



ASSESSMENT OF AGRO-MORPHOLOGICAL VARIABILITY IN RICE BY MULTIVARIATE ANALYSIS

Verica Ilieva*, Natalija Markova Ruzdik*, Ljupco Mihajlov*, Mite Ilievski*

* Faculty of Agriculture, "Goce Delcev" University – Stip, Krste Misirkov bb, 2000 Stip, Republic of North Macedonia



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INTRODUCTION

The presence of genetic diversity in the initial material is the basic prerequisite for the success of each breeding program 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 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 program, 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 utility in any breeding program. Agro-morphological characterization of germplasm variety is fundamental in order to provide information for plant breeding programs (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).

Statistical analyzes 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 methods, such as Principal Component Analysis, significantly contribute to reducing the data and highlighting the properties that most influence the sample's variability.

Multivariate analysis is the most commonly used approach for genetic variability estimation to illuminate the patterns of variation in germplasm collections. 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). 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 (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 Field experiment

Fourteen Italian rice varieties were used as an experimental material for this research (Arsenal, Nembo, Ronaldo, Galileo, Sprint, Ulisse, Krystalino, Mirko, Sfera, Gloria, Pato, Creso, Vasco and San Andrea). 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 varieties were new introduced.

The trials were set up during the period 2014 and 2015, using randomized block design in three replications.

Methods and Data processing

Ten randomly selected plants from each repetition have been analyzed for the plant height, panicle length, number of grains per panicle and weight of grains per panicle. The number of plants per m² was determined by counting the plants from m² of each repetition. 1 000 grain weight, has been determined to measure 1 000 grain of each repetition. Grain yield obtained from the 5 m² was calculated in t ha⁻¹.

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

RESULTS AND DISCUSSION

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 principal component analysis (PCA) from our research are depicted in Table 1.

Three main components in the PCA analysis with Eigenvalues > 1 contributed 75.59% variability existing in the rice varieties for yield contributing traits. 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 m² (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.

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 Eigenvalue greater than 1 and explained 72.48% of the total variance were recorded by Pachauri et al. (2017).

	Principal Components		
	PC1	PC2	PC3
Eigenvalue	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 analyzed rice varieties. Only two varieties showed positive values by all main components (Ulisse and San Andrea). Those varieties had a higher value for grain yield and favorable values by other yield-related components.

Table 2. Factor loadings by main components of the analyzed 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

The result from performed phenotypic correlation is depicted in Table 3. 1 000 grain weight was highly and significantly negative correlated with number of grains per panicle ($r = -0.752$). Negative correlation was established also between the number of plants per m² and weight of grains per panicle ($r = -0.593$). On the other hand, the number of plants per m² was positive significantly correlated with grain yield ($r = 0.185$). Significant correlations of yield and yield-related traits were reported by other workers in inbred lines, hybrids, varieties and landrace rice (Chakravorty et al., 2013; Janwan et al., 2013).

Cluster analysis was carried out based on available data for grain yield and yield related components (Figure 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.

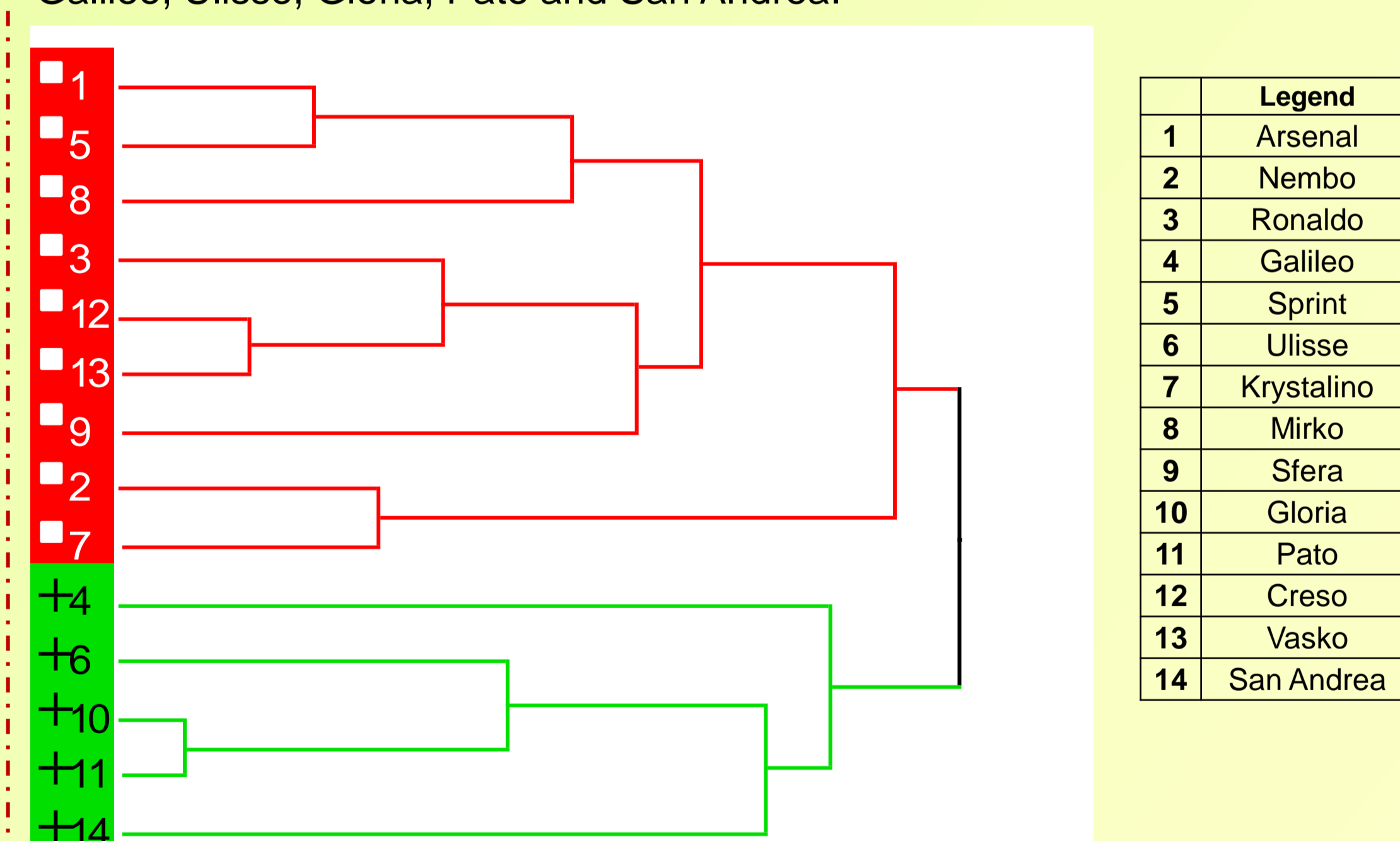


Figure 1. Cluster analysis of rice varieties based on grain yield and yield related components

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

CONCLUSION

The performed research showed variability between tested rice varieties. The morphological trait value of each trait measures the importance and contribution of each component. The results of PCA revealed that the first three principal components explained 75.59% of the total variation. Only Ulisse and San Andrea had a positive values by all main components. Positive significant correlation between number of plants per m² and grain yield was established, but also the significant high factor loading values for panicle length and 1 000 grain weight indicate on importance of those traits in breeding programs for yield improvement.

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