

GENOTYPE X ENVIRONMENT INTERACTIONS FOR POD NUMBER AND 1000 SEED WEIGHT IN RAPESEED

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ABSTRACT

The objective of this study was to assess the genotype (G) by environment (E) interaction of pod number and 1000-seed weight of rapeseed (*Brassica napus* L.) based on parametric model - additive main effects and multiplicative interaction (AMMI). Thirty genotypes were evaluated across three environments (growing seasons). The best genotype for pod number was UM-12 with 170.8 pods in average, while the best genotype for 1000-seed weight was UM-2 with average 1000-seed weight of 4.2 g. Combined analysis of variance showed that the environment (E) accounted for a high percentage of sums of squares. AMMI model analysis showed that PCA1 explains up to 68% and PCA2 - 31.84% of the interaction effects for pod number, as well as 62% and 38% of the interaction effects for 1000-seed weight. The biplot graphics indicated that the most suitable genotypes for the cultivation across the tested environments were Sremica and UM-8, for pod number, as well as UM-2, for seed weight. However, none of the tested genotypes had superior performance in all environments. The differential response of genotypes observed in this study reaffirms the necessity of multi environment evaluations to identify superior and stable genotypes.

Keywords: AMMI; *Brassica napus*; genotype by environment interaction; pod number and 1000 seed weight

INTRODUCTION

Brassica napus L. is one of the main oil and protein producing plants grown in Europe; therefore, its culture is of the utmost importance (www.faostat.org). Beside high oil and protein content, rapeseed became interesting for production of biodiesel that is important source of bio-renewable energy (Jovičić et al. 2011).

Rapeseed breeding strategies primarily deal with developing new genotypes for human consumption, characterized by high and stable grain yield and oil content as well as low glucosinolate and erucic acid (Sabaghnia et al. 2010). Seed yield depends on pod number and 1000-seed weight (Friedt and Snowdon 2009). Genotype, environment and their interaction have a great influence on quantitative traits of rapeseed, such as yield and oil and protein content (Huhan and Leon 1985). Genotype, environment and interaction effect analysis on tested parameters could be done with the use of different statistical models. One of the methods in a G X E interaction study is the Additive Main Effects and Multiplicative Interaction (AMMI) model which combines the conventional analyses of variance for additive main effects with the principal components analysis (PCA) for the non-additive residuals. AMMI is frequently applied in yield trials in agricultural research when both main effects and interaction are important (Gauch and Zobel 1996).

The objective of this study was to assess the genotype (G) by environment (E) interaction of pod number and 1000-seed weight of rapeseed based on AMMI parametric model.

MATERIAL AND METHODS

Nineteen winter rapeseed cultivars were used in the experiment: two varieties from Hungary (Oktavija, Jana), two varieties from Serbia (Sremica, Banačanka), three varieties from France (Samuray, Jet Neuf, B-009), one variety from Germany (Falcon), and 11 experimental lines from Serbia (UM-1, UM-

2, UM-5, UM-6, UM-8, UM-9, UM-10, UM-11, UM-12, UM-13, UM-14). Cultivars were grown during three growing seasons (from 1996 to 1999) at the experimental fields of Institute of Field and Vegetable Crops, Novi Sad, Serbia. The field trial was arranged in a randomized complete block design with three replications. Seed was sown by hand in four rows, 4 m long, with a between-row spacing of 25 cm, provided within-row spacing of 5 cm. The trial was set up in chernozem type of soil. Before tillage, 250 kg ha⁻¹ NPK fertilizer was applied. Other agricultural practices were optimal in all investigated seasons. Pod number per plant (PNP) was determined on 33 plants. 1000-seed weight (SW) was determined according ISTA rules (1996). AMMI model was used for genotype x environment interaction (GxE) analysis (Zobel et al. 1988). Statistical analysis of data was done with SAS program (SAS Institute Inc. 1990).

RESULTS AND DISCUSSION

Variance analysis for PNP showed that all variation sources were highly significant (Table 1). In PNP, environment made 48.94% of total variation. Genotype share in total variation was 24.45%, while GxE share was 26.29%. Share of the environment in total variation for PNP was two times higher compared to other sources of variation. Furthermore, even interaction share was higher than genotype share in total variation. The first main component (PCA1) covered the greatest part of variation within multivariate variance part i.e. 68.16%, while the second component (PCA2) covered 31.84% of variation.

Table 1. Sum square (SS) and mean square (MS) of variance analysis for AMMI model for pod number per plant and 1000-seed weight in three years for 30 rapeseed cultivars.

Var source	df	SS (%)		MS		F _{experimental}		F _{theoretical}	
		No pods	1000-seed weight	No pods	1000-seed weight	No pods	1000-seed weight	0.05	0.01
Rep	2	0.32	0.03	0.63	0.01	2.55	0.59	1.46	1.69
Years (E)	29	48.94	12.22	94.37	6.11	383.17**	277.73**	2.99	4.60
Gen (G)	2	24.45	15.69	3.25	0.54	13.22**	24.59**	1.46	1.69
GxE	58	26.29	7.08	1.75	0.12	7.11**	5.55**	2.99	4.60
PCA1	30	68.16	4.40	66.64	0.15	9.36**	6.73**	1.36	1.52
PCA2	28	31.84	2.68	33.36	0.10	4.69**	4.37**	1.46	1.69
Error	178		3.97		0.02				

Based on AMMI biplot presentation of GxE interaction for pod number it could be observed that genotypes UM12, B-900 and Duna had higher PNP compared to average and that those genotypes had positive interaction with the 1998/99 production year (Figure 1). The lowest values for PNP were obtained in 1997/98. Genotypes Jana and Samuray had positive interaction with 1997/98 production year. 1999/00 was stable and at its proximity, around zero PCA value, are the genotypes H-450, Aligator and UM-13. Other genotypes differ in average value and in interaction, but these variations are not as distinctive as in above-mentioned genotypes.

AMMI model enables graphical presentation of the results in the form of biplot that facilitates their further analysis. This way of result presentation it is easy to determine average trait value and environmental effect on genotype values (Kaya et al. 2002). Compared to traditional regression model, AMMI model is more efficient for interaction studies (Marjanović-Jeromela 2008). Yan et al. (2000)

noted successful use of biplot for multi-year results, as well as for determination of genotypes most convenient for further use in breeding, or cultivation in certain environment.

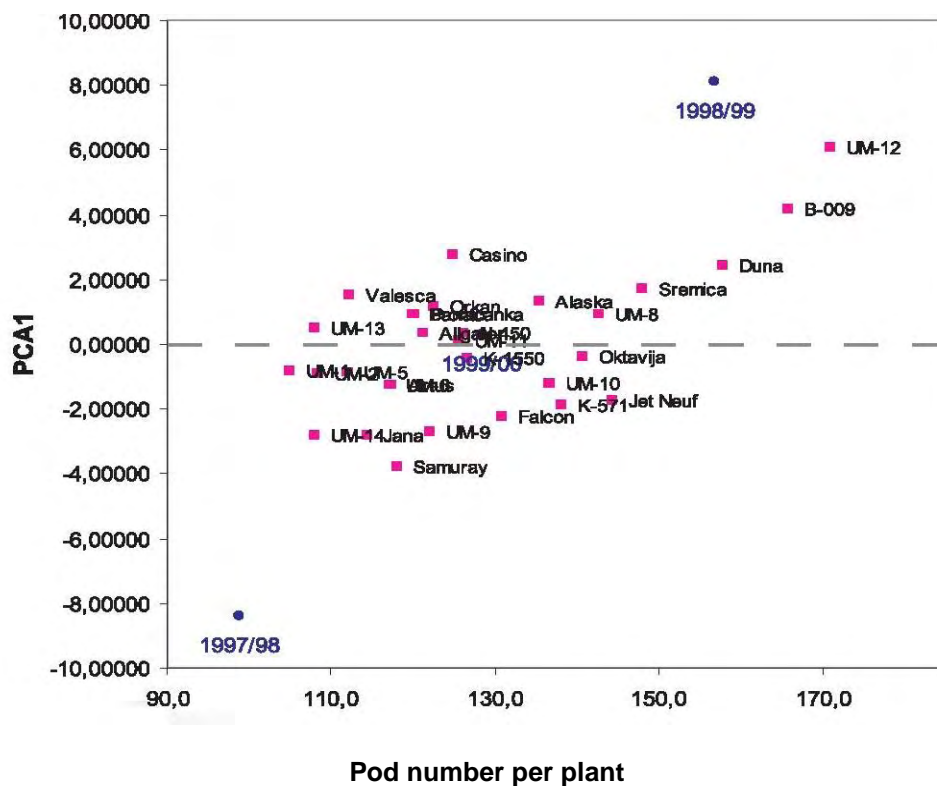


Figure 1. Biplot of AMMI model for mean value and the first PCA axis of 30 rapeseed cultivars for pod number per plant in three-year period

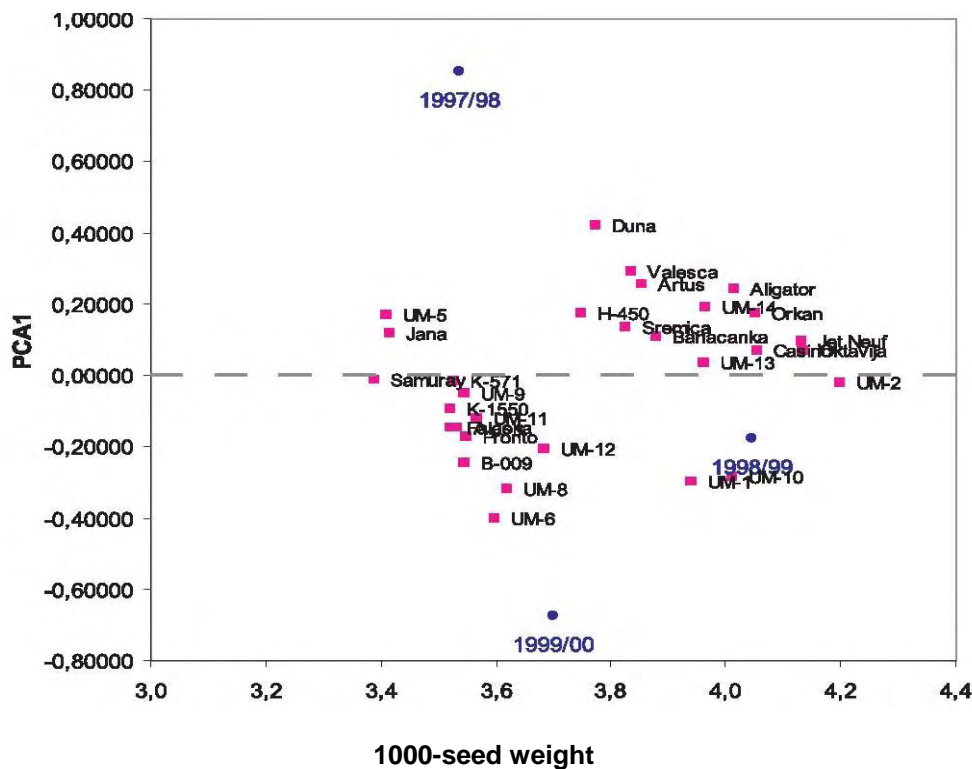


Figure 2. Biplot of AMMI model for mean value and the first PCA axis of 30 rapeseed genotypes for 1000-seed weight in three-year period

In 1000-seed weight expression in observed period, all variation sources, main additive (environment and genotype), as well as non-additive (GxE) were highly significant (Table 1). Effect of environment in total variation was 94.37%, while the effect of genotype was 3.25%. Effect of GxE was only 1.75%. PCA1 covered 66.64% within multivariate part, while PCA2 covered 33.36%.

SW in observed period ranged from 3.41 to 4.20 g. AMMI biplot showed the differences both in main effect and in GxE effect (Figure 2). Genotype UM-2 had the highest value of SW. The same genotype showed high stability for this trait. The high stability was observed in genotype Samuray, as well, but its SW was under average value. The most positive effect on SW was expressed in 1998/99 and positive interaction was achieved with genotypes UM-1 and UM-10. These genotypes had positive correlation with 1999/00 production year. Relatively higher variation was observed in genotype Drina that had positive reaction to environmental conditions in 1997/98.

CONCLUSIONS

The environment had the highest influence on pod number per plant and 1000-seed weight.

Use of graphical presentation of AMMI analysis in the form of biplot facilitates the selection of stable genotypes with high values of the desired trait.

Genotype UM-2 had the high stability and high 1000-seed weight value. This genotype should be included in breeding programme.

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