

Genotype-by-environment interaction for seed quality traits in interspecific cross-derived *Brassica* lines using additive main effects and multiplicative interaction model

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Received: 2 October 2018 / Accepted: 20 December 2018 / Published online: 24 December 2018
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Abstract The aim of this study was to assess genotype by environment interaction for seed quality traits in interspecific cross-derived *Brassica* lines by the additive main effects and multiplicative interaction (AMMI) model. The study comprised of 25 winter rapeseed genotypes i.e.: *B. napus* cultivar Californium, twenty three cross-derived *Brassica* lines and male sterile line of an F₈ generation of *B. napus* (MS8), selected from resynthesized oilseed rape (*B. rapa* ssp. *chinensis* × *B. oleracea* var. *gemmifera*) using in vitro cultures of isolated embryos. Field trials were performed at three locations in 3 years in a randomized complete block design, with three replicates. AMMI analyses revealed significant genotype and environmental effects as well as genotype by environmental interaction with respect to all five

observed traits. The lines 16 (*B. napus* line MS8 × *B. rapa* ssp. *pekinensis*) and 7 (*B. napus* line MS8 × *B. carinata*) are recommended for further inclusion in the breeding programs because their stability and good average values of observed traits, except total glucosinolates content for line 16 (the best total genotype selection indexes were equal to 81 and 97, respectively).

Keywords Acid detergent fiber · Adaptability · AMMI · Biplot · *Brassica* lines · Total glucosinolates content · Oil content · Neutral detergent fiber · Protein content · Stability

Introduction

Brassica L. is a diverse genus that includes six species cultivated as important crops, which yield edible oil and condiment seeds, roots, leaves, stems, vegetative and floral buds and meristems. Due to their wide adaptation and ability to thrive under varying agroclimatic conditions, brassica crops are grown throughout the world for food, animal forage, fodder and industrial applications (Eckes et al. 2017). In Poland within *Brassica* species, winter oilseed rape is the most important oil–protein plant (Liersch et al. 2016; Szała et al. 2016; Sosnowska et al. 2017).

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Given the importance of *Brassica* species worldwide, integrated approaches to research and plant breeding for crop improvement are required to address future global challenges, such as satisfying increased demand for higher quality and nutritious food, the reduction of waste, and producing predictable yields in a more variable environment. Researchers have evaluated many aspects of *Brassica* phenotypic diversity to assist in crop improvement, including yield, resistance to pathogens and pests and the composition of industrially important compounds.

Nowadays, development of oilseed rape cultivars with good quality i.e. high oil, protein as well as low erucic acid, glucosinolate and fiber content is a challenging objective for many rapeseed breeding programs (Bocianowski et al. 2014; Niemann et al. 2012; Zou et al. 2016). It is known that all these seed quality traits are influenced by genetic and environmental factors, so their precise estimation requires phenotyping in replicated multi-environmental field trials.

In field crop trials, genotype-by-environment (GE) interaction is often analyzed by the additive main effects and multiplicative interaction (AMMI) model (Zobel et al. 1988). The AMMI model is a combination of the analysis of variance (ANOVA) with additive parameters and the principal component analysis (PCA) with multiplicative parameters in a single analysis. The AMMI biplot graphic display simultaneously both main and interaction effects for genotypes and environments, and enables a single analysis of the genotype by environment interaction. The AMMI is, therefore, also known as interaction PCA (Gauch and Zobel 1990).

The aim of this paper was to assess genotype by environment interaction for five quantitative traits (oil content, protein content, total glucosinolates content, acid detergent fiber and neutral detergent fiber) in interspecific cross-derived *Brassica* lines grown in three locations in the Greater Poland by the AMMI model.

Materials and methods

Plant material for field trials consisted of 25 winter rapeseed genotypes i.e.: *B. napus* cv. Californium, twenty three interspecific cross-derived *Brassica* lines and male sterile line of an F₈ generation of *B. napus*

(MS8). MS8 line was selected from resynthesized oilseed rape (*B. rapa* ssp. *chinensis* × *B. oleracea* var. *gemmifera*) using in vitro cultures of isolated embryos (Table 1). F₅–F₇ generation of tested lines as well as control genotypes i.e. *B. napus* cv. Californium and MS8 line were selected from the rapeseed breeding program of the Department of Genetics and Plant Breeding, Poznań University of Life Sciences (PULS). The study was carried out in three locations i.e. the PULS experimental station Dłóń (51°41'23"N, 17°04'10"E) located 100 km south of Poznań, Złotniki (52°25'18"N, 16°50'41"E) located 15 km west from Poznań and in the experimental fields in Poznań–Sołacz (52°25'18"N, 16°54'26"E). The field trials at all locations were arranged in a randomized complete block design with three replicates. Each genotype was grown in a three row plot of 9.0 m² with a 0.30 row distance and a sowing density of 60 seeds/m². Agricultural practices were optimal for local agroecological conditions in all investigated locations. Plots were harvested using a plot harvester. These locations have different types of soil and weather conditions. The field experiment in Dłóń was conducted on typical heavy soil of III quality class. The field experiment in Sołacz was conducted on typical light, sandy soil of IV quality class. The field experiment in Złotniki was conducted on typical luvisols soil of IVa quality class. Complex of agricultural usefulness were: good rye in Dłóń, good wheat in Sołacz and very good rye in Złotniki. In crop seasons 2010/2011, 2011/2012 and 2012/2013 weather conditions were normal for Poland. The sums of precipitation during vegetation season of winter oilseed rape in 2011, 2012 and 2013 were, respectively, in Dłóń: 465, 631 and 565 mm, in Sołacz: 477, 514 and 607 mm, in Złotniki: 402, 678 and 581 mm. Mean annual temperature during vegetation season of winter oilseed rape in 2011, 2012 and 2013 were, respectively, in Dłóń: 10.0, 10.1 and 9.7 °C, in Sołacz: 9.6, 9.4 and 9.2 °C, in Złotniki: 15.2, 9.1 and 9.8 °C.

Quality analysis

The seed samples for the analysis of protein content (in %), oil content (in %), total glucosinolates content (in μmol/gsm) and fiber content (in %) were collected from five self-pollinated plants from each tested line in each replication. The fiber content in the cross-derived lines and control seeds was expressed as the average

Table 1 Code and origin of the genotypes tested

Genotypes	Code
<i>B. napus</i> cv. Californium	1
<i>B. napus</i> line MS8 × <i>B. rapa</i> ssp. <i>pekinensis</i>	2, 3, 4
<i>B. napus</i> line MS8 × <i>B. carinata</i>	5, 7, 8, 9, 23
<i>B. napus</i> line MS8 × <i>B. rapa</i> ssp. <i>pekinensis</i>	6, 13, 14, 15, 16, 17, 18, 22
<i>B. napus</i> line MS8 × <i>B. rapa</i> ssp. <i>trilocularis</i>	10, 11, 12, 20, 21
<i>B. napus</i> line MS8 × <i>B. juncea</i>	19, 24
<i>B. napus</i> line MS8	25

value of the neutral detergent fiber (NDF) and the acid detergent fiber (ADF) as a subfraction of the NDF. The seed quality traits content was determined by near-infrared reflectance spectroscopy (NIRS) (Velasco et al. 1999). These analyses were performed at the Małyszyn Laboratory that belongs to Plant Breeding Strzelce in triplicate. For NIRS analysis minimum 3 g of intact seeds were used. Every seed probe was scanned on the NIRS Systems monochromator model 6500 (NIR Systems, Inc. Silver Springers, MD, USA).

Statistical analysis

A two-way fixed effect model was fitted to determine the magnitude of the main effects of variation and their interaction on each trait. Least-squares means were simultaneously produced for the AMMI model. The model first fits additive effects for the main effects of genotypes (G) and environments (E) followed by multiplicative effects for GE interaction by principal component analysis. Environments were defined as combinations of locations and years (E1—Dłóń, 2011; E2—Poznań–Sołacz, 2011; E3—Złotniki, 2011; E4—Dłóń, 2012; E5—Poznań–Sołacz, 2012; E6—Złotniki, 2012; E7—Dłóń, 2013; E8—Poznań–Sołacz, 2013; E9—Złotniki, 2013). The AMMI model (Gauch and Zobel 1990; Nowosad et al. 2016) is given by:

$$y_{ge} = \mu + \alpha_g + \beta_e + \sum_{n=1}^N \lambda_n \gamma_{gn} \delta_{en} + Q_{ge},$$

where y_{ge} is the trait mean of genotype g in environment e , μ is the grand mean, α_g is the genotypic mean deviations, β_e is the environmental mean deviations, N is the number of PCA axis retained in the adjusted model, λ_n is the eigenvalue of the PCA axis n , γ_{gn} is the genotype score for PCA axis n , δ_{en} is the score eigenvector for PCA axis n , Q_{ge} is the residual,

including AMMI noise and pooled experimental error. Expected distribution of Q_{ge} is normal. The AMMI stability values (ASVs) were used to compare the stability of genotypes as described by Purchase et al. (2000):

$$ASV = \sqrt{\left[\frac{SS_{IPCA1}}{SS_{IPCA2}} (IPCA_1) \right]^2 + (IPCA_2)^2},$$

where SS was the sum of squares, $IPCA_1$ and $IPCA_2$ —the first and the second interaction principal component axes, respectively; the $IPCA_1$ and $IPCA_2$ scores were the genotypic scores in the AMMI model. ASV was the distance from zero in a two-dimensional scatterplot of $IPCA_1$ scores against $IPCA_2$ scores. Since the $IPCA_1$ score contributes more to GE sum of square, it has to be weighted by the proportional difference between $IPCA_1$ and $IPCA_2$ scores to compensate for the relative contribution of $IPCA_1$ and $IPCA_2$ total GE sum of squares. The higher the $IPCA$ score, either negative or positive, the more specifically adopted a genotype is to certain environments. Lower ASV score indicate a more stable genotype across environments (Nowosad et al. 2017).

Genotype selection index (GSI) was calculated for each genotype which incorporates both mean of trait and ASV index in single criteria (GSI_i) as (Farshadfar and Sutka 2003)

$$GSI_i = RM_i + RA_i,$$

where GSI_i is genotype selection index for i th genotype, RM_i is rank of trait mean (from maximal to minimal for oil content and protein content, and from minimal to maximal for total glucosinolates content, ADF and NDF) for i th genotype, RA_i is rank of the AMMI stability value for the i th genotype. Finally, total genotype selection index (TGSI) was

calculated for each genotype as sum of GSIs for all five traits of study. All the analyses were conducted using the GenStat v. 18 statistical software package.

Results

Oil content

The three sources of variation were highly significant. In the analysis of variance, the sum of squares for environment main effect represented 16.69% of the total oil content variation. The differences between genotypes explained 9.37% of the total oil content variation, while the effects of GE interaction explained 25.70% (Table 2). Values for the three principal components were also highly significant and accounted jointly for 85.38% of the whole effect it had on the variation of oil content. The first principal component (IPCA 1) accounted for 51.68% of the variation caused by interaction, while IPCA 2 and IPCA 3 accounted for 18.23 and 15.47%, respectively. Genotype stability is considered as non significant reaction to changing environmental conditions, agronomic factors, weather conditions, biotic and abiotic stresses. In this study, climatic conditions were the source of this variation component. The stability of tested genotypes can be evaluated according to biplot for oil content (Fig. 1). Interspecific *Brassica* cross-derived lines interacted differently with climate

conditions in the observed environments. The lines 2, 4, 5, 12 and 13 interacted positively with the E2, E5, E6 and E8 environments, but negatively with the E4 (Fig. 1). The lines 20, 21, 22, 23, 24 and 25 interacted positively with the E1 and E7 environments, but negatively with the E3 and E9. The analysis showed that some genotypes have high adaptation; however, most of them have specific adaptability. AMMI stability values (ASV) revealed variations in oil content stability among the 25 genotypes (Table 3). According to Purchase et al. (2000), a stable variety is defined as one with ASV value close to zero. Consequently, the lines 10 and 1 with ASV of, respectively, 0.271 and 0.476, were the most stable, while the lines 9 and 3 were the least stable (Table 3). The line 16 with the highest average oil content (44.20%) and ASV equal to 0.939 is line with the best genotype selection index (7). A group of lines: 7, 8, 11 and 19 had high averages of oil content and show high stability (Fig. 1, Table 3). These lines had good genotype selection index, respectively, 11, 11, 11 and 12 (Table 3).

Protein content

The three sources of variation for the protein content were highly significant. In the ANOVA, the sum of squares for environment main effect represented 50.08% of the total protein content variation. The differences between genotypes explained 10.03% of

Table 2 Analysis of variance of main effects and interactions for seed quality traits in interspecific cross-derived *Brassica* lines and variability explained (ve, in %)

Source of variation	d.f.	Oil content		Protein content		Total glucosinolates content		ADF		NDF	
		m.s.	ve (%)	m.s.	ve (%)	m.s.	ve (%)	m.s.	ve (%)	m.s.	ve (%)
Treatments	224	62.1***	52.12	58.3***	83.16	2103***	82.49	49.4***	84.55	86.1***	77.72
Genotypes (G)	24	108***	9.73	65.6***	10.03	18,470***	77.63	70.6***	12.95	345***	33.39
Environments (E)	8	557***	16.69	983***	50.08	764***	1.07	686***	41.98	711***	22.92
GE Interactions	192	35.8***	25.70	18.8***	23.05	112***	3.78	20.2***	29.62	27.7***	21.41
IPCA 1	31	114***	51.68	63.8***	54.68	382***	54.89	62.8***	50.22	66.6***	38.86
IPCA 2	29	43.1***	18.23	23.7***	19.01	111***	14.91	46.4***	34.74	49.2***	26.87
IPCA 3	27	39.3***	15.47	17***	12.71	104***	13.02	11.8***	8.18	46.6***	23.67
Residuals	105	9.56***		4.7***		35		2.52***		5.4***	
Error	3132	4.04		0.8		32		0.61		1.7	

*** $P < 0.001$

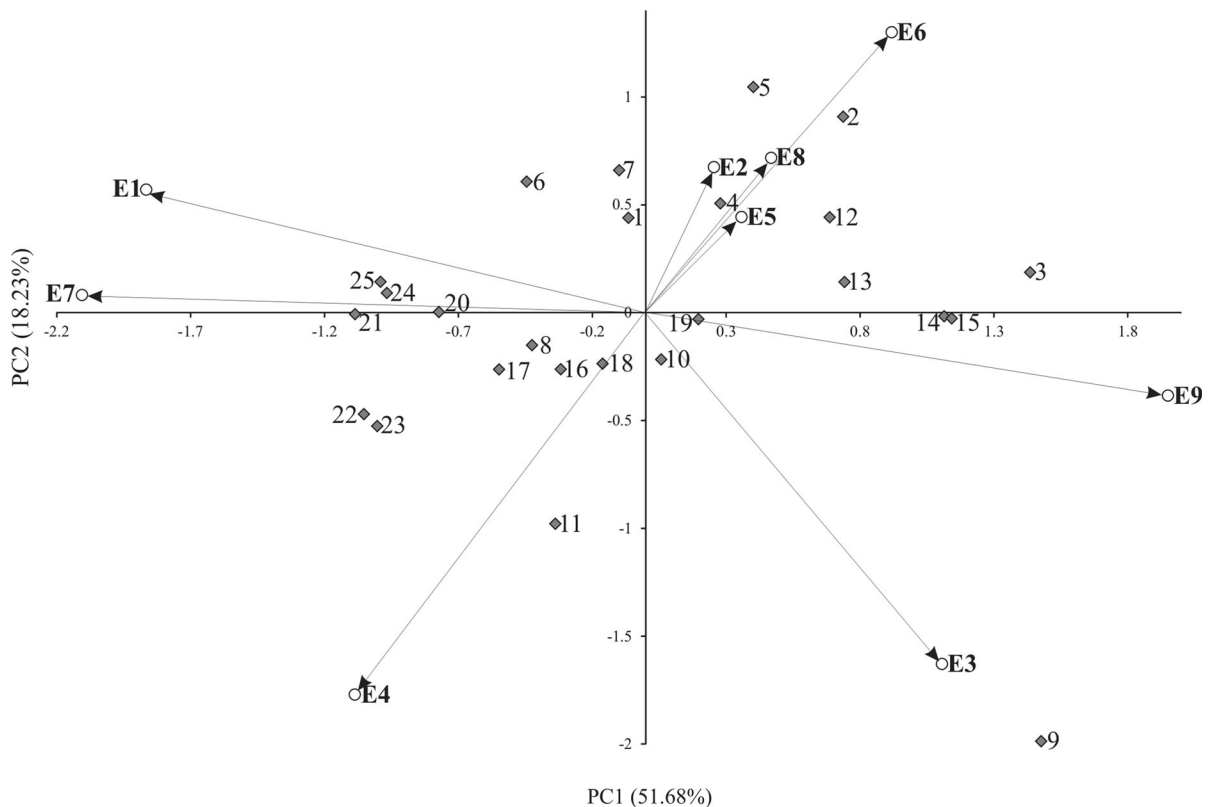


Fig. 1 Biplot for genotype by environment interaction of oil content in interspecific cross-derived *Brassica* lines in nine environments, showing the effects of primary and secondary components (IPCA 1 and IPCA 2, respectively) (E1—Dłóń,

2011; E2—Poznań-Sołacz, 2011; E3—Złotniki, 2011; E4—Dłóń, 2012; E5—Poznań-Sołacz, 2012; E6—Złotniki, 2012; E7—Dłóń, 2013; E8—Poznań-Sołacz, 2013; E9—Złotniki, 2013)

the total oil content variation, while the effects of GE interaction explained 23.05% (Table 2). Values for the three principal components were also highly significant and accounted jointly for 86.40% of the whole effect it had on the variation of protein content. The first principal component (IPCA 1) accounted for 54.68% of the variation caused by interaction, while IPCA 2 and IPCA 3 accounted for 19.01 and 12.71%, respectively. The stability of tested genotypes can be evaluated according to biplot for protein content (Fig. 2). The lines 2, 3, 5, 6, 18 and 19 interacted positively with the E1 and E4 environments, but negatively with the E3 and E6 (Fig. 2). The lines 9 and 14 interacted positively with the E7 environment, but negatively with the E9. The line 1 interacted positively with the E2, E5 and E8 environments. The lines 6, 1 and 17 with ASV of, respectively, 0.352, 0.410 and 0.454, were the most stable, while the lines 3 and 9 were the least stable (Table 3). The lines 6 and 16 with

high average protein content (21.34% and 21.37%, respectively) and ASV equal to 0.352 and 0.454, respectively, are lines with the best genotype selection index (6).

Total glucosinolates content

In the ANOVA, the sum of squares for genotypes main effect represented 77.63% of the total, and this factor had the highest effect on the total glucosinolates content. The differences between environments explained 1.07% of the total glucosinolates content variation, while the effects of GE interaction explained 3.78% (Table 2). Values for the three principal components were also highly significant. The three principal components of GE interaction accounted jointly for 82.82% of the whole effect it had on the variation of total glucosinolates content. The first principal component (IPCA 1) accounted for

Table 3 Average values of observed traits for genotypes, AMMI stability value (ASV), rank of the AMMI stability value (RA), rank of trait mean [RM, from maximal to minimal for oil content (%) and protein content (%), and from minimal to maximal for total glucosinolates content (umol/gsm), ADF (%) and NDF (%)], genotype selection index (GSI) and total genotype selection index (TGSI)

Code	Oil content					Protein content					Total glucosinolates content				
	Mean	ASV	RA	RM	GSI	Mean	ASV	RA	RM	GSI	Mean	ASV	RA	RM	GSI
1	42.83	0.476	2	15	17	20.12	0.41	2	20	22	12.65	1.648	9	4	13
2	42.51	2.28	16	18	34	21.38	1.033	8	2	10	31.48	1.053	7	18	25
3	42.54	4.076	24	17	41	21.35	4.768	25	4	29	28.53	1.994	10	12	22
4	42.11	0.939	7	21	28	20.47	0.569	4	16	20	13.60	0.723	5	5	10
5	42.75	1.547	11	16	27	19.83	0.977	6	23	29	29.93	2.81	15	14	29
6	41.24	1.402	10	24	34	21.34	0.352	1	5	6	53.73	9.437	25	25	50
7	43.09	0.718	5	6	11	20.63	1.177	11	12	23	15.00	0.636	4	7	11
8	43.54	1.214	8	3	11	20.09	1.8	18	21	39	13.77	2.126	12	6	18
9	43.47	4.637	25	4	29	18.96	4.724	24	24	48	31.02	4.416	20	16	36
10	42.33	0.271	1	20	21	20.43	1.516	14	17	31	11.93	0.517	2	3	5
11	43.87	1.369	9	2	11	18.79	1.947	21	25	46	10.47	1.445	8	1	9
12	42.86	1.997	13	12	25	20.19	1.53	16	19	35	16.23	3.625	16	8	24
13	42.89	2.11	14	10	24	20.33	1.912	19	18	37	11.50	4.661	21	2	23
14	41.32	3.161	22	23	45	20.84	3.612	23	8	31	35.94	0.346	1	19	20
15	43.09	3.241	23	7	30	20.68	1.052	9	10	19	23.83	2.241	13	9	22
16	44.20	0.939	6	1	7	20.90	0.82	5	7	12	37.25	3.646	17	20	37
17	42.42	1.577	12	19	31	21.37	0.454	3	3	6	27.17	9.091	24	11	35
18	39.92	0.515	3	25	28	21.77	2.63	22	1	23	41.55	0.546	3	23	26
19	43.03	0.558	4	8	12	20.06	1.52	15	22	37	31.45	4.069	18	17	35
20	43.02	2.19	15	9	24	20.64	1.375	12	11	23	28.82	2.615	14	13	27
21	42.87	3.079	21	11	32	20.55	1.51	13	13	26	30.42	6.511	23	15	38
22	42.84	3.022	20	14	34	20.54	1.76	17	14	31	38.59	2.059	11	22	33
23	41.66	2.894	19	22	41	20.78	1.16	10	9	19	43.03	4.354	19	24	43
24	43.15	2.745	17	5	22	21.11	0.997	7	6	13	37.96	6.153	22	21	43
25	42.85	2.814	18	13	31	20.48	1.921	20	15	35	24.12	0.726	6	10	16
Code	ADF					NDF					TGSI				
	Mean	ASV	RA	RM	GSI	Mean	ASV	RA	RM	GSI					
1	21.83	0.2797	3	22	25	27.73	0.614	8	22	30	107				
2	21.00	2.5457	25	14	39	24.74	0.951	12	11	23	131				
3	21.05	1.9016	23	15	38	24.85	2	24	12	36	166				
4	22.51	0.9802	18	25	43	26.58	1.573	20	20	40	141				
5	21.00	1.8341	22	13	35	23.56	1.181	15	3	18	138				
6	20.84	0.2938	4	12	16	22.24	2.16	25	1	26	132				
7	21.44	0.3366	5	20	25	24.12	1.338	19	7	26	96				
8	21.88	0.7492	12	23	35	26.95	1.609	22	21	43	146				
9	20.77	1.738	21	11	32	26.55	1.824	23	19	42	187				
10	22.34	0.395	7	24	31	27.97	0.394	3	23	26	114				
11	21.60	0.5188	10	21	31	28.12	0.555	6	25	31	128				
12	21.23	2.4224	24	18	42	28.09	0.513	5	24	29	155				
13	20.46	0.236	2	7	9	26.26	0.656	10	18	28	121				

Table 3 continued

Code	ADF					NDF					TGSI
	Mean	ASV	RA	RM	GSI	Mean	ASV	RA	RM	GSI	
14	19.99	0.7648	13	3	16	24.15	1.293	18	8	26	138
15	21.18	1.4395	20	17	37	24.94	0.894	11	13	24	132
16	20.11	0.7161	11	5	16	24.10	0.506	4	5	9	81
17	19.94	1.3789	19	1	20	24.07	1.069	13	4	17	109
18	19.97	0.8656	16	2	18	23.24	0.623	9	2	11	106
19	20.64	0.105	1	10	11	25.00	0.392	2	14	16	111
20	20.46	0.448	9	8	17	25.28	0.574	7	17	24	115
21	20.37	0.9653	17	6	23	25.14	1.604	21	16	37	156
22	21.08	0.3542	6	16	22	24.62	1.089	14	10	24	144
23	20.47	0.4429	8	9	17	24.38	0.377	1	9	10	130
24	20.06	0.7975	14	4	18	24.12	1.207	16	6	22	118
25	21.32	0.8567	15	19	34	25.08	1.226	17	15	32	148

54.89% of the variation caused by interaction, IPCA 2 accounted for 14.91% while IPCA 3 accounted for 13.02% (Fig. 3, Table 2). The stability of tested lines can be evaluated according to biplot for total glucosinolates content (Fig. 3). The lines 6, 19, 20 and 21 interacted positively with the E4, but negatively with the E3, E6 and E9 environments (Fig. 3). The lines 15, 22, 23 and 24 interacted positively with the E7, but negatively with the E3. The lines 14, 10 and 18 with ASV of, respectively, 0.346, 0.517 and 0.546 were the most stable, while the lines such as 6, 17, 21 and 24 were the smallest stable (Table 3). A group of lines: 11, 13, 10 and 1 had the least averages of total glucosinolates content. The line 10 has the best genotype selection index, equal to 5 (Table 3). However, the line 6 has the worst genotype selection index (50).

ADF

The three sources of variation were highly significant. In the ANOVA, the sum of squares for environment main effect represented 41.98% of the total, and this factor had the highest effect on ADF (Table 2). The

differences between genotypes explained 12.95% of the total ADF variation, while the effects of GE interaction explained 29.62%. Values for the three principal components were also highly significant. The three principal components of GE interaction accounted jointly for 93.14% of the whole effect it had on the variation of ADF. The first principal component (IPCA 1) accounted for 50.22% of the variation caused by interaction, while IPCA 2 and IPCA 3 accounted for 34.74 and 8.18%, respectively. The lines 3 and 9 interacted positively with the E3 and E9 environments, but negatively with the E1 and E7 (Fig. 4). The lines 2, 5 and 12 interacted positively with the E6 environment, but negatively with the E4. The highest stability on ADF we observed for line 19 (ASV = 0.105). The best genotype selection index, equal to 9, has line 13, with small ADF (20.46) and ASV = 0.236 (Table 3).

NDF

The sum of squares for environment main effect represented 22.92% of the total NDF variation. The differences between genotypes explained 33.39% of the total NDF variation, while the effects of GE

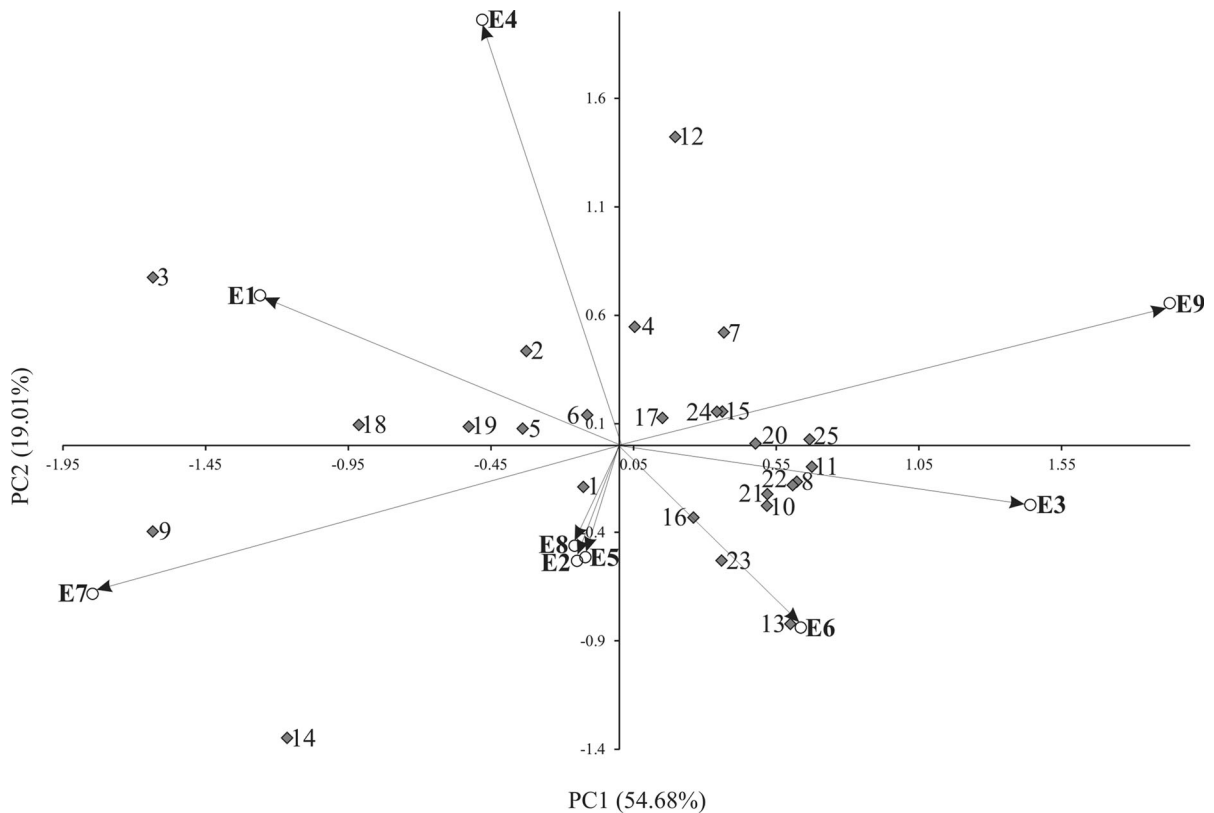


Fig. 2 Biplot for genotype by environment interaction of protein content in interspecific cross-derived *Brassica* lines in nine environments, showing the effects of primary and secondary components (IPCA 1 and IPCA 2, respectively)

(E1—Dłóń, 2011; E2—Poznań–Sołacz, 2011; E3—Złotniki, 2011; E4—Dłóń, 2012; E5—Poznań–Sołacz, 2012; E6—Złotniki, 2012; E7—Dłóń, 2013; E8—Poznań–Sołacz, 2013; E9—Złotniki, 2013)

interaction explained 21.41% (Table 2). Values for the three principal components were also highly significant and accounted jointly for 89.40% of the whole effect it had on the variation of NDF. The IPCA 1 accounted for 38.86% of the variation caused by interaction, while IPCA 2 and IPCA 3 accounted for 26.87 and 23.67%, respectively. The lines 4, 6 and 14 interacted positively with the E3, E6 and E9 environments, but negatively with the E1 and E7 (Fig. 5). The lines 17, 22, 24 and 25 interacted positively with the E1 and E7 environments, but negatively with the E3, E4, E6 and E9. The lines 23, 19 and 10 with ASV of, respectively, 0.377, 0.392 and 0.394, were the most

stable, while the lines 6 and 3 were the least stable (Table 3). The line 16 with small average NDF (24.10%) and ASV equal to 0.506 is line with the best genotype selection index (9).

The best total genotype selection index we observed for line 16 (TGSI = 81) and line 7 (TGSI = 97), while the worst—line 9 (TGSI = 187). The lines 16 (*B. napus* line MS8 × *B. rapa* ssp. *pekinensis*) and 7 (*B. napus* line MS8 × *B. carinata*) are recommended for further inclusion in the breeding programs because of their stability and good average values of observed traits, except total glucosinolates content for line 16.

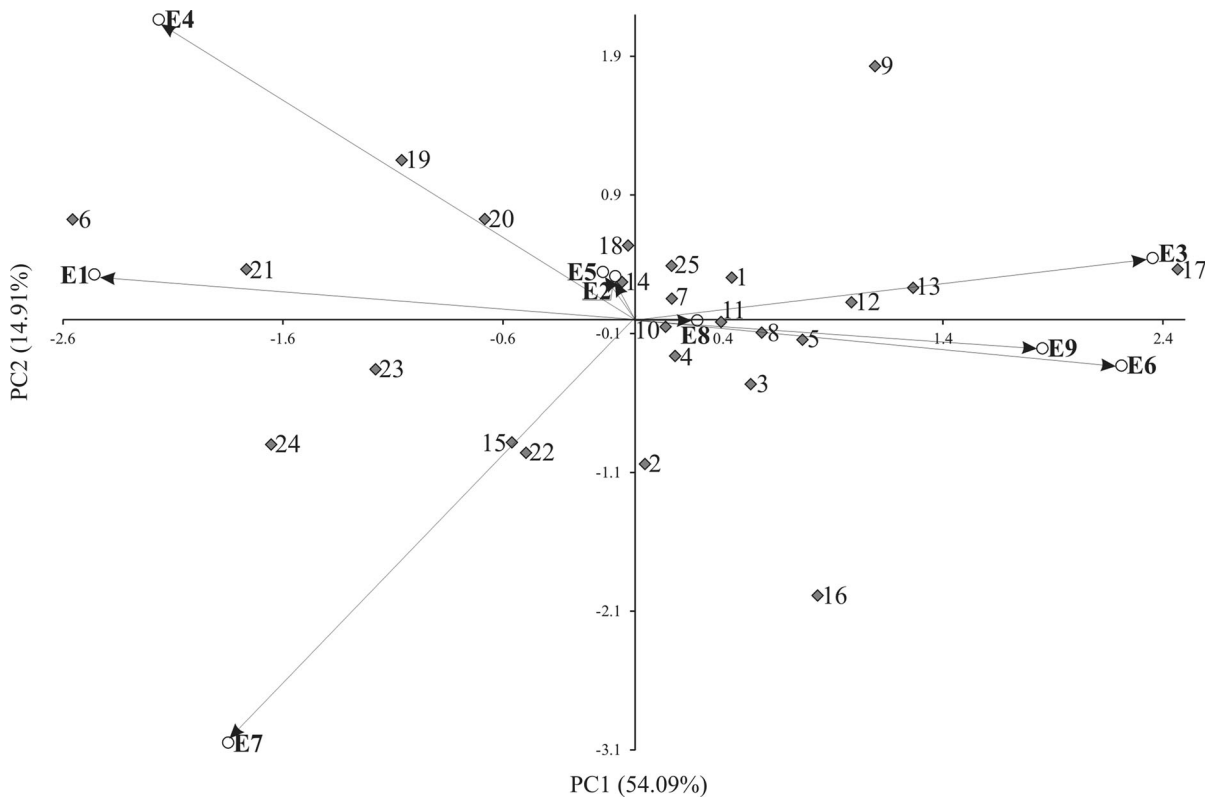


Fig. 3 Biplot for genotype by environment interaction of total glucosinolates content in interspecific cross-derived *Brassica* lines in nine environments, showing the effects of primary and secondary components (IPCA 1 and IPCA 2, respectively)

(E1—Dłóń, 2011; E2—Poznań–Sołacz, 2011; E3—Złotniki, 2011; E4—Dłóń, 2012; E5—Poznań–Sołacz, 2012; E6—Złotniki, 2012; E7—Dłóń, 2013; E8—Poznań–Sołacz, 2013; E9—Złotniki, 2013)

Discussion

In *Brassica* species and especially in *Brassica napus* breeding, traits related to commercial success are of highest importance (Friedt and Snowdon 2010). However, such traits in many cases can only be assessed in an advanced developmental stage (Körber et al. 2016). The oil content, protein content, total glucosinolates content, ADF and NDF in winter rapeseed are traits determined by multiple genes that cause change in the performance of genotypes depending on the cultivation environment. That is why the importance of GE interactions in plant breeding programs have been a focus of attention for breeders (Golkari et al. 2016; Nowosad et al. 2016;

Chen et al. 2017). Genotype by environment interaction is an important and challenging issue for plant breeders especially in developing new improved varieties. Multi-environment trials are used to determine sites representing the target environment and can identify superior lines or cultivars for recommendation to breeders (Golkari et al. 2016). Data collected from such trials are needed for precise estimation of genotype value and yield stability (Yan and Hunt 2001). These trials facilitate quantification of the environment and GE interactions. Differences in environmental conditions may cause large GE interactions, especially under drought-prone environments. The interpretation of GE interactions can be facilitated using several statistical models.

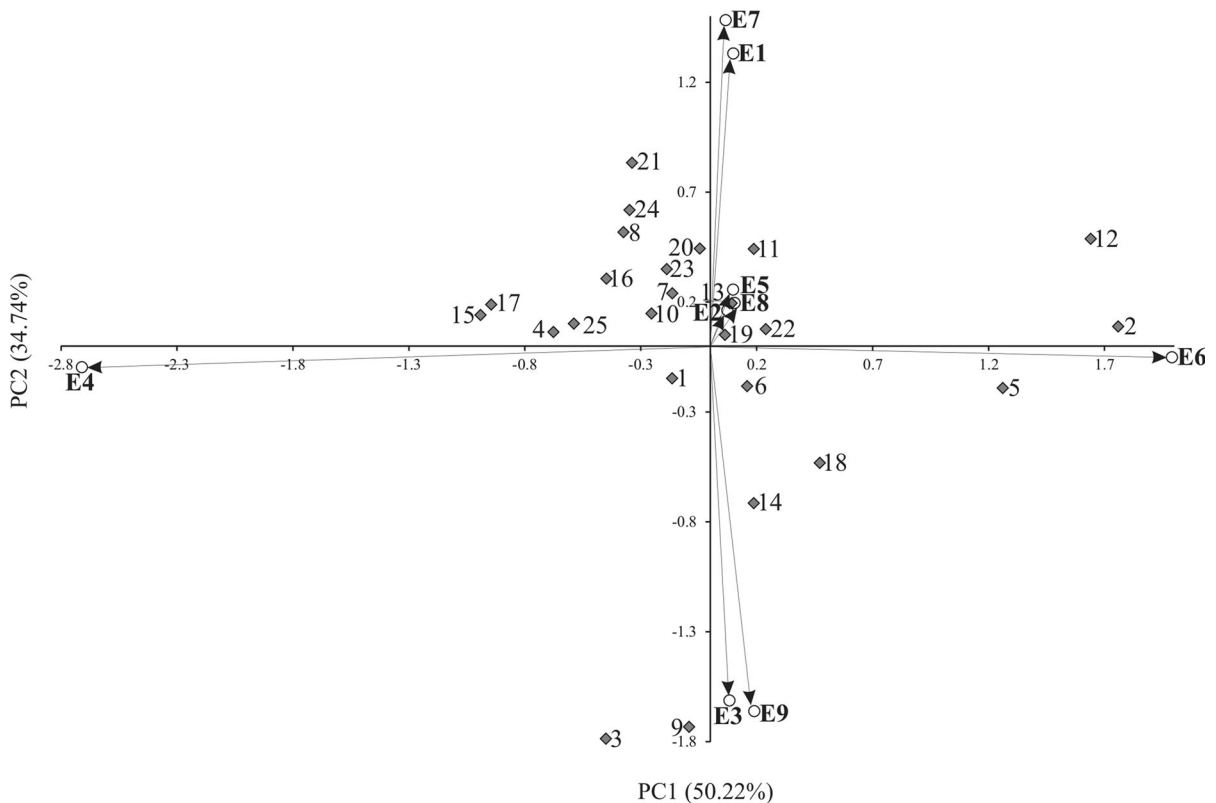


Fig. 4 Biplot for genotype by environment interaction of ADF in interspecific cross-derived *Brassica* lines in nine environments, showing the effects of primary and secondary components (IPCA 1 and IPCA 2, respectively) (E1—Dłoń, 2011;

E2—Poznań-Sołacz, 2011; E3—Złotniki, 2011; E4—Dłoń, 2012; E5—Poznań-Sołacz, 2012; E6—Złotniki, 2012; E7—Dłoń, 2013; E8—Poznań-Sołacz, 2013; E9—Złotniki, 2013)

Traditional, statistical methods as linear regression ANOVA and PCA are often not effective for understanding and evaluating complex data from multi-environments yield trials. In contrast to the standard statistical analyses, AMMI incorporates ANOVA and PCA into a single model and enables simple visual interpretation of the GE interaction. AMMI model is usually constructed from the first two IPCA axes. Measuring GE interaction is very important to determine an optimum breeding strategy for releasing genotypes with an adequate adaptation to target environments (Fox et al. 1997). The AMMI model was often used in study of many species (Abakemal

et al. 2016; Edwards 2016; Nowosad et al. 2016). The AMMI model provides a useful tool in diagnosing GE interaction patterns and improving the accuracy of response estimates. It enables clustering of genotypes based on similarity of response characteristics and identifying potential trends across environments (Bocianowski et al. 2018). The suggested strategy could extract more information from the GE interaction, thereby aiding researchers in identifying specific genotypes with competitive yields across diverse environments. The genotype and environment main effects as well as GE interaction had the strongest effect on all five observed traits (oil content, protein

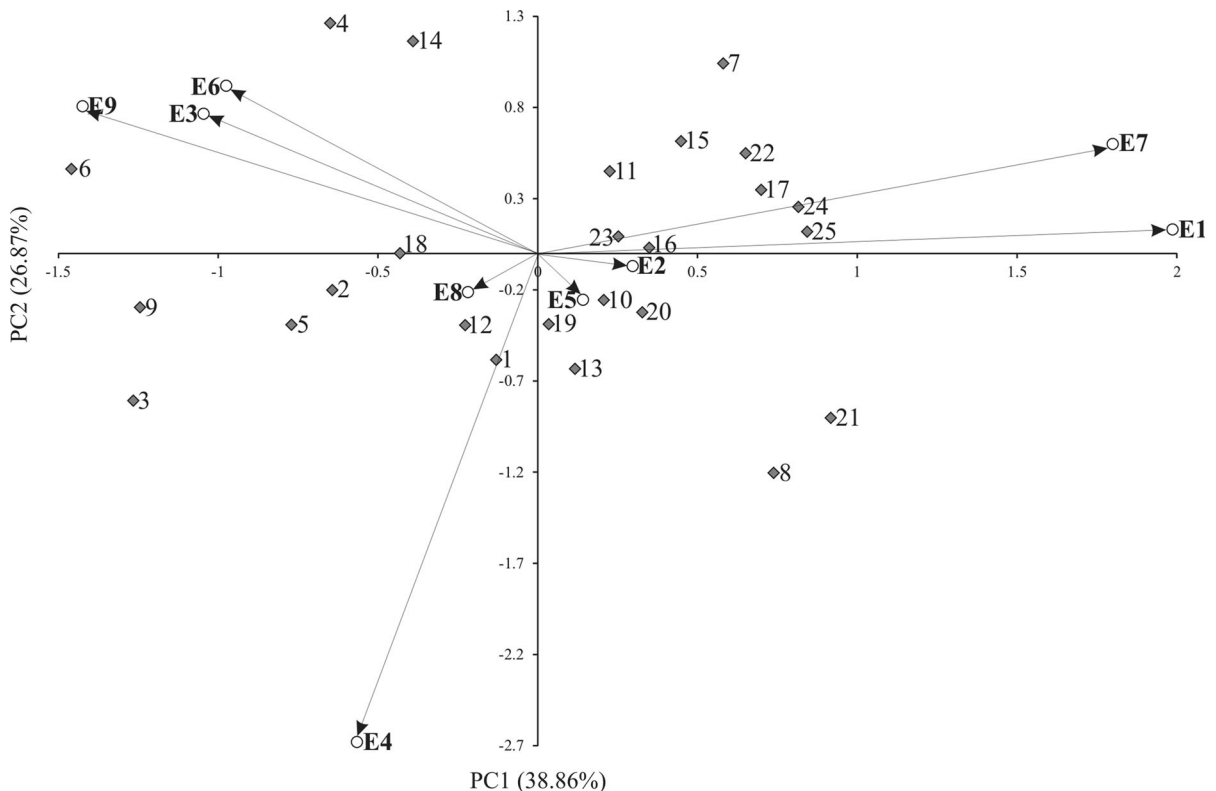


Fig. 5 Biplot for genotype by environment interaction of NDF in interspecific cross-derived *Brassica* lines in nine environments, showing the effects of primary and secondary components (IPCA 1 and IPCA 2, respectively) (E1—Dłóń, 2011;

E2—Poznań–Sołacz, 2011; E3—Złotniki, 2011; E4—Dłóń, 2012; E5—Poznań–Sołacz, 2012; E6—Złotniki, 2012; E7—Dłóń, 2013; E8—Poznań–Sołacz, 2013; E9—Złotniki, 2013)

content, total glucosinolates content, ADF, NDF) expression in Greater Poland. AMMI analyses permits estimation of interaction effect of a genotype in each environment and it helps to identify genotypes best suited for specific environmental conditions. AMMI analyses revealed significant GE interaction with respect to all five traits. The AMMI stability value exposed high genotypes stability. The AMMI results displayed on the GE biplot enables determination of the main effect of the genotype, the environment, and the most meaningful GE interactions.

In general, environments with scores near zero have little interaction across genotypes and provide low discrimination among genotypes (Anandan et al. 2009). In this study, these patterns were observed in

E2, E5 and E8 environments (Figs. 1, 2, 3, 4, 5). AMMI models are capable of measuring the weight of the environments, the genotypes and their interactions throughout a value that measures how stable a genotype is in all environments in terms of particular observed traits. The lines 16 (*B. napus* line MS8 × *B. rapa* ssp. *pekinensis*) and 7 (*B. napus* line MS8 × *B. carinata*) are recommended for further inclusion in the breeding programs because their stability and good average values of observed traits, except total glucosinolates content for line 16. For these lines we obtained the best total (calculated for all five traits) genotype selection index (TGSI = 81 and 97 for line 16 and line 7, respectively).

Conclusions

The interspecific cross-derived *Brassica* lines have not been extensively used in breeding programs because of their low seed yield, low oil content and not-canola quality. However, such plant material is essential for plant breeders to produce cultivars that can develop higher level of resistance to biotic and abiotic stresses.

Acknowledgements This study was funded by the Polish Ministry of Agriculture and Rural Development.

Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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