

MULTIVARIATE ASSESSMENT OF WHEAT YIELD AND GRAIN QUALITY TRAITS UNDER DIFFERENT CULTIVAR × SOWING DENSITY COMBINATIONS ON CHERNOZEM SOIL

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Abstract. The optimization of sowing density requires simultaneous consideration of grain yield and technological quality, because genotype responses may differ when several correlated traits are evaluated together. The present study used principal component analysis (PCA) to characterize the multivariate response of three winter wheat (*Triticum aestivum* L.) cultivars—Glosa, Anapurna and Biharia—grown on chernozem soil at three sowing densities: 780, 650 and 530 viable grains m^{-2} . The multivariate model included mean grain yield, crude protein content, wet gluten content, Zeleny sedimentation value and thousand-kernel weight (TKW). PC1 had an eigenvalue of 3.8835 and explained 77.67% of total variance, whereas PC2 explained 14.07%; together, the first two components accounted for 91.74% of the information contained in the five original variables. PC1 was strongly and positively associated with protein ($r = 0.9420$), TKW ($r = 0.9376$), wet gluten ($r = 0.9143$) and yield ($r = 0.8546$), while Zeleny sedimentation value showed a negative loading ($r = -0.7422$). The Biharia treatments occupied the positive side of PC1 at all three sowing densities, with the highest PC1 score recorded for Biharia × 650 viable grains m^{-2} (1.4381), followed by Biharia × 780 (1.2361) and Biharia × 530 (0.9862). In contrast, the Anapurna combinations had negative PC1 scores, while Glosa occupied mainly intermediate positions. PC2 was determined especially by Zeleny sedimentation value, which contributed 53.19% to this component. The results demonstrate that PCA efficiently separates cultivar × density combinations according to an integrated yield–quality profile and reveals cultivar-specific responses that are not evident when traits are interpreted separately. The multivariate approach can therefore complement univariate analyses when selecting sowing density for wheat production systems on chernozem soils.

Keywords: winter wheat; principal component analysis; sowing density; grain yield; protein; wet gluten; Zeleny; thousand-kernel weight

INTRODUCTION

Winter wheat (*Triticum aestivum* L.) productivity and end-use quality are jointly determined by genotype, environment and crop management. Among management factors, sowing density modifies crop establishment, tillering, spike number, competition for light, water and nutrients, and consequently both yield formation and grain composition. The response is not universal because modern cultivars differ in tillering capacity, stand plasticity and their ability to compensate for low or high plant populations (Bastos et al., 2020; Stanley et al., 2020).

Plant density can influence quality traits as well as yield. Studies conducted under contrasting environments have shown that increasing plant density may alter grain protein concentration, wet gluten, test weight and thousand-kernel weight, while the magnitude and even direction of these effects depend on genotype, nitrogen supply and climatic conditions (Lachutta and Jankowski, 2024; Feng et al., 2026). Therefore, a density that maximizes yield does not necessarily provide the most favorable technological quality profile.

For Romanian wheat production, cultivar choice remains especially important because locally adapted and introduced cultivars differ substantially in productive potential and quality.

Recent Romanian research confirmed that cropping system and genotype significantly affect yield, protein, wet gluten and sedimentation-related traits, and that Biharia and Anapurna can express distinct responses to technological management (Paunescu et al., 2023). Physicochemical investigations of wheat cultivated in Romania also emphasize strong associations among protein, gluten and other grain-quality variables (Golea et al., 2023).

The three cultivars evaluated here—Glosa, Anapurna and Biharia—have previously shown contrasting productive and quality responses across sowing densities. In an earlier univariate evaluation of this experimental system, Anapurna had the highest mean yield, while density also influenced production and grain quality (Naghiu et al., 2025). The present paper does not repeat that univariate analysis; instead, it evaluates the joint structure of yield and quality variables through principal component analysis.

Principal component analysis is particularly useful when agronomic and quality variables are correlated. It reduces a complex set of traits to a small number of orthogonal components and allows treatments to be positioned according to integrated response patterns. PCA has been successfully applied to wheat datasets involving yield, protein, gluten, thousand-kernel weight and technological quality traits (Mitura et al., 2023; Golea et al., 2023). The objective of this study was therefore to identify the main multivariate gradients governing yield and grain quality and to discriminate the nine cultivar $\times$ sowing density combinations under chernozem soil conditions.

MATERIAL AND METHODS

The experiment comprised three winter wheat cultivars, Glosa, Anapurna and Biharia, each tested at three sowing densities: D1 = 780, D2 = 650 and D3 = 530 viable grains m^{-2} . The nine cultivar $\times$ density combinations were coded in the original statistical dataset as s1d1–s3d3, where s1 = Glosa, s2 = Anapurna and s3 = Biharia. The soil considered in the present analysis was chernozem.

The multivariate dataset contained five variables calculated as treatment means: grain yield (Yield), crude protein content (Protein), wet gluten content (Wet gluten), Zeleny sedimentation value (Zeleny) and thousand-kernel weight (TKW). These traits represent complementary dimensions of crop performance, including productivity, grain protein accumulation, gluten quantity, sedimentation behavior and kernel size.

Principal component analysis was performed on the correlation matrix, thereby standardizing variables measured in different units. Eigenvalues, percentage of explained variance, factor–variable correlations (loadings), variable contributions, eigenvectors and factor scores were examined. The first two components were retained for graphical interpretation because together they explained more than 90% of the total variance. The equations obtained from the correlation-matrix eigenvectors were: $PC1 = 0.4336 \times \text{Yield} + 0.4780 \times \text{Protein} + 0.4640 \times \text{Wet gluten} - 0.3766 \times \text{Zeleny} + 0.4758 \times \text{TKW}$; $PC2 = 0.3983 \times \text{Yield} - 0.2976 \times \text{Protein} - 0.2491 \times \text{Wet gluten} - 0.7293 \times \text{Zeleny} - 0.3985 \times \text{TKW}$. Treatment scores were used to compare cultivar $\times$ density combinations in the PC1–PC2 plane.

The interpretation focused on the magnitude and sign of loadings, contributions of variables to each component and the relative position of treatments. Because the source dataset supplied for this paper contains the PCA output rather than replicate-level raw observations, inferential tests of individual treatment means are not recalculated here; the paper therefore interprets the multivariate structure supported directly by the available PCA results.

Table 1

Component	Eigenvalue	Variance (%)	Cumulative (%)
PC1	3.8835	77.6700	77.6700
PC2	0.7034	14.0672	91.7372
PC3	0.3142	6.2840	98.0212
PC4	0.0955	1.9096	99.9308
PC5	0.0035	0.0691	99.9999

RESULTS AND DISCUSSION

The eigenvalue structure indicates a highly concentrated multivariate pattern. PC1 had an eigenvalue of 3.8835 and accounted for 77.67% of total variance, while PC2 had an eigenvalue of 0.7034 and explained a further 14.07%. Consequently, 91.74% of the total information contained in the five variables was represented in a two-dimensional solution. PC3 increased cumulative explained variance to 98.02%, whereas PC4 and PC5 together added less than 2%. The scree pattern therefore supports the use of the first two axes for agronomic interpretation.

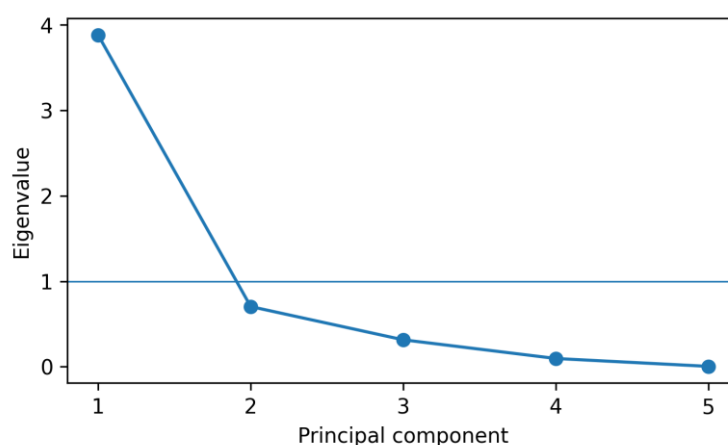


Figure 1. Scree plot of eigenvalues for the five principal components.

PC1 represented an integrated productivity–grain composition axis. Protein had the strongest positive loading (0.9420), followed closely by TKW (0.9376) and wet gluten (0.9143), while yield also showed a strong positive association (0.8546). By contrast, Zeleny sedimentation value loaded negatively (−0.7422). Thus, treatments with high positive PC1 scores were characterized by a joint tendency toward higher values of yield, protein, gluten and kernel weight within this dataset, whereas the Zeleny response moved in the opposite direction. Similar PCA-based approaches in wheat have shown that yield and quality variables can form either convergent or contrasting multivariate gradients depending on genotype and environment (Mitura et al., 2023; Golea et al., 2023; Lachutta and Jankowski, 2024).

The contribution analysis confirmed that PC1 was broadly shared among the principal productive and compositional traits. Protein contributed 22.85% to PC1, TKW 22.64%, wet

gluten 21.53%, yield 18.80% and Zeleny 14.19%. This relatively balanced structure indicates that PC1 should not be interpreted as a single-trait axis. Rather, it summarizes a coordinated yield–quality profile. Such an integrated interpretation is useful in cultivar management because plant density can modify yield components and grain composition simultaneously, and responses may differ among genotypes (Bastos et al., 2020; Stanley et al., 2020).

PC2 was primarily a Zeleny sedimentation axis. Zeleny had a loading of -0.6117 and accounted for 53.19% of the contribution to PC2. Yield loaded positively (0.3340), whereas TKW (-0.3342), protein (-0.2496) and wet gluten (-0.2089) loaded negatively. The contrast between wet gluten/protein and sedimentation behavior is agronomically plausible because gluten quantity and gluten strength are related but not interchangeable quality dimensions. Recent work has similarly shown that changes in sowing strategy can increase protein or wet gluten without necessarily improving sedimentation-related gluten strength (Lachutta and Jankowski, 2024).

Table 2

Variable	Factor–variable correlations and contributions to PC1 and PC2					
	loading	PC1	loading	PC2	contribution	PC1
Yield		0.8546		0.3340		18.80%
Protein		0.9420		-0.2496		22.85%
Wet		0.9143		-0.2089		21.53%
gluten						
Zeleny		-0.7422		-0.6117		14.19%
TKW		0.9376		-0.3342		22.64%
						53.19%
						15.88%

Treatment scores revealed a marked cultivar effect in the multivariate space. All three Biharia combinations had positive PC1 scores: 1.2361 at 780 viable grains m⁻², 1.4381 at 650 viable grains m⁻² and 0.9862 at 530 viable grains m⁻². The highest PC1 score of the entire dataset was therefore obtained by Biharia at 650 viable grains m⁻². This position indicates the strongest combined expression of the variables positively associated with PC1, rather than superiority for every individual trait. Biharia at 780 viable grains m⁻² was also clearly positive on PC1 and moderately positive on PC2.

Anapurna occupied the negative side of PC1 at all densities, with scores of -0.9705 , -1.1181 and -0.9157 for 780, 650 and 530 viable grains m⁻², respectively. The three Anapurna treatments were differentiated mainly along PC2: the 780-grain treatment had a positive PC2 score (0.9578), whereas the 530-grain treatment was negative (-0.8679). This demonstrates that density changed the internal quality balance of the cultivar even though its PC1 position remained consistently negative. Genotype-specific responses to density are well documented and are one reason why a universal seeding-rate recommendation is rarely optimal across cultivars and environments (Bastos et al., 2020).

Glosa occupied a more central region of the multivariate space. Its PC1 scores ranged from -0.6262 at 780 viable grains m⁻² to 0.0491 at 650 viable grains m⁻² and -0.0791 at 530 viable grains m⁻². The 650-grain treatment had the highest PC2 score among Glosa treatments (1.0023). This central position suggests a more balanced multivariate response, without the pronounced positive PC1 displacement observed for Biharia or the negative displacement observed for Anapurna.

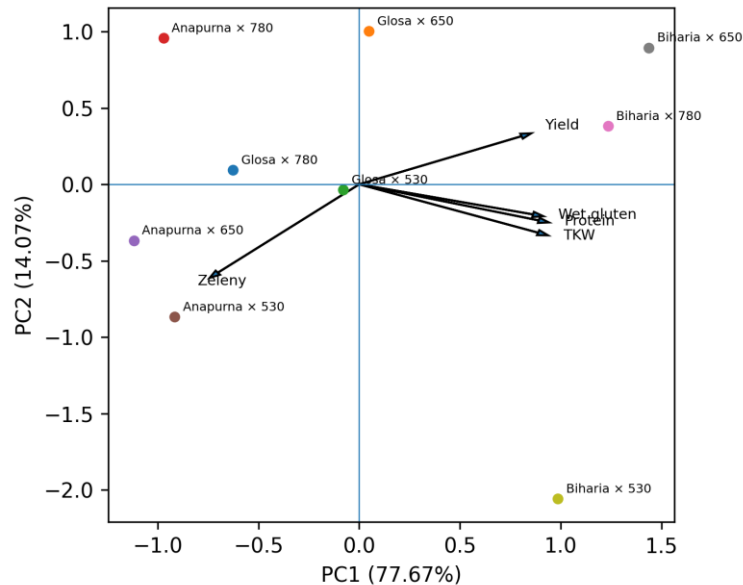


Figure 2. PC1–PC2 biplot of yield and quality variables and the nine cultivar × sowing density combinations.

Table 3

PC1 and PC2 scores of cultivar × sowing density combinations			
Cultivar	Density (viable grains m ⁻²)	PC1	PC2
Glosa	780	-0.6262	0.0930
Glosa	650	0.0491	1.0023
Glosa	530	-0.0791	-0.0358
Anapurna	780	-0.9705	0.9578
Anapurna	650	-1.1181	-0.3681
Anapurna	530	-0.9157	-0.8679
Biharia	780	1.2361	0.3822
Biharia	650	1.4381	0.8942
Biharia	530	0.9862	-2.0576

The strongest differentiation on PC2 was observed for Biharia at 530 viable grains m⁻², which had a score of -2.0576 and contributed 52.92% to PC2. This treatment therefore largely defines the negative extreme of the second axis. Since Zeleny sedimentation value is the dominant contributor to PC2 and also has a negative loading, the position of this treatment reflects a distinct sedimentation-related profile relative to the other combinations. However, because PCA describes covariance structure rather than statistical significance of raw means, this result should be interpreted as multivariate separation and not as an independent proof of a treatment effect on Zeleny value.

The findings support the use of multivariate methods as a complement to classical analysis of variance. In a previous evaluation of the same cultivar and density factors, the highest mean yield was associated with Anapurna and the highest density produced the highest density-level mean yield (Naghiu et al., 2025). The PCA presented here adds a different layer of information: when yield is considered simultaneously with protein, gluten, Zeleny and TKW,

Biharia treatments are displaced toward the positive side of the dominant multivariate axis. This difference illustrates why a treatment selected solely for maximum yield may not coincide with the treatment having the strongest integrated yield–quality profile.

Recent studies reinforce this interpretation. Higher sowing density can increase spike number and alter yield formation, but genotype and environmental productivity modify the optimum population (Bastos et al., 2020; Stanley et al., 2020). In technological-quality studies, density has been associated with changes in protein and gluten traits, and the response is strongly conditioned by nitrogen management and sowing strategy (Lachutta and Jankowski, 2024; Feng et al., 2026). PCA studies of wheat quality likewise show that protein, wet gluten, kernel characteristics and yield may cluster differently depending on cultivar and production environment (Mitura et al., 2023; Golea et al., 2023). Therefore, cultivar-specific density recommendations should consider both productive and quality objectives.

CONCLUSIONS

Principal component analysis efficiently summarized the joint variation of grain yield, protein, wet gluten, Zeleny sedimentation value and thousand-kernel weight in the Glosa, Anapurna and Biharia winter wheat cultivars grown at 780, 650 and 530 viable grains m⁻² on chernozem soil.

The first two principal components explained 91.74% of total variance. PC1 alone explained 77.67% and was strongly positively associated with protein, TKW, wet gluten and yield, while Zeleny sedimentation value was negatively associated with this axis. PC2 explained 14.07% and was governed primarily by the Zeleny variable.

Biharia showed positive PC1 scores at all three densities, with the highest integrated PC1 score at 650 viable grains m⁻². Anapurna remained on the negative side of PC1 at all densities, while Glosa occupied mainly intermediate positions. Density nevertheless changed the PC2 position within each cultivar, demonstrating that plant population can modify the balance among quality traits even when the cultivar effect remains evident.

The multivariate results should be used together with univariate yield and quality analyses rather than as a substitute for them. For practical technological recommendations, the next analytical step should integrate year, soil, cultivar and density effects using the complete replicate-level dataset and validate the PCA patterns by analysis of variance and multiple-comparison procedures.

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