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ASSESSMENT OF AGRO-MORPHOLOGICAL VARIABILITY IN RICE USING MULTIVARIATE ANALYSIS

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Abstract

The research was carried out to assessment the agro-morphological variability in fourteen rice varieties using principal component analysis, linear correlation and cluster analysis. All rice varieties have Italian origin and were grown in 2014 and 2015 under agroecological conditions in Kocani, the Republic of North Macedonia. Principal component analysis was utilized to examine the variation and to estimate the contribution of traits for total variability. Three components in the PCA analysis with Eigen value > 1 contributed 75.59% variability existing in the rice varieties for yield contributing traits. PC1 accounted 30.81% of the total variability, contributed by traits like 1 000 grain weight, panicle length, weight of grains per panicle and plant height. PC2 had the contribution from the traits as number of plants per m^2, plant height and panicle length which accounted for 25.08% of the total variation. Grain yield and panicle length had contributed 19.71% of the total variation in PC3. Only Ulisse and San Andrea showed positive values among all three main components. Grain yield showed positive correlation with number of plants per m^2 (r= 0.185). On the other side, number of plants per m^2 was in negative correlation with weight of grains per panicle (r= -0.593). Also, negative correlation was established between number of grains per panicle and 1 000 grain weight (r= -0.752). Using cluster analysis, two main cluster groups with subgroups were extracted. The results revealed existence of variability in the studied varieties which can help breeders to achieve higher yield in rice.

Key words: *Oryza sativa* L., *principal component analysis, cluster analysis, linear correlation*

INTRODUCTION

The existence of genetic diversity in the initial material is one of the basic prerequisites for the success of each breeding programme and the achievement of the basic goals for plant improvement, such as increasing the yield potential, adaptability, quality and resistance to biotic and abiotic stress. For this aim, breeders use the natural populations, wild relatives of cultivated species, populations created by hybridization, induced mutations and other biotechnological methods. Introduction is also one of the methods used to increase genetic variability. Using introduction as a method in breeding programme, it is necessary to have the correct characterization and evaluation of the introduced material, especially from geographically more remote regions. Characterization of rice germplasm increases its value in any breeding programme. Agro-morphological characterization of germplasm variety is fundamental in order to provide information for plant breeding programmes (Lin, 1991; Nascimento et al., 2011). The use of agro-morphological traits is the most common approach utilized to estimate relationships between genotypes (Bajracharya et al., 2006).

Genetic diversity has an important and significant role in plant production. It is considered as a means of survival and adaptation to changing environments (Rao and Hodgkin, 2002; Gao, 2003). Evaluation of genetic resources for various agronomic traits and the assessment of the amount of genetic variation within them are useful to allow more efficient genetic improvement (Haussmann et al., 2004). Assessment of genetic and agro-morphological variability is very important in rice breeding from the standpoint of selection, conservation of different land races variety of rice and proper utilization (Jayasudha and Sharma, 2010).

Statistical analyses are necessary for proper examination and analysis of agro-morphological properties. The application of statistical methods gives an insight into the legality of the relationship between the tested properties, genotypes and factors that influence the development of the culture itself. The large number of agro-morphological properties and their interconnectedness make the statistical analysis extremely complex, especially if a large number of genotypes are examined.

Multivariate analysis is the most commonly used approach for genetic variability, estimation to illuminate the patterns of variation in germplasm collections. Principal component analysis (PCA), cluster analysis (CA) and correlation are the most important multivariate analysis methods (Oyelola, 2014). Among multivariate techniques, PCA and cluster analysis are preferred tools for morphological characterization of genotypes and their grouping on similarity basis (Peeters and Martinelli, 1989; Mohammadi and Prasanna, 2003). Principal component analysis, significantly contribute to reducing the data and highlighting the properties that most influence the sample's variability. Combination of these two approaches gives comprehensive information of characters which are critically contributing for genetic variability in crops (Rachovska et al., 2002).

Many researchers had successfully used agro-morphological characters to classify and estimate diversity in a variety of rice using multivariate analyses (Nachimuthu et al., 2014; Ravikumar et al., 2015; Pachauri et al., 2017).

The objective of this study was to characterize and classify 14 new introduced rice varieties from Italy and also to identify morphological traits responsible for selection of important characters and study the interrelationship among the traits.

MATERIAL AND METHODS

Plant material and experimental design

Fourteen rice varieties were used as an experimental material for this research. All rice varieties have Italian origin. San Andrea variety for a long period is used as a main cultivar in commercial rice production in the Republic of North Macedonia, while the other Italian varieties (Arsenal, Nembo, Ronaldo, Galileo, Sprint, Ulisse, Krystalino, Mirko, Sfera, Gloria, Pato, Creso and Vasco) were newly introduced. The trials were set up during the period 2014 and 2015, on alluvial soil type in the region of Kocani. The experimental material was placed by using randomized block design in three replications. The standard agronomic packages of practices were followed throughout the season for regular growth of crop.

Determination of agro-morphological traits

Ten randomly selected plants from each repetition have been analysed for some agro-morphological traits such as plant height (cm), panicle length (cm), number of grains per panicle and weight of grains per panicle (g). The number of plants per m^2 was determined by counting the plants from m^2 of each repetition. 1 000 grain weight, has been determined to measure 1 000 grain of each repetition. Grain yield obtained from the 5 m^2 was calculated in t·ha^{-1}. When calculating the 1000 grain weight and grain yield, the moisture content was reduced in 14%.

Statistical analyses

All tested traits were statistical analysed by SPSS (2010) system and JMP 5.0.1 (2002) software. Principal component analysis and cluster analysis were done using the methodology given by Gomez and Gomez (1984). The correlation between yield and yield components was calculated according Singh and Chaudhary (1985).

RESULTS AND DISCUSSION

Principal component analysis (PCA) is one of the important multivariate tool of diversity analysis. This statistical technique analyses a data table in which observations are described by several inter-correlated quantitative dependent variables and can be helpful for identification of plant character that categorize the distinctiveness among promising varieties. The objective of principal component analysis is reduction of dimensionality of a data set with a large number of correlated variable or traits (Jolliffe, 2002).

The results of PCA from our research are depicted in Table 1. PCA was carried out by using 14 rice varieties and seven agro-morphological traits. Three main components in the PCA analysis with Eigen value > 1 contributed 75.59% variability existing in the rice varieties for yield contributing traits. In this study, PC1 accounted 30.81% of the total variability, PC2 showed 25.08% and PC3 accounted 19.71% of variations among characters. PC1 accounted for the maximum variability and highly loaded with characters such as 1 000 grain weight (0.65), panicle length (0.54), weight of grains per panicle (0.36) and plant height (0.32) contributed in positive direction. The second principal component accounted 25.08% of the total variation and was in positive correlation with number of plants per m^2 (0.56), plant height (0.32) and panicle length (0.30). Grain yield (0.74) and panicle length (0.62) were important traits contributing to the third PC, which accounted 19.71% of the total variation (Tab. 1).

Through PCA we could identify the number of plant characters, which are responsible for the observed genotypic variation within a group. Four principal components with Eigen value greater than >1 and explained 72.48% of the total variance were recorded by Pachauri et al. (2017).

PCA has been used by various researchers like Gana et al. (2013), Asfaq et al. (2014), Worede et al. (2014), Kumar et al. (2015), Ravikumar et al. (2015), Ojha et al. (2017), Pachauri et al. (2017) and Yugandhar et al. (2018) for characterization different rice germplasm lines.

Table 1. Eigen value, contribution of variability and factor loadings for the principal component.

	Principal Components		
	PC1	PC2	PC3
Eigen value	2.16	1.76	1.38
Percentage of variability (%)	30.81	25.08	19.71
Cumulative percentage (%)	30.81	55.88	75.59
Traits	**Factor loadings**		
Plant height	0.32	0.32	-0.10
Panicle length	0.54	0.30	0.62
Number of grains per panicle	-0.47	-0.43	-0.01
Weight of grains per panicle	0.36	-0.54	0.20
1 000 grain weight	0.65	0.03	0.13
Number of plants per m^2	-0.30	0.56	0.07
Grain yield	-0.19	-0.13	0.74

In Table 2 are given the factor loadings by main components of the analysed rice varieties. Only two varieties, Ulisse and San Andrea, showed positive values by all main components. Those varieties had a higher value for grain yield and favourable values by other yield-related components.

Table 2. Factor loadings by main components of the analysed rice varieties.

Rice varieties	PC1	PC2	PC3
Arsenal	-0.94	0.2	-1.02
Nembo	0.34	-1.94	-1.93
Ronaldo	-0.73	-1.02	1.71
Galileo	1.77	-1.98	2.26
Sprint	-1.22	1.52	-0.30
Ulisse	1.41	0.75	0.80
Krystalino	-0.98	-2.10	-1.17
Mirko	-2.47	0.64	0.57
Sfera	-1.97	0.72	0.54
Gloria	1.76	0.90	-1.09
Pato	1.73	0.23	-1.02
Creso	-0.25	-0.59	0.01
Vasko	-0.11	0.35	0.33
San Andrea	1.66	2.10	0.31

Correlations help the breeder to understand the mutual component characters on which selection can be based for genetic improvement (Chakravorty et al., 2013). In order to assess trait association, phenotypic correlation analysis was done and the result is depicted in Table 3. 1 000 grain weight was highly and significantly negative correlated with number of grains per panicle (r = -0.752). Positive significant correlation was established between the number of plants per m^2 and grain yield (r= 0.185). On the other hand, the number of plants per m^2 was negatively correlated with weight of grains per panicle (r= -0.593).

Significant phenotypic correlations of yield and yield-related traits were reported by other workers in inbred lines, hybrids, varieties and landrace rice (Sürek and Beşer 2003; Bastian et al., 2008; Chakravorty et al., 2013; Janwan et al., 2013; Seesang et al., 2013).

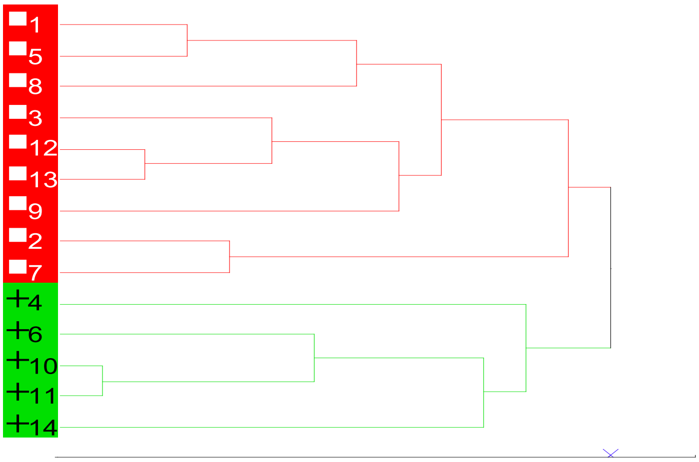
Table 3. Phenotypic linear correlation between grain yield and yield components.

Traits	Plant height	Panicle length	Number of grains per panicle	Weight of grains per panicle	1 000 grain weight	Number of plants per m^2	Grain yield
Plant height	1	0.128	-0.246	0.167	0.317	0.248	-0.292
Panicle length		1	-0.208	-0.125	0.113	0.126	0.337
Number of grains per panicle			1	0.180	-0.752**	-0.056	0.224
Weight of grains per panicle				1	0.485	-0.593*	0.207
1 000 grain weight					1	-0.326	-0.098
Number of plants per m^2						1	0.185*
Grain yield							1

** Correlation is significant at the P<0.01

* Correlation is significant at the P<0.05

Cluster analysis was carried out based on available data for grain yield and yield related components (Fig. 1). Two main cluster groups were extracted. The first one contains 9 varieties: Arsenal, Sprint, Mirko, Ronaldo, Creso, Vasko, Sfera, Nembo and Krystalino. The varieties Creso and Vasko were genetically the closest with the least remote units, forming subgroup in the first cluster. The second cluster group contains the remaining varieties Galileo, Ulisse, Gloria, Pato and San Andrea (Fig. 1).



	Legend
1	Arsenal
2	Nembo
3	Ronaldo
4	Galileo
5	Sprint
6	Ulisse
7	Krystalino
8	Mirko
9	Sfera
10	Gloria
11	Pato
12	Creso
13	Vasko
14	San Andrea

Figure 1. Cluster analysis of rice varieties based on grain yield and yield related components.

CONCLUDING REMARKS

The performed research showed variability between analysed agro-morphological traits. Principal component analysis was utilized to estimate the relative contribution of different traits for total variability. This tool has identified some characters that plays prominent role in classifying the variation existing in the germplasm. The results of the PCA revealed that the 75.59% of the total variability was explained by the first three main principal components. The analysis identified that traits such as 1 000 grain weight, panicle lenght, number of plants per m^2 and grain yield in different principal components are the most important for classifying the variation. Only Ulisse and San Andrea had positive values by all main components. Positive correlation between number of plants per m^2 and grain yield was established, but also the significant high factor loading values for panicle length and 1 000 grain weight were determinate which indicate on the importance of those traits in breeding programs for yield improvement.

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ПРОЦЕНКА НА АГРО-МОРФОЛОШКАТА ВАРИЈАБИЛНОСТ КАЈ ОРИЗОТ СО МУЛТИФАКТОРИЈАЛНА АНАЛИЗА

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Резиме

Целта на овој труд е да се изврши проценка на агроморфолошката варијабилност на четиринаесет сорти ориз, користејќи ги компонентната векторска анализа, линеарната корелација и кластер анализата. Сите анализирани сорти имаат италијанско потекло и се одгледувани во 2014 и 2015 година во агроеколошки услови во Кочани, Република Северна Македонија. Со цел да се утврди варијабилноста на својствата и да се процени уделот на анализираните својства во однос на вкупната варијабилност беше применета компонентна векторска анализа. Со оваа анализа се добиени три главни компоненти со гранична вредност на оптоварување поголема од 1, а кумулативниот процент на овие три главни компоненти изнесува 75.59% од вкупното варирање. Првата главна компонента учествува со 30.81% и е позитивно поврзана со следниве својства: маса на 1000 зрна, должина на метличка, маса на зрна од метличка и висина на растение. Втората главна компонента учествува со 25.08% од вкупното варирање и е во корелација со позитивните вредности на својствата: број на растенија на m^2, висина на растение и должина на метличка. Третата главна компонента учествува со 19.71% од вкупното варирање и е позитивно поврзана со приносот на зрно и должина на метличката. Само сортите Ulisse и San Andrea покажаа позитивни вредности кај сите три главни компоненти. Приносот на зрно покажа позитивна корелација со бројот на растенија на m^2 ($r = 0.185$). Од друга страна, бројот на растенија на m^2 беше во негативна корелација со масата на зрна од метличка ($r = -0.593$). Исто така, беше утврдена негативна корелација помеѓу бројот на зрна од метличка и масата на 1000 зрна ($r = -0.752$). Со кластер анализа се издвоени две главни кластер групи со подгрупи. Резултатите укажуваат на постоење на варијабилност во проучуваните сорти која може да им помогне на селекционерите за постигнување на повисок принос кај оризот.

Клучни зборови: *Oryza sativa L., компонентна векторска анализа, кластер анализа, линеарна корелација.*