

MULTIVARIATE STATISTICAL ANALYSIS OF PRODUCTIVE TRAITS IN POA PRATENSIS UNDER WESTERN ROMANIAN CONDITIONS

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Abstract

*This study evaluated the growth performance and productive potential of smooth meadow-grass genotypes under the pedoclimatic conditions of western Romania. The local populations were analyzed from which 20 genotypes were selected, evaluated based on morphological and productive characters, such as bush diameter, plant height, number of generative shoots, leaf area and green mass per clone. Pearson correlation analysis revealed very strong positive relationships between green mass, bush diameter and number of generative shoots, underlining the importance of these characters in determining biomass production. Principal component analysis (PCA) and cluster analysis revealed the existence of significant phenotypic variability between genotypes and allowed the identification of groups with different levels of productivity. Overall, the results demonstrate that environmental conditions strongly influence vegetative development and the expression of productive characters, highlighting at the same time the potential for selection of valuable genotypes for *Poa pratensis* breeding programs.*

Key words: smooth meadow-grass, biochemical composition, biomass quality, generative shoots.

INTRODUCTION

In Europe, the multifunctional nature of permanent grassland ecosystems is particularly appreciated as a fundamental element of the rural landscape, contributing not only to fodder production, but also to biodiversity conservation, soil protection, hydrological stability and a host of social aspects (Hopkins & Holz, 2006; Peeters, 2009; Conant et al., 2017; Samfira et al., 2022; Butnariu, 2026).

Recent studies indicate that appropriate grassland management can increase carbon sequestration capacity and reduce the impact of climate change on agricultural systems (Frame et al., 1998; Hoskin et al., 1999; White & Hodgson, 1999; Soussana et al., 2019).

The genus *Poa*, belonging to the *Poaceae* family, includes over 500 species distributed in different climatic regions of the globe (Soreng et al., 2017). Among them, *Poa pratensis* L., commonly known as smooth meadow-grass, is one of the most important species from an agronomic and ecological point of view. This species is naturally distributed in temperate

regions of Europe, Asia, and North America and is appreciated for its high adaptability to different environmental conditions (Beard, 2002; Turgeon, 2011; Parker & Roberts, 2016). In forage production systems, smooth meadow-grass is valued for its ability to produce high-nutritional-quality plant biomass. Under favorable soil and climate conditions, dry matter production can range from 4 to 8 t/ha, depending on fertilization, the cropping system, and the meadow's floristic composition (Hopkins & Holz, 2006). In grasslands dominated by perennial grasses, this species frequently contributes to a significant proportion of total forage production.

In addition to biomass production, forage quality is an essential indicator of the agronomic value of grass species. The main parameters used to assess forage quality include crude protein content, organic matter digestibility, and structural fiber content (Van Soest, 1994; Butnariu et al., 2012). In the case of *Poa pratensis*, crude protein content can range from 10 to 18% of the dry matter, depending on

vegetation stage and growing conditions (White et al., 1999).

The digestibility of organic matter is an important indicator of forage nutritional value. Studies on the digestibility of grassland forages show that plant biomass from *Poa pratensis* can have digestibility values between 60 and 70%, depending on the stage of the plant development and management practices (Hopkins & Holz, 2006).

The content of structural fibers, as measured by neutral detergent fiber (NDF) and acid detergent fiber (ADF), directly influences the digestibility and energy value of forages (Orloff & Putnam, 2007; Rayburn et al., 2007).

The leaf/stem ratio is another important indicator of forage quality, since leaves contain higher concentrations of nutrients compared to stems. In this species, the high proportion of leaves improves the nutritional value of the forage and increases palatability for animals (Frame et al., 1998).

In recent years, much research has focused on improving the agronomic performance of *Poa pratensis* by selecting genotypes with high tolerance to abiotic stresses, such as high temperatures or water deficit (Bonos & Huff, 2013; Huang et al., 2021; Chen et al., 2021; Butnariu & Koirala, 2025). In the context of climate change, these characteristics are becoming increasingly important for maintaining the productivity of grassland ecosystems (IPCC, 2021).

The smooth meadow-grass exhibits morphological peculiarities that distinguish it from other *Poa pratensis* varieties, especially its narrower leaves and greater adaptability to variable pedoclimatic conditions. Some studies suggest that this variety may exhibit greater stability in biomass production and better tolerance to climatic stress conditions (Chen et al., 2021).

In Europe, the evaluation of grass species' performance under regional pedoclimatic conditions is essential for optimizing forage production systems. The productivity and nutritional value of plant biomass can vary considerably depending on climatic conditions, soil fertility, and agricultural management practices (Peeters, 2009). In Romania, grassland productivity is an important component of the agricultural system, offering high potential for

forage production, but it depends on the floristic composition and local pedoclimatic conditions (Ciobanu et al., 2012; Samuil et al., 2012). In this context, the evaluation of the productive and qualitative parameters of this variety, cultivated in the pedoclimatic conditions of western Romania, can provide relevant information regarding the agronomic potential of this species and its adaptability to regional conditions.

MATERIALS AND METHODS

The **purpose** of the work was to study, under the specific cultivation conditions of the Banat Plain, the phenotypic externalization of the morpho-productive traits in smooth meadow-grass and to identify productively valuable clones. This objective is important because the species is allelogamous and apomictic (many selected descendants reproduce by seeds that largely preserve the maternal genotype). The improvement process is largely based on selecting valuable clones.

The **biological material** consisted of local genotypes collected from the spontaneous flora of the Banat area, Romania. The genotypes were introduced into the collection field where 20 genotypes were selected and subjected to mass selection to eliminate the unvalued provenances. The identification of the parents required the investigation of the following characters throughout the vegetation period: bush diameter (cm), bush height (cm), number of generative shoots, number of leaves per main shoot, foliar surface (cm²), green mass/clone (g).

The **soil conditions** are typical of a chernozem, weakly gleyed, medium clay-clayey. The pH value indicates a weakly alkaline reaction (7.3-8.4) at 20-100 cm, and a moderately alkaline reaction (8.5-9.0) between 100-130 cm.

Climatic conditions. The observation period exhibited a rainfall regime with values well below the multiannual monthly average in the majority of months. The total amount of precipitation available to plants was 499.2 mm, with a negative deviation of 22.2 mm from the multiannual average. The precipitation deficit, together with excessive temperatures, induced an atmospheric heatwave and exacerbated pedological and atmospheric drought.

Statistical Analyses and Software Used. The relationships between morphological and

productivity characters were evaluated using the Pearson correlation coefficient (r). The Pearson coefficient measures the intensity and direction of the linear relationship between two variables. The statistical significance of the correlations was assessed based on the p-value, using the following significance thresholds: • $p < 0.05$ – significant (*) • $p < 0.01$ – highly significant (**) • $p < 0.001$ – very highly significant (***). The correlation matrix enabled the identification of associations between characters contributing to biomass production and plant architecture. Principal Component Analysis (PCA) was used to evaluate the structure of phenotypic variability between genotypes. Before performing the PCA analysis, all variables were standardized (z-score transformation) to eliminate the effects of differences in units of measurement. PCA reduces the dimensionality of the data set by transforming the original variables into a smaller set of principal components that explain most of the variation in the data. The first two principal components (PC1 and PC2) were used to create a biplot, which visualizes the distribution of genotypes across the analyzed characters. This analysis facilitates the identification of groups of genotypes with similar morphological and productive characteristics. The similarity between genotypes, based on the analyzed morphological characters, was evaluated through hierarchical cluster analysis.

The grouping procedure was performed using Euclidean distance as a measure of similarity and Ward's method as a clustering algorithm. The results of the analysis were graphically represented as a dendrogram, which illustrates the relationships among genotypes and allows the identification of clusters with similar phenotypic characteristics. Cluster analysis is frequently used in plant breeding studies to identify groups of genotypes with similar agronomic performances and valuable potential for breeding programs.

RESULTS AND DISCUSSIONS

To highlight the relationships between the main morphological and productivity characters of the smooth meadow-grass genotypes, a Pearson correlation matrix was performed using the mean values of the following variables: bush diameter, bush height, number of generative shoots, number of leaves on the main shoot, leaf area, and green mass per clone (Table 1). In this table, the first two columns show the variable pairs analyzed for correlations. The obtained correlations highlight the degree of association between these characters and identify those that significantly influence biomass production. Interpretation of correlation coefficients provides important information for selecting valuable genotypes in breeding programs.

Table 1. Expressing the degree of linear association of productive characters in *Poa pratensis* in Pearson's correlation matrix

The pairs of variables analyzed for correlation		Pearson's r	p	Lower 95% CI	Upper 95% CI
Bush diameter cm	Bush height cm	0.325	.162	-0.137	0.671
Bush diameter cm	Generative shoots	0.827***	< .001	0.607	0.929
Bush diameter cm	Leaves per main shoot	-0.215	.364	-0.600	0.252
Bush diameter cm	Leaf area cm ²	0.730***	< .001	0.425	0.886
Bush diameter cm	Green mass g	0.903***	< .001	0.768	0.962
Bush height cm	Generative shoots	0.362	.117	-0.096	0.693
Bush height cm	Leaves per main shoot	0.300	.198	-0.164	0.656
Bush height cm	Leaf area cm ²	0.427	.061	-0.020	0.731
Bush height cm	Green mass g	0.428	.060	-0.018	0.732
Generative shoots	Leaves per main shoot	-0.123	.605	-0.537	0.338
Generative shoots	Leaf area cm ²	0.538*	.014	0.125	0.792
Generative shoots	Green mass g	0.908***	< .001	0.778	0.963
Leaves per main shoot	Leaf area cm ²	-0.092	.699	-0.514	0.365
Leaves per main shoot	Green mass g	-0.010	.968	-0.450	0.435
Leaf area cm ²	Green mass g	0.730***	< .001	0.424	0.886

Significance: * $p < .05$, ** $p < .01$, *** $p < .001$.

The interpretation of the Pearson correlation matrix results highlights strong and very strong correlations among the main productivity characters of the *Poa pratensis* genotypes. These relationships indicate that certain morphological characters are closely related to plants' ability to produce biomass.

The analysis of the relationship between the Green Mass – Generative shoots characters shows a correlation coefficient $r = 0.91$ and a statistical significance level of $p < 0.001$, indicating a very strong, highly statistically significant correlation. This result suggests that the number of generative shoots is one of the main factors influencing green mass production, since a higher shoot density implicitly determines greater biomass accumulation.

Also, the analysis of the relationship between the Green Mass – Bush diameter characters shows a high correlation coefficient ($r = 0.90$), with a significance level $p < 0.001$.

These results indicate that genotypes with larger bush diameters generally produce more green mass. The biological explanation for this relationship is that plants with a more developed bush have a more complex vegetative structure, being able to support a higher biomass production. Similarly, the analysis of the relationship between Bush diameter and Generative shoots revealed a correlation coefficient of $r = 0.83$, with a significance level $p < 0.001$, indicating a very strong correlation between these two characters. This result suggests that genotypes that develop larger bushes also tend to produce a greater number of generative shoots, thereby increasing the plants' productive capacity.

Important interrelationships were also observed between the Leaf area – Green mass characters, with a correlation coefficient of $r = 0.73$ and a significance level of $p < 0.01$, indicating a strong, statistically significant correlation. This relationship can be explained by the fact that a larger leaf area indicates higher photosynthetic capacity, which favors the accumulation of more organic matter and, implicitly, higher biomass production.

On the other hand, the Pearson correlation matrix also highlights weak or insignificant correlations among certain characters. In this sense, the Leaves per main shoot character shows no significant correlations with the other

variables analyzed. This result suggests that the number of leaves per main shoot does not directly influence total biomass production; rather, the main role is attributed to the characters that determine bush architecture and shoot density.

Overall, the results of the correlation analysis indicate that bush diameter, number of generative shoots, and leaf area are the characters that contribute most to green mass production in smooth meadow-grass genotypes. These characters may represent important selection criteria in breeding programs, being relevant indicators of the productive potential of the studied genotypes.

To more clearly highlight the relationships among the analyzed characters, the Pearson correlation matrix was also presented as a heat map (Figure 1). This graphic representation allows for a quick observation of the intensity of the correlations between the variables, by means of a color scale, where the more intense shades indicate strong positive correlations, and the open ones weak or non-existent correlations. The heat map confirms strong correlations among green mass, the number of generative shoots, and bush diameter, as well as between leaf area and green mass, highlighting the importance of these characters in determining the productivity of *Poa pratensis* genotypes. In contrast, the character number of leaves on the main shoot shows low correlations with the other analyzed variables.

To highlight the variability structure among the analyzed characters and identify the main factors contributing to the differentiation of *Poa pratensis* genotypes, Principal Component Analysis (PCA) was performed.

This multivariate statistical method allows the reduction of the dimensionality of the data set by transforming the initial variables into a smaller number of principal components, which together explain most of the total variation. The significance of the PCA model was evaluated using the Chi-square test, which yielded $\chi^2 = 17.447$, $df = 9$, and $p = 0.042$, confirming that the model is statistically significant and adequate for interpreting the relationships among the analyzed variables. The Scree plot highlights the contribution of each component to explaining the total variability of the data. According to the eigenvalue criterion

(eigenvalue > 1) and parallel analysis, the first principal component (RC1) explains most of the variation, which indicates that most of the

analyzed characters are influenced by a common factor associated with plant productivity and vigor.

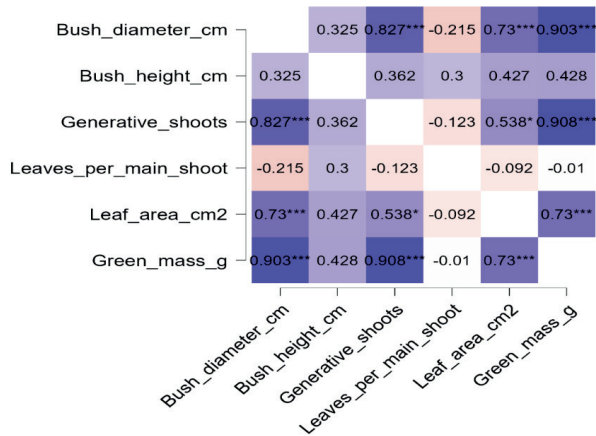


Figure 1. Heat map of the Pearson correlation matrix between morphological and productivity characters of the *Poa pratensis* genotypes

The component loadings show the contribution of each variable to the formation of the principal component RC1. The highest values are recorded for green mass (0.966), bush diameter (0.935), and the number of generative shoots (0.894), indicating that these characters have the greatest influence on the variability between genotypes (Table 2). Also, leaf area (0.819) contributes significantly to this component, suggesting the leaf apparatus plays an important role in biomass accumulation. In contrast, the character number of leaves per main shoot makes a very low contribution, an aspect also highlighted by the high uniqueness value (0.992), which indicates a limited influence on overall variability (Table 3).

The graphic representation of the relationships between the principal component and the analyzed variables, illustrated by a path diagram, confirms that the main characters that determine the variability of genotypes are those associated with productivity and bush size, respectively green mass, bush diameter, and number of generative shoots (Figure 2).

The Scree plot of the eigenvalues from the PCA, together with the results of the parallel analysis, used to determine the optimal number of components to retain in the model (Figure 3). In this representation, the eigenvalues obtained from the experimental data set are compared

with the values generated by a simulated model based on random data.

Table 2. Chi-square test used to check the adequacy of the PCA model

	Value	Df	p
Model	17.447	9	0.042

Table 3. Loadings of variables in the principal component RC1 resulting from PCA analysis

Component Loadings	RC1	Uniqueness
Green mass g	0.966	0.066
Bush diameter cm	0.935	0.125
Generative shoots	0.894	0.201
Leaf area cm ²	0.819	0.329
Bush height cm	0.531	0.718
Leaves per main shoot		0.992

Parallel analysis is a robust method for validating PCA, as it compares the observed structure of the data with a theoretical model in which the variables exhibit no significant correlations. Thus, the principal components are considered relevant when the eigenvalues obtained from the experimental data exceed those generated by the simulated model.

Therefore, the Scree plot analysis confirms that the first principal component explains the dominant factor explaining the variability in the analyzed characters, being mainly associated with productivity characters and bush size. This

observation also supports the results obtained in the analysis of component loadings, where variables such as green mass, bush diameter, and

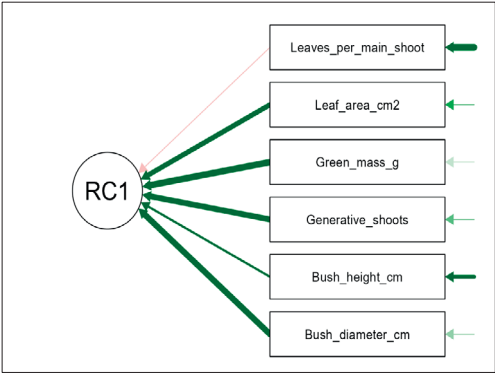


Figure 2. Scree plot of the eigenvalues resulting from principal component analysis (PCA) for the analyzed characters in *Poa pratensis* genotypes

Figure 4 shows the distribution of the 20 *Poa pratensis* genotypes in the plane of the first two principal components (PC1 and PC2), resulting from the PCA analysis. The graphic representation highlights the degree of similarity or differentiation between the genotypes based on the morphological and productivity characters analyzed.

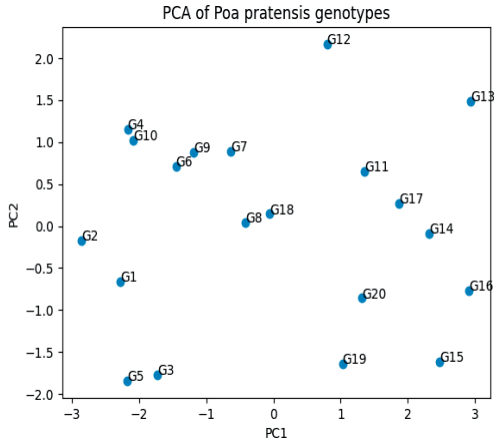


Figure 4. Representation of *Poa pratensis* genotypes in the PC1 and PC2 principal components plot

A clear separation of genotypes is observed along the PC1 axis, which mainly reflects variation in characters associated with productivity, such as green mass, bush diameter, and number of generative shoots. The genotypes

number of generative shoots contribute the most to the formation of the principal component.

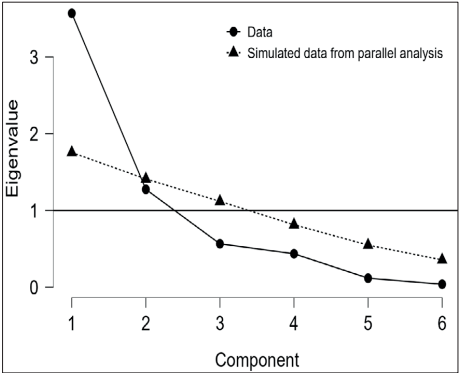


Figure 3. Scree plot of the eigenvalues resulting from principal component analysis (PCA) for the analyzed characters in *Poa pratensis* genotypes

located on the right side of the graph, such as G13, G16, G15, G14 and G17, are characterized by high values of these characters and can be considered genotypes with higher productive potential. In contrast, the genotypes located on the left side of the graph, such as G2, G1, G5 and G3, exhibit lower values for productivity characters, indicating lower productive potential compared to the other genotypes analyzed. The genotypes positioned in the central area of the graph, such as G7, G8, G6, G9 and G18, exhibit intermediate characteristics, suggesting moderate variability in the analyzed characters. It is also noted that certain genotypes, such as G12 and G13, are located at a relatively large distance from the rest of the points on the graph, indicating a high degree of phenotypic differentiation compared to the other genotypes studied. These genotypes may represent valuable sources of genetic variability and are of interest to breeding programs. Overall, the distribution of genotypes on the PCA plot highlights considerable phenotypic variability within the analyzed biological material, offering opportunities to select genotypes with superior performance.

To assess the structure of phenotypic variability and highlight the similarity relationships among the studied genotypes, hierarchical cluster analysis was performed using Euclidean distance and the Ward agglomeration method. The results are presented as a dendrogram,

which illustrates the degree of proximity or differentiation among genotypes based on the morphological and productivity characters analyzed (Figure 5).

The structure of the dendrogram highlights the formation of two main clusters, separated by a relatively high similarity distance, indicating considerable phenotypic diversity within the analyzed biological material.

The first cluster includes genotypes G6, G10, G8, G7, G9, G3, G5, G4, G1 and G2, which are relatively similar and, in general, characterized by moderate values of characters associated with productivity and vegetative development.

The second cluster brings together genotypes G18, G11, G12, G13, G14, G17, G15, G16, G19 and G20, which are clearly differentiated from the first group and are associated with higher values of important morphological characters,

such as bush diameter, number of generative shoots, and green mass. Within this cluster, internal subgroups are also observed, reflecting varying degrees of similarity among genotypes. The clear separation of these two groups confirms the results of the PCA analysis, in which genotypes with higher productive potential were predominantly distributed in the positive area of principal component PC1. Thus, cluster analysis provides a complementary view of phenotypic variability and contributes to identifying genotypes with valuable agronomic characteristics. Overall, the dendrogram results highlight a differentiated genetic structure within the analyzed population, indicating strong potential for these genotypes in *Poa pratensis* breeding programs to obtain varieties with superior productive performance.

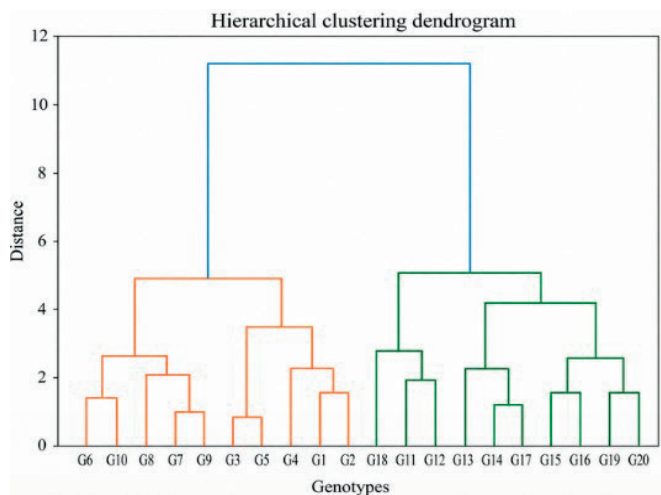


Figure 5. Dendrogram of *Poa pratensis* genotypes obtained by hierarchical cluster analysis based on the morphological and productivity characters analyzed

The statistical analyses performed highlight significant phenotypic variability among the studied *Poa pratensis* genotypes. The Pearson correlation matrix and heat map demonstrated strong correlations among the main productivity characters, especially among green mass, bush diameter, and number of generative shoots, confirming the role of these characters in determining the productive potential of the genotypes.

The principal component analysis highlighted that most of the variability is explained by characters associated with plant vigor and

vegetative development, and the distribution of genotypes on the first principal components plane allowed the identification of genotypes with superior performance.

The results of the cluster analysis, illustrated by a dendrogram, confirm these observations and highlight the formation of two distinct genotype groups, corresponding to different levels of development and productivity. Overall, these multivariate analyses provide valuable information on the structure of phenotypic variability and the relationships between genotypes, contributing to the identification of

genetic material with high potential for *Poa pratensis* breeding programs.

The cluster analysis presented in Figure 5 highlights the formation of two main genotype groups. Group 1 includes genotypes G1-G10 and is characterized by a lower productive potential. Genotypes in this group generally have smaller bushes, fewer generative shoots, and lower biomass production, indicating a moderate level of productive performance. Group 2 includes genotypes G11-G20, which are distinguished by a higher vegetative vigor. These genotypes are characterized by more developed bushes, a larger leaf area, a greater number of generative shoots, and higher green mass production. Within this group, genotypes G13, G14, G15 and G16 stand out for the highest values of productivity traits. Depending on the objectives of breeding programs, this classification of genotypes can be a useful tool for guiding selection, facilitating the identification of genetic material with superior potential for developing new productive varieties. Cluster analysis is frequently used in decision making related to the breeding process, particularly in crop science such as maize, highlighting the practical importance of this method in selecting the most appropriate fertilization response (Agapie & Sala, 2022).

CONCLUSIONS

The results of statistical analyses on smooth meadow-grass genotypes highlight significant phenotypic variability among the studied materials.

Pearson correlation analysis demonstrated very strong correlations among green mass, bush diameter, and the number of generative shoots, indicating that these characters play an essential role in determining the productive potential of the genotypes. In contrast, the character number of leaves per main shoot does not show significant correlations with the other variables analyzed, suggesting a reduced influence on total biomass production.

Principal component analysis showed that the first two principal components explain over 80% of the total variability, confirming that most of the differences between genotypes are determined by a small number of characters,

mainly associated with vegetative vigor and productive capacity.

The results of cluster analysis highlighted the separation of genotypes into two main groups, corresponding to different levels of development and productivity. The first group comprises genotypes characterized by lower values for the analyzed characters, whereas the second group comprises vigorous genotypes with high values for bush diameter, number of generative shoots, and green mass production. Within this superior group, genotypes G13, G14, G15 and G16 stand out for their highest productive potential and are considered valuable genetic materials for breeding programs of the smooth meadow-grass species to obtain new varieties with superior productive performance.

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