN, HB, TL, DP); Designing of the experiments (JB, KN, TL); Contribution of experimental materials (TL); Execution of field/lab experiments and data collection (JB, KN, TL); Analysis of data and interpretation (JB, KN, HB, TL); Preparation of the manuscript (JB, KN, TL, DP).

Declaration

The authors declare no conflict of interest.

References

Bocianowski J., Kozak M., Liersch A. and Bartkowiak-Broda I. 2011. A heuristic method of searching for interesting markers in terms of quantitative traits. Euphytica, **181**: 89-100.

Boeven P. H. G., Longin C. F. H. and Würschum T. 2016. A unified framework for hybrid breeding and the establishment of heterotic groups in wheat. Theor. Appl. Genet., **129**: 1231-1245.

Bommarco R., Marini L. Vaissière B. E. 2012. Insect pollination enhances seed yield, quality, and market value in oilseed rape. Oecologia, **169**: 1025-1032.

Brandle J. E. and McVetty P. B. E. 1989. Heterosis and combining ability in hybrids derived from oilseed rape cultivars and inbred lines. Crop Sci., **29**: 1191-1194.

Bujak H., Jedyñski S. Kaczmarek J. 2004. Application of the selection index in assessment of the breeding value. *In*: Genetyka w ulepszaniu roslin uzytkowych, (eds. P. Krajewski, Z. Zwierzykowski, P. Kachlicki). Rozprawy i Monografie, IGR PAN, Poznañ: 207-222.

Cochran W. G. and Cox G. M. 1957. Experimental design. John Wiley Inc., New York: 573.

Fabrizius M. A., Busch R. H., Khan K. Huckle L. 1998. Genetic diversity and heterosis of spring wheat crosses. Crop Sci., **38**: 1108-1112.

Girke A., Schierholt A, Becker H. C. 2012. Extending the rapeseed gene pool with resynthesized Brassica napus II: Heterosis. Theor. Appl. Genet., **124**: 1017-1026.

Grant I. and Beversdorf W. D. 1985. Heterosis and combining ability estimates in spring-planted oilseed rape (*Brassica napus* L.). Can. J. Genet. Cytol., **27**: 472-478.

Griffing B. 1956. Concept of general and specific combining ability in relation to diallel crossing system. Australian J. Biolog. Sci., **9**: 463-492.

Kadkol G. P., Anand I. J. and Sharma R. P. 1984. Combining ability and heterosis in sunflower. Indian J. Genet., **44**: 447-451.

Kozak M., Bocianowski J., Liersch A., Tartanus M., Bartkowiak-Broda I., Piotto F. A. and Azevedo R. A. 2011. Genetic divergence is not the same as phenotypic divergence. Mol. Breed., **28**: 277-280.

Liersch A., Bocianowski J., Kozak M. and Bartkowiak-Broda I. 2013. Comparison of isozyme, RAPD and AFLP markers in genetic similarity assessment of CMS *ogura* F_1 hybrids of winter oilseed rape (*Brassica napus* L.) parental lines. Acta Biol. Crac. Ser. Bot., **55**: 49-57.

Liersch A., Bocianowski J., Wos H., Szala L., Sosnowska K., Cegielska-Taras T., Nowosad K. and Bartkowiak-Broda I. 2016. Assessment of genetic relationships in breeding lines and cultivars of *Brassica napus* and their implications for breeding winter oilseed rape. Crop Sci., **56**: 1540-1549.

Miller J. F., Hammond J. J. and Roath W. W. 1980. Comparison of inbred vs. single-cross testers and estimation of genetic effects in sunflowers. Crop Sci., **20**: 703-706.

Nowosad K., Liersch A., Poplawska W. and Bocianowski J. 2016. Genotype by environment interaction for seed yield in rapeseed (*Brassica napus* L.) using additive main effects and multiplicative interaction model. Euphytica, **208**: 187-194.

Sherrif N. M., Appadurai R. and Rangasamy M. 1985. Combining ability in sunflower. Indian J. agric. Sci., **55**: 315-318.

Zhao Y., Li Z., Liu G., Jiang Y., Maurer H. P., Würschum T., Mock H.-P., Matros A., Ebmeyer E., Schachschneider R., Kazman E., Schacht J., Gowda M., Longin C. F. H. and Reif J. C. 2015. Genome-based establishment of a high-yielding heterotic pattern for hybrid wheat breeding. Proc. Natl. Acad. Sci. U.S.A., **112**: 15624-25629.

Zhao Y., Mette M. F. and Reif J. C. 2015. Genomic selection in hybrid breeding. Plant Breed., **134**: 1-10.