AGRICULTURAL UNIVERSITY – PLOVDIV
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An Efficient Methodology for the Identification of High-Yielding and Stable Winter Wheat Genotypes through the Integration of Traditional and Innovative Statistical Approaches

AUTHOR'S ABSTRACT
of a dissertation

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Content

I. GENERAL CHARACTERISTICS OF THE DISSERTATION

I.1. Relevance of the Research Topic

I.1.1. Importance of Winter Wheat in a Global and Regional Context

Winter wheat (Triticum aestivum L.) is one of the most important agricultural crops worldwide and plays a key role in ensuring global food security. It provides approximately 20% of the total caloric intake and a substantial share of plant-based proteins in the human diet, which defines it as a strategic crop for the sustainable development of the agricultural sector (FAO, 2017). The projected growth of the global population and the increasing demand for food impose a pressing need for the sustainable enhancement of wheat yields under conditions of limited and increasingly variable natural resources.

At the global level, the rate of genetic progress in wheat over recent decades has been assessed as insufficient to offset climate-related risks and to meet future production demands. Analyses based on long-term datasets indicate that in many regions the annual increase in wheat yield remains below 1%, which is considerably lower than that observed for other major cereal crops (Ray et al., 2013; Fischer et al., 2014). This slowdown is attributed both to the biological characteristics of wheat as a predominantly self-pollinating species and to the increasing frequency of extreme climatic events. Rising temperatures, recurrent droughts, and uneven precipitation patterns adversely affect critical developmental stages such as flowering and grain filling, resulting in pronounced interannual yield variability (Asseng et al., 2015; Jagadish et al., 2021).

The importance of winter wheat is particularly pronounced in Europe, where it represents a core component of crop rotations and a leading crop in terms of cultivated area and economic value. At the regional level, including Southeastern Europe and Bulgaria, wheat production is of fundamental importance for farm-level stability and national food security. Bulgaria is characterized by a temperate continental climate, under which winter wheat traditionally occupies a dominant position in crop production systems. At the same time, wheat yields are strongly influenced by climatic variability, including frequent spring–summer droughts, elevated temperatures during reproductive stages, and substantial interannual differences in precipitation regimes (Asseng et al., 2015; Uhr et al., 2023).

Under such conditions, the role of the environment as a dominant factor in yield formation becomes increasingly pronounced, and genotype × environment interaction (GEI) emerges as a key determinant in the ranking and evaluation of wheat varieties. Numerous studies have demonstrated that GEI is the primary reason why genotypes exhibiting high yield potential in specific years or environments may display unstable or inferior performance under different conditions (Annicchiarico, 2002; Crossa et al., 2021). Consequently, yield stability must be considered a criterion of equal importance to mean productivity, particularly in regions characterized by high climatic variability, such as Bulgaria.

In this context, the relevance of the present study is defined by the need for reliable identification of high-yielding and stable winter wheat genotypes under contrasting environmental conditions. The integration of traditional evaluation approaches with modern statistical and multivariate methods for analyzing genotype × environment interaction provides opportunities for a more precise assessment of breeding potential and for the development of robust selection strategies. Thus, winter wheat is established not only as a key crop for food security but also as a model system for the development and application of effective methodologies for evaluating productivity and stability under conditions of increasing climatic variability.

I.1.2. Climatic Constraints and Genetic Progress

Climate change over recent decades has become one of the major limiting factors for the sustainable production of winter wheat at both global and regional scales. The increasing frequency and intensity of extreme climatic events, including prolonged droughts, elevated temperatures, and abrupt temperature fluctuations, exert a substantial impact on physiological processes and final crop productivity.

At the global level, numerous studies indicate that the negative effects of rising temperatures already partially offset the genetic progress achieved in wheat. Analyses based on long-term experimental and production data show that for each 1 °C increase in mean temperature, potential wheat yield may decline by 5–7%, depending on the region and agronomic conditions (Asseng et al., 2015; Zhao et al., 2017). These yield losses raise serious concerns regarding the capacity of existing cultivars to maintain stable and high productivity under changing climatic conditions.

Against this background, genetic progress in winter wheat achieved through conventional breeding is considered relatively slow. In many regions, the annual yield increase attributable to breeding improvements remains below 1%, which is insufficient to compensate for climatic pressure and resource degradation (Ray et al., 2013; Fischer et al., 2014). This limitation can be explained by both the complex genetic architecture of yield as a quantitative trait and the constraints of breeding strategies predominantly focused on mean productivity under optimal conditions.

Under the conditions of Bulgaria, climatic constraints are particularly evident due to pronounced interannual variability in weather patterns. Frequent spring and early summer droughts, combined with high temperatures, result in unstable expression of yield potential even in cultivars with proven high productivity. Consequently, breeding progress measured under controlled or favorable conditions does not translate directly into stable yields under practical farming conditions.

In this context, the need to reconsider the criteria for genetic progress in winter wheat becomes increasingly evident. Modern breeding objectives should extend beyond the pursuit of maximum yield under optimal environments and incorporate indicators of adaptability and stability across a wide range of conditions. Numerous authors emphasize that future genetic progress in wheat will largely depend on the ability of breeding programs to identify genotypes that combine high productivity with resilience to climatic stress (Annicchiarico, 2002; Crossa et al., 2021).

Therefore, climatic constraints not only reduce current yield levels but also limit the effectiveness of classical breeding approaches. This necessitates the integration of advanced analytical methods for genotype evaluation, enabling a more precise separation of true genetic progress from environmentally induced variation. This need defines the scientific and practical significance of studies focused on genotype × environment interaction and on the identification of stable and adaptive winter wheat genotypes.

I.1.3. Role of Genotype × Environment Interaction (GEI) and Yield Stability

Genotype × environment interaction (GEI) represents a fundamental biological and statistical phenomenon that determines how different genotypes respond to variations in environmental conditions. In winter wheat, GEI is of particular importance due to the crop's wide geographic distribution and its high sensitivity to climatic and agroecological factors. The presence of significant GEI implies that the relative ranking of genotypes by yield is not constant across years or environments, thereby complicating the processes of varietal evaluation and recommendation for agricultural practice (Crossa, 1990; Yan & Kang, 2003).

In conventional breeding practice, cultivar evaluation is often based on mean yield values obtained across a limited number of environments. Under conditions of pronounced GEI, this approach may be misleading, as high mean productivity can result from superior performance in a small number of favorable environments that compensates for poor performance under stress conditions. Numerous studies indicate that in wheat, the proportion of total variation explained by GEI is often comparable to or even exceeds that attributable to the genotype main effect, particularly in multi-environment trials (Zobel et al., 1988; Crossa et al., 2017). This underscores the necessity not only to detect GEI, but also to quantify and analyze it in detail.

Yield stability is considered an integrative trait reflecting the ability of a genotype to maintain relatively consistent productivity across a wide range of environments. Different stability concepts are described in the literature, including biological stability, associated with minimal yield variation, and agronomic stability, which seeks an optimal balance between high mean yield and predictable performance under variable conditions (Becker & Léon, 1988; Annicchiarico, 2002). Under conditions of increasing climatic variability, agronomic stability has gained primary importance, as the breeding value of genotypes is determined not only by their performance under optimal conditions, but also by their capacity to limit yield losses under stress.

In regions characterized by pronounced climatic fluctuations, such as Bulgaria, yield stability becomes a key breeding and production criterion. Frequent changes in temperature and precipitation regimes lead to strong interannual environmental variability, under which genotypes with high average yields may pose economic risks due to unstable performance. In this context, GEI analysis enables the identification of genotypes with broad adaptation as well as those with specific adaptation to particular types of environments. This is essential for optimizing varietal structure and enhancing the sustainability of wheat production systems (Yan et al., 2007; Crossa et al., 2021).

The development of modern statistical approaches has substantially expanded the possibilities for studying GEI and yield stability. Methods such as AMMI, REML/BLUP, and various stability indices allow the simultaneous assessment of productivity and adaptability, providing deeper insights into the structure of genotype × environment interaction. These approaches support more objective genotype evaluation and facilitate the formulation of reliable recommendations for agricultural practice.

Consequently, the role of GEI and yield stability is central to contemporary research on winter wheat. The analysis of these factors not only increases the efficiency of breeding programs but also contributes to the development of sustainable production strategies aimed at risk reduction and at maximizing the expression of genetic potential under diverse and changing environmental conditions.

I.1.4. Need for Integrated Methodologies

The increasing complexity of the factors determining productivity and yield stability in winter wheat necessitates the application of analytical approaches that go beyond the capabilities of individual classical evaluation methods. Under conditions characterized by pronounced genotype × environment interaction, high climatic variability, and the multidimensional nature of yield as a trait, the use of isolated statistical criteria often leads to partial or even contradictory interpretations. This highlights the need to explore integrated methodologies that combine different analytical approaches in order to achieve a more comprehensive and objective characterization of genotypes.

Traditional analytical methods, such as analysis of variance and linear regression models, provide fundamental information on the significance and relative contribution of the main sources of variation. They allow quantitative partitioning of genotype, environment, and genotype × environment interaction effects; however, their capacity to interpret the complex structure of GEI and to visualize genotype adaptability is limited (Zobel et al., 1988; Piepho et al., 2008). These limitations become particularly evident in multi-location trials, where the results are often difficult to translate directly into breeding and production practice.

The development of multivariate methods for GEI analysis, such as AMMI and related biplot approaches, has substantially expanded the possibilities for interpreting experimental data. By combining additive effects with interaction principal components, these methods enable the identification of stable genotypes, the differentiation between specific and broad adaptation, and a clearer understanding of genotype performance across environments (Crossa et al., 2017; Gauch, 2013). Nevertheless, AMMI analysis alone does not provide direct predictions of genotype performance and does not fully account for the hierarchical structure of experimental data.

In this context, mixed linear models and approaches based on REML/BLUP have emerged as a key component of contemporary integrated methodologies. They allow the simultaneous modeling of fixed and random effects, provide more reliable estimates of genotypic effects, and enable prediction of genotype performance across environments (Piepho et al., 2008; Smith et al., 2005). When combined with classical and multivariate approaches, these models establish a robust statistical framework for genotype evaluation.

An additional argument supporting the use of integrated methodologies is the multifactorial nature of yield formation, which results from complex interactions among multiple yield components. One-dimensional evaluation of genotypes based on a single trait, even when that trait is as central as grain yield, does not fully reflect their breeding value. In this regard, multi-trait indices and comprehensive evaluation methods allow the simultaneous consideration of productivity, stability, and structural yield components, thereby more closely aligning analytical outcomes with actual breeding objectives (Annicchiarico, 2002; Olivoto et al., 2020).

Consequently, the well-founded need for integrated methodologies arises from the pursuit of higher accuracy, reliability, and applicability of research results. The combination of traditional statistical approaches, multivariate methods, and modern predictive models enables a more complete expression of the genetic potential of winter wheat. This, in turn, creates favorable conditions for the effective selection of genotypes that combine high productivity with stable performance under conditions of increasing climatic variability.

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I.2. Aim, Objectives, and Working Hypotheses of the Study

The aim of the present study is to assess the feasibility of combining traditional and innovative statistical approaches for the comprehensive evaluation of winter wheat cultivars, with simultaneous determination of productivity, yield stability, and adaptability under contrasting growing conditions.

Specific objectives:

1. To analyze the effect of genotype × environment interaction on grain yield and yield stability in winter wheat.

2. To investigate the relationships between the main yield components and final grain yield.

3. To apply multivariate statistical methods for grouping genotypes based on yield and structural traits.

4. To evaluate the stability of productivity using integrated indices that combine yield performance and stability.

5. To apply multi-trait approaches for grouping and classification of the studied genotypes in order to formulate recommendations for breeding practice.

Working hypotheses:

1. Genotype × environment interaction has a significant effect on winter wheat yield, determining the stability and adaptability of individual cultivars.

2. The relationships between the main yield-related traits and grain yield vary in strength and direction depending on the combined effects of environmental factors and their interaction with genotype.

3. Grouping genotypes using multivariate analysis reveals real differences in phenotypic and genetic potential and contributes to a more comprehensive characterization of their performance.

4. Winter wheat cultivars can be reliably evaluated using combined indices and/or models for productivity and stability.

5. The integration of multi-trait indices (MGIDI, MTSI, WAASBY) and their comparison through consensus approaches provides a more precise and reproducible assessment of genotypes.

I.3. Materials and Methods

I.3.1. Genotypes and Experimental Design

The present study is based on 118 winter wheat (Triticum aestivum L.) genotypes. These genotypes were selected to represent a broad genetic base encompassing wide variation in agronomic, physiological, and adaptive traits related to their breeding origin. The experimental set includes both domestic Bulgarian cultivars developed by national breeding institutes and foreign genotypes provided by leading public and private breeding centers in Europe, Asia, and North America. The large number of genotypes posed a substantial challenge for detailed characterization of their productive potential and performance under variable environmental conditions. Their inclusion in breeding programs may represent a key element for further effective enrichment of the national genetic pool and for achieving sustained and substantial increases in productivity potential. Table 1 presents the distribution of the studied genotypes by country of origin and breeding center. The Bulgarian cultivars (32 in total) include well-established standards such as Aglika, Pryaspa, Enola, Sadovo 1, and Pobeda, as well as newer cultivars such as Yoana, Gizda, Slaven, and others. These genotypes were used both as reference standards and for monitoring breeding progress under the conditions of Northeastern Bulgaria. The foreign genotypes originate from leading institutes and companies with a proven contribution to modern wheat breeding. These include PKB, Serbia (PKB Rodika, PKB Vizelka, PKB Kristina); Fundulea, Romania (Litera, Otilia, Glosa); Krasnodar and Myronivka, Russia and Ukraine (Nota, Grom, Yunona, Esaul); Martonvásár and Szeged, Hungary (GK Csillag, Mv Kikelet, GK Vitorlás); Limagrain, France (Azimut, Midas, Apach); as well as universities in the United States (Wahoo, Cougar, Wesley). Many of these cultivars have been bred for tolerance to abiotic and biotic stress factors, allowing for an objective evaluation of their adaptability under the conditions of Northeastern Bulgaria.

Field experiments were conducted at the experimental station of the Dobrudzha Agricultural Institute, General Toshevo, over three consecutive growing seasons (2012–2013, 2013–2014, and 2014–2015). Each year was treated as a separate environment, enabling analysis of interannual climatic variability and its role in the expression of genotype × environment interaction. The selected seasons differed markedly in temperature and precipitation patterns, forming a natural experimental gradient ranging from relatively favorable to distinctly stress-prone conditions.

Table 1. Origin of the studied genotypes.

Region/Country	Region/Country	Region/Country
Bulgaria	Dobrudzha Agricultural Institute – General Toshevo; Institute of Plant Genetic Resources – Sadovo; Institute of Agriculture and Seed Science “Obraztsov Chiflik” – Ruse	32
Serbia	PKB Belgrade; Institute of Field and Vegetable Crops – Novi Sad	10
Romania	Fundulea – National Agricultural Research Institute	9
Russia	Krasnodar Research Institute of Agriculture	13
Ukraine	Myronivka Institute of Wheat; Odessa Agricultural Institute	10
Moldova	Balti Research Institute of Field Crops	8
France	Limagrain, Boreal (private companies)	7
Hungary	Agricultural Institute – Martonvásár; Cereal Research Institute – Szeged	13
Czech Republic	SELGEN	4
Slovakia	Slovak Agricultural Research Institute	1
Austria	Pioneer	2
USA	Colorado State University; Washington State University; University of Nebraska–Lincoln; Kansas State University	9

The experimental design was a randomized complete block design (RCBD) with three replications, widely used in field trials due to its effectiveness in reducing spatial variability and ensuring reliable statistical comparability among genotypes. Each experimental plot covered an area of 7.5 m^2. Sowing was performed within the optimal agronomic window and completed within a single day for all genotypes in each experimental year. The seeding rate was 550 viable seeds m^{-2}, with a row spacing of 10.5 cm.

Fertilization was uniform across all treatments and included pre-sowing application of phosphorus and potassium, as well as split nitrogen fertilization: a basal pre-sowing application and two top-dressings during the growing season at tillering and stem elongation stages according to the Zadoks scale. Weed control against both grass and broadleaf weeds was implemented through herbicide applications at the recommended crop growth stages. All agronomic and plant protection practices were applied simultaneously to all genotypes, without individual adjustments.

The uniform growing conditions, combined with the broad genetic base and the multi-environment nature of the experiment, provide a reliable experimental framework for analyzing productivity, yield stability, and adaptability of the studied genotypes. This enables an objective assessment of their responses to climatic variability and creates a sound basis for formulating scientifically grounded breeding and practical recommendations.

I.3.2. Measured Traits

For all 118 winter wheat genotypes, an agronomic evaluation of the main yield components was conducted in each replication and in each of the three experimental years. This resulted in a comprehensive dataset suitable for the application of statistical analyses consistent with the objectives and working hypotheses of the study. Measurements were performed following the standard methodology for field agronomic experiments (Gomez & Gomez, 1984), and phenological stages were recorded according to the Zadoks scale (Zadoks et al., 1974). The analysis included four key traits directly or indirectly related to grain yield formation.

The number of productive tillers (NPT) represents the number of ear-bearing stems per unit area and serves as an indicator of productive tillering capacity. It was determined by counting ear-bearing stems within a 50 × 50 cm quadrat at physiological maturity, with values subsequently recalculated on a per-square-meter basis. This trait is closely associated with crop stand density and plays a direct role in yield formation.

The number of grains per spike (NGS) was determined as the average number of grains from at least 10 spikes randomly sampled from each plot. This trait reflects spike fertility and is strongly influenced by environmental conditions during flowering. It has a well-documented positive relationship with grain yield, although it is often affected by interactions with other yield components, particularly NPT (Reynolds et al., 2007).

The number of grains per square meter (NGM) represents an integrated indicator expressing the total number of grains formed per unit area. It results from the interaction between the number of productive tillers and the number of grains per spike and is widely recognized as a primary determinant of yield level in wheat (Sadras & Lawson, 2011; Slafer et al., 2014; Fischer, 2008).

Thousand-grain weight (TGW, g) was measured by weighing three subsamples of 1,000 grains from each plot. This trait characterizes grain size and is associated with the grain-filling process up to physiological maturity. Although TGW is considered a relatively stable varietal characteristic, compensatory effects with other yield components are observed in some genotypes, and it is often negatively correlated with NGM due to competition for assimilates and other resources (Fischer & Rebetzke, 2018).

Grain yield (GY, t ha^{-1}) was considered the resultant trait reflecting the complex interaction among all yield components and environmental conditions. Variation in grain yield among genotypes and across years results from the specific seasonal balance among NPT, NGS, NGM, and TGW, which underlines the central role of this trait in breeding and adaptation studies.

I.3.3. Statistical Methods and Models

The study applied an integrated statistical framework combining traditional and modern approaches for the analysis of grain yield, yield components, and genotype × environment interaction (GEI), aiming to provide a reliable multivariate and prediction-oriented evaluation of 118 winter wheat genotypes tested across three climatically contrasting years. At the initial stage, descriptive statistics were calculated for the traits NPT, NGS, NGM, TGW, and GY at the genotype level, enabling assessment of variability, distributional properties, and the presence of outliers. This represents a standard step in the preparation of agronomic datasets for multifactorial analyses (Gomez & Gomez, 1984; Montgomery, 2017). Data were subjected to structured pre-processing, including checks for missing values and anomalies, as well as trait standardization. Outlier detection was based on classical approaches relying on approximate normality assumptions (Grubbs, 1969).

All analyses were conducted in the R statistical environment (R Core Team, 2025) using a combination of specialized packages: metan for stability indices and multi-trait indices (Olivoto & Lúcio, 2020), lme4 for linear mixed models and REML estimation (Bates et al., 2015), lavaan for structural equation modeling (Rosseel, 2012), along with base procedures for clustering and visualization. The application of multivariate evaluation techniques and machine learning algorithms followed general principles of modern statistical and predictive methodology (James et al., 2021).

Genotype × environment interaction was analyzed using the AMMI model, which combines analysis of variance (ANOVA) and principal component analysis (PCA). ANOVA was used to partition the additive effects of genotype and environment, while PCA was applied to structure the multiplicative component of the interaction and to extract interaction principal component axes (IPCA) for interpretation and biplot visualization (Gauch, 2013; Hongyu et al., 2014). In parallel, PCA was also applied to environmental covariates to identify major agrometeorological gradients (Jolliffe & Cadima, 2016).

In addition, linear mixed models (LMMs) estimated by restricted maximum likelihood (REML) were employed, allowing simultaneous modeling of fixed and random effects and providing objective estimates of variance components, including under unbalanced data conditions (Patterson & Thompson, 1971; Piepho & Möhring, 2007; Bates et al., 2015). Within the LMM framework, genotype was treated as a random effect in order to obtain best linear unbiased predictions (BLUPs) and to derive key genetic parameters, including the relative contribution of GEI (Smith et al., 2005; Piepho et al., 2008; Cullis et al., 2006). To elucidate causal relationships among traits and grain yield, a structural equation model (SEM) was applied using the lavaan package. Direct and indirect effects of TGW, NGM, NGS, and NPT on GY were estimated while simultaneously accounting for inter-trait relationships and inter-environmental variation (Jöreskog, 1970; Rosseel, 2012). Model evaluation and comparison were supported by information criteria (AIC and BIC) (Akaike, 1974), in accordance with established principles for selecting among competing models (Burnham & Anderson, 2004).

For additional predictive assessment of trait importance, the Random Forests algorithm was employed. This method captures nonlinear relationships and provides robust predictor ranking even in the presence of multicollinearity. Variable importance was evaluated using metrics such as mean decrease in accuracy (MDA) and mean decrease in impurity (MDI) (Breiman, 2001; Liaw & Wiener, 2002; Grömping, 2009; Nicodemus, 2011).

Genotype stability and adaptability were assessed using a set of established indices, including YSI, Pi, Kang's Stability Index, as well as the modern WAASB and WAASBY indices based on BLUP and AMMI components, which enable a balanced evaluation of productivity and stability (Bouslama & Schapaugh, 1984; Lin & Binns, 1988; Kang, 1993; Olivoto et al., 2019; Olivoto & Nardino, 2021). Similarities and complementarities among indices were examined using Spearman's rank correlation for ordinal variables (Spearman, 1904; Zar, 1972).

Multivariate classification of genotypes was performed using k-means clustering applied to Z-standardized values of key traits. The optimal number of clusters was determined using criteria based on within-cluster variation and the silhouette coefficient (Hartigan & Wong, 1979; Kassambara, 2017). Multi-trait selection was further supported by the MTSI and MGIDI indices, which reduce dimensionality through factor analysis and evaluate the distance of genotypes from an ideotype with optimal trait values (Rocha et al., 2018; Olivoto et al., 2019; Olivoto & Nardino, 2021).

Finally, to integrate results from multiple indices and reduce method dependency, Robust Rank Aggregation (RRA) was applied, providing a consensus ranking of genotypes with stable superiority regardless of the specific index used (Kolde et al., 2012)).

I.4. Soil and Climatic Characterization

Soil Characteristics of the Study Area

The soil–geographical conditions of the area of the Dobrudzha Agricultural Institute, General Toshevo, form a specific environment that combines high natural fertility with certain climatic and agronomic constraints. The experimental area is located in the central part of the Dobrudzha Plateau, developed on deep loess deposits, with flat to gently undulating relief and an elevation of approximately 230–240 m above sea level. These conditions favor the development of chernozem soils, which represent one of the most valuable agronomic resources in Bulgaria.

According to the FAO–UNESCO soil classification system, the chernozems in the region are classified as Luvic Phaeozems, while under the current World Reference Base for Soil Resources (WRB) they are defined as Haplic Chernozems and Vertic Chernozems, reflecting differences in methodological approaches to soil classification (Filcheva et al., 2018). Both classification systems emphasize the presence of a deep humus horizon, high inherent fertility, and the dominant role of loess as the parent material. Bulgarian studies confirm that Dobrudzha is the most representative region for the development of this soil type and that its agronomic advantages constitute a strategic factor for winter wheat production (Nankova & Yankov, 2015; Nankov et al., 2014).

Climatic Characteristics of the Study Area

The climate of the Dobrudzha Agricultural Institute area in General Toshevo is a key factor influencing the development, productivity, and yield stability of winter wheat. The region is situated in northeastern Bulgaria and belongs to the temperate continental climatic subzone, characterized by pronounced seasonal temperature amplitudes, limited water availability, and high solar radiation. The interior of the Dobrudzha Plateau exhibits a predominantly continental climate, while the influence of the Black Sea basin is weak and mainly confined to coastal areas (NIMH, 2020; Copernicus Climate Service, 2023).

The mean annual air temperature in the region is approximately 11 °C, according to the climatic norm of the National Institute of Meteorology and Hydrology (1991–2020) and international climate databases (World Bank Climate Data, 2022). Average minimum temperatures in January are around 0 °C, while mean temperatures in July reach 20.8–21.0 °C. The summer temperature maximum coincides with the grain-filling stage, during which temperatures exceeding the physiological optimum may accelerate plant senescence and reduce grain weight. Winter wheat tolerance to low temperatures depends largely on the degree of autumn hardening and the presence of snow cover; snowless winters increase the risk of frost damage and crop injury (Nankova & Atanasov, 2024).

The precipitation regime represents one of the main limiting factors for crop productivity. The average annual precipitation ranges from 500 to 550 mm, with seasonal distribution being of greater importance than the total amount. Spring precipitation (110–130 mm) generally supports tillering and the onset of stem elongation but is often insufficient for optimal crop development. Summer precipitation (150–170 mm) is characterized by high variability and uneven distribution, and moisture deficits during the April–June period are a primary cause of sharp yield reductions, regardless of fertilization level (Atanasov & Nankova, 2023). September is traditionally the driest month, which negatively affects soil moisture reserves prior to sowing.

Agrometeorological Conditions During the Winter Wheat Growing Seasons

Agrometeorological conditions during the three years of the study had a substantial impact on the development and productivity of the analyzed winter wheat genotypes. The growing seasons 2012–2013, 2013–2014, and 2014–2015 were characterized by pronounced deviations in temperature and precipitation patterns from the long-term climatic norm, forming a natural gradient ranging from favorable to distinctly stress-prone conditions. Percentage deviations of the main meteorological elements relative to the multiannual average are presented in Figure 1.

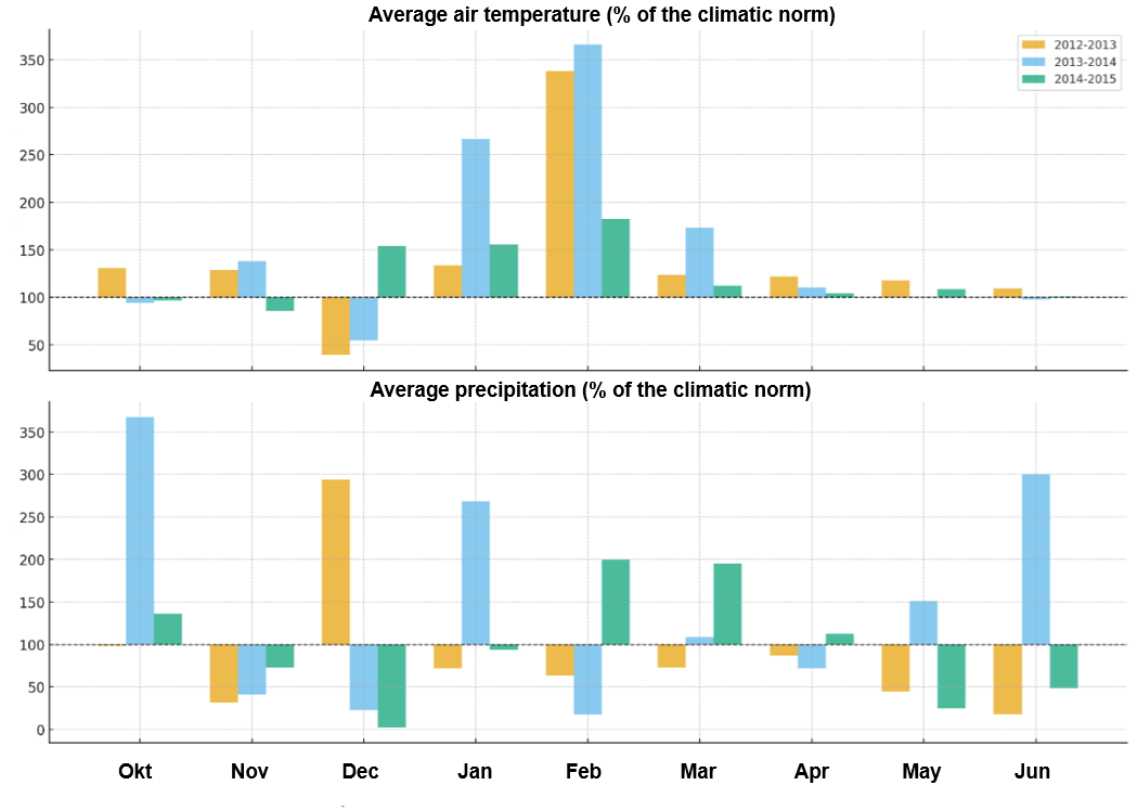


Figure 1. Meteorological elements

Temperature anomalies were most pronounced during the winter months, when values above the climatic norm were recorded in all three years. Elevated winter temperatures exert a dual effect on winter wheat: on the one hand, they reduce the risk of frost injury, while on the other hand they disrupt hardening and vernalization processes that are critical for the normal transition to reproductive stages (Wu et al., 2017). Unusually warm winter and early spring periods accelerate metabolic processes and shorten the duration of biomass accumulation, which may ultimately lead to yield reduction (Xu et al., 2024). Global assessments confirm that an increase of 1 °C in mean temperature results in a significant decrease in wheat yield, particularly in regions experiencing pronounced climatic warming, such as Southeastern Europe (Zhang et al., 2022).

The 2012–2013 growing season was characterized by a relatively favorable climatic profile. Despite elevated temperatures, minimum values remained sufficiently low to ensure normal vernalization. Precipitation in December reached 293.9% of the long-term average, providing adequate soil moisture reserves and stimulating effective tillering. The combination of moderate temperatures and sufficient soil moisture during the heading and grain filling period created favorable conditions for the formation of a high number of grains per unit area and stable grain filling, resulting in the highest average yield of the study period, at 9.07 t ha⁻¹ (Atanasov & Nankova, 2023).

The 2013–2014 growing season emerged as the most unfavorable. At the beginning of the season, precipitation substantially exceeded the long-term average (October – 367%), and during winter this excess coincided with anomalously high temperatures, reaching up to 365% above normal in February. This combination of excessive moisture and thermal stress led to prolonged vegetative growth, increased lodging risk, and heightened susceptibility to diseases. Similar effects have been reported in international studies, indicating that high humidity combined with above-normal temperatures limits photosynthetic activity and reduces the number of fertile florets (Asseng et al., 2015). Excessive rainfall during the grain-filling period further restricted assimilate accumulation and resulted in a pronounced reduction in grain weight (Semenov & Stratonovitch, 2013). Consequently, grain yield in this season was the lowest, averaging 5.50 t ha⁻¹.

The climatic profile of the 2014–2015 season represented an intermediate stress scenario. At the onset of the growing season, precipitation was markedly below normal (73% in November and only 2.5% in December), leading to significantly reduced tillering and a limited potential for forming a high number of productive tillers (Nankova & Atanasov, 2024). Higher precipitation in February and March (199% and 195%, respectively) partially compensated for the early moisture deficit; however, in combination with elevated temperatures, it accelerated crop development and shortened the period for reproductive structure formation. As a result, intermediate yield levels were recorded, with an average grain yield of 7.20 t ha⁻¹.

The analysis of the three growing seasons clearly demonstrates that deviations in temperature and precipitation patterns determine both the rate of phenological development and the formation of yield components. Elevated winter temperatures influence the degree of hardening, while the moisture regime during early growth stages is critical for productive tiller formation. Conditions during grain filling are decisive for grain weight, one of the most climate-sensitive yield components under stress conditions (Asseng et al., 2015; Zhang et al., 2022).

II. RESULTS AND DISCUSSION

II.1. Descriptive Statistics

The first stage of the analysis comprised descriptive statistics and boxplot diagrams (Figure 2), which illustrate the variability of the agronomic traits (NPT, NGS, NGM, TGW, and GY) across the three investigated growing seasons (2013–2015). This approach is widely applied for the preliminary assessment of genotype × environment interaction, as it combines visual inspection with quantitative interpretation (Hongyu et al., 2014; Olivoto et al., 2019).

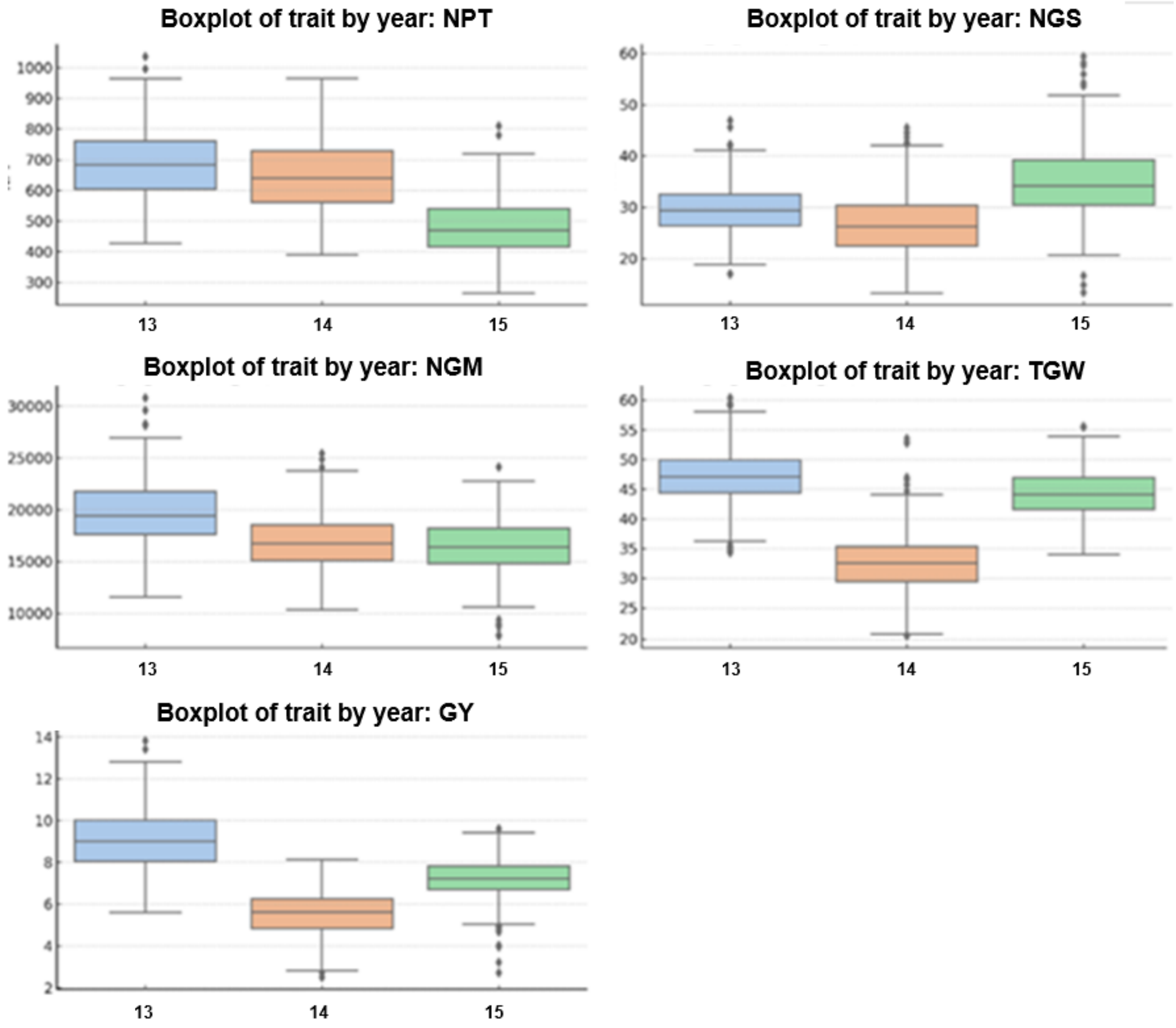


Figure 2. Boxplot diagrams illustrating the variation of agronomic traits (NPT, NGS, NGM, TGW, and GY) by year (2013–2015)

In 2013, the highest values of grain yield (GY), thousand-grain weight (TGW), and number of grains per square meter (NGM) were observed, accompanied by relatively low variability. This pattern indicates favorable growing conditions and a full expression of the genetic potential of the studied genotypes (Stoyanov & Baychev, 2021).

In 2014, the median values of GY and TGW decreased markedly, while the range of variation expanded. This reflects unfavorable climatic conditions and increased differences in genotype adaptability (Sadras & Lawson, 2011; Dragov et al., 2024).

In 2015, partial recovery was recorded, with mean values of grain yield and grain weight approaching the overall experimental average, albeit with a wider range of variation. This was particularly evident for NPT and NGS, indicating a stronger environmental influence on the responses of individual genotypes (Peltonen-Sainio et al., 2007).

Table 2. Descriptive statistics of agronomic traits by year and coefficient of variation (CV)

Season	NPT (no.)	NGS (no.)	NGM (grains m^{-2})	TGW (g 1000 grains^{-1})	GY (t ha^{-1})
2012 –2013	691.22 (16.0%)	29.54 (16.4%)	19 731 (15.7%)	47.11 (9.6%)	**9.07 (16.1%)**
2013 –2014	648.83 (18.0%)	26.74 (22.0%)	16 883 (15.8%)	32.69 (15.5%)	**5.50 (18.8%)**
2014 –2015	476.88 (18.6%)	35.22 (20.0%)	16 398 (15.7%)	44.23 (9.0%)	**7.21 (13.7%)**
Mean (3 years)	605.64 (17.5%)	30.50 (19.5%)	17 671 (15.7%)	41.34 (11.3%)	**7.26 (16.2%)**

Table 2 presents the mean values and relative variability (CV) of the main agronomic traits across the three investigated growing seasons. The data clearly demonstrate pronounced seasonal dynamics and differing degrees of stability among traits.

During the 2012–2013 season, the highest values of GY (9.07 t ha^{-1}), NGM (19,731 grains m^{-2}), and TGW (47.11 g) were recorded, accompanied by low variability (CV below 10% for TGW). This indicates favorable climatic conditions and a full expression of genetic potential.

In 2013–2014, grain yield declined to 5.50 t ha^{-1} and TGW to 32.69 g, accompanied by increased variability (CV up to 22% for NGS and 18.8% for GY). This reflects the stronger influence of unfavorable environmental factors and increased differences in genotype adaptability.

In 2014–2015, partial recovery of GY (7.21 t ha^{-1}) and TGW (44.23 g) was observed, while NPT and NGS exhibited the highest sensitivity (CV above 18%). This pattern indicates a pronounced interaction with environmental conditions.

Overall, NGM and TGW emerged as the most stable traits, whereas NPT and NGS showed greater variability, reflecting genotype responses to climatic fluctuations. This pattern confirms the compensatory relationship between grain number and grain weight, as widely reported in the literature (Sadras & Lawson, 2011).

II.2. Assessment of the Effects of Environment, Genotype, and Their Interaction on Grain Yield and Its Components

Understanding the relative contribution of genotype (G), environment (E), and their interaction (GEI) is essential for the selection of stable wheat cultivars. Under conditions of climatic variability, GEI often exceeds the pure genetic effect, thereby determining interannual differences in productivity (Yan & Kang, 2002; Crossa et al., 2021).

Table 3 summarizes the results of the AMMI analysis and shows that the environment (ENV) plays a dominant role in the expression of thousand-grain weight (TGW; 66.3%) and grain yield (GY; 68.6%), whereas the genetic contribution is stronger for the number of grains per spike (NGS; 27.7%) and the number of grains per square meter (NGM; 25.4%). This confirms that growing conditions are the main source of variation for grain yield, while grain number-related traits exhibit higher heritability.

Table 3. AMMI analysis of grain yield and its main components (TSS%)

Trait	ENV	GEN	GEI
NPT	43.4	18.8	12.8
NGS	25.8	27.7	16.4
TGW	**66.3**	6.7	16.7
NGM	21.8	**25.4**	**29.4**
GY	**68.6**	13.2	18.2

Climatic factors play a decisive role in the formation of grain yield and its components. TGW and GY are most strongly affected by temperature and precipitation during the late stages of the growing season (Calderini & Reynolds, 2000), whereas NGS and NGM display greater genetic robustness and a more linear response to environmental variation (Araus et al., 2008).

The case of NGM is particularly informative, as it combines a substantial genetic contribution with a pronounced GEI component, indicating that this trait integrates both genotypic potential and adaptive response. Consistently, Fischer (2011) identified NGM as a primary determinant of wheat yield and a reliable predictive indicator under conditions of strong genotype × environment interaction.

II.3. Analysis of Interrelationships among Traits and Their Effects on Productivity

Analyses based on structural equation modeling (SEM), linear mixed models (LMM), and Random Forests (RF) were conducted to identify the direct and indirect effects on grain yield (GY), the sensitivity of genotypes to environmental conditions, and the relative importance of the studied traits.

The RF results (Table 4) indicate that the number of grains per square meter (NGM) and thousand-grain weight (TGW) are the leading explanatory factors for yield variation. Their high values of mean decrease in impurity (MDI) and mean decrease in accuracy (MDA) confirm their importance both for internal model structure and for predictive performance. In contrast, the number of productive tillers (NPT) and the number of grains per spike (NGS) show negligible contributions (low MDI/MDA values), suggesting that their effects on yield are predominantly indirect, mediated through NGM, and compensated in interaction with TGW. From a practical perspective, this implies that managing NGM and maintaining adequate TGW represent the most effective levers for increasing and stabilizing grain yield (Breiman, 2001).

Table 4. Trait importance ranking with respect to grain yield (Random Forests)

Trait	MDI (Gini)	MDA (perm ΔRMSE)
NGM	0.4626	0.9105
TGW	0.5322	0.9029
NGS	0.0028	0.0009
NPT	0.0024	0.0002

NGM – number of grains per square meter; TGW – thousand-grain weight; NGS – number of grains per spike; NPT – number of productive tillers; MDI – Mean Decrease in Impurity (Gini, 1912); MDA – Mean Decrease in Accuracy, estimated using permutation-based approaches; ΔRMSE – change in root mean square error. Random Forests is an ensemble machine-learning algorithm based on multiple decision trees (Breiman, 2001).

The results of the linear mixed model (LMM), presented in Table 5, corroborate the RF findings and demonstrate that NGM exerts the strongest positive effect on grain yield. The estimated coefficient ($\beta = 0.0004$, $p < 0.0001$) indicates that an increase of 1,000 grains m^{-2} results in an approximate yield increase of 0.4 t ha^{-1}. Given the observed range of NGM values (8,000–30,000 grains m^{-2}), this effect explains a substantial proportion of yield variation (Slafer et al., 2014).

TGW also exhibits a significant positive effect ($\beta = 0.16$, $p < 0.0001$); however, due to its narrower range of variation (20–60 g), its contribution is more limited and largely compensatory. In contrast, NPT ($\beta = -0.0005$) and NGS ($\beta = -0.0135$) display negative relationships with grain yield, likely reflecting internal compensation mechanisms whereby excessive tillering or an overly high grain number per spike reduces assimilate availability, leading to lower grain weight and final yield (Sadras & Lawson, 2011).

Table 5. Estimated effects of yield-related traits on grain yield (LMM)

Trait	Coefficient (β)	Std. Error	t-value	p-value
NPT	-0.0005	0.0002	-2.32	0.0202
NGS	-0.0135	0.0039	-3.48	0.0005
NGM	0.0004	0.0000	60.14	0.0000
TGW	0.16	0.0017	91.98	0.0000

LMM – Linear Mixed Model; the environment (ENV) was modeled as a random effect; NPT – number of productive tillers; NGS – number of grains per spike; NGM – number of grains per square meter; TGW – thousand-grain weight; β – fixed regression coefficient; t – t-statistic; p – level of statistical significance.

A comparison of RF and LMM results reveals a high degree of consistency in identifying the primary yield-determining traits, alongside methodological differences in interpretation. Both models independently identify NGM and TGW as the main drivers of grain yield formation, confirming their central role (Slafer et al., 2014; Jeong et al., 2016). In RF, this is reflected in high MDI and MDA values (Breiman, 2001), whereas in LMM it is demonstrated through statistically significant regression coefficients (Piepho et al., 2008).

The most pronounced discrepancies between the two approaches concern NGS and NPT. RF classifies these traits as unimportant for prediction, whereas LMM reveals significant negative effects, particularly for NGS. This divergence stems from the different nature of the models: RF captures nonlinear relationships and interactions but does not provide parametric estimates (Cutler et al., 2007), whereas LMM yields linear quantitative estimates while explicitly accounting for environmental effects (Smith et al., 2005).

Overall, RF is more suitable for ranking traits by importance and evaluating predictive accuracy, whereas LMM provides statistically interpretable parameter estimates. Their combined application integrates the strengths of both approaches, ensuring robust prediction alongside biologically meaningful interpretation as an essential requirement for effective winter wheat breeding (Olivoto & Nardino, 2021).

Following the identification of traits with direct effects on yield, a structural equation model (SEM) was applied to investigate indirect effects among yield components. The model included NGM and TGW as direct determinants and NPT and NGS as indirect contributors, with GY specified as the dependent variable.

The SEM results (Table 6) indicate that NGM ($\beta = 0.726$) and TGW ($\beta = 0.719$) exert the strongest direct effects on grain yield, whereas NGS ($\beta = 0.331$) and NPT ($\beta = 0.212$) show moderate but statistically significant influences ($p < 0.001$). Internal relationships among traits were also identified: NPT negatively affects NGS ($\beta = -0.684$) but positively influences NGM ($\beta = 0.450$), confirming the compensatory dynamics among yield components.

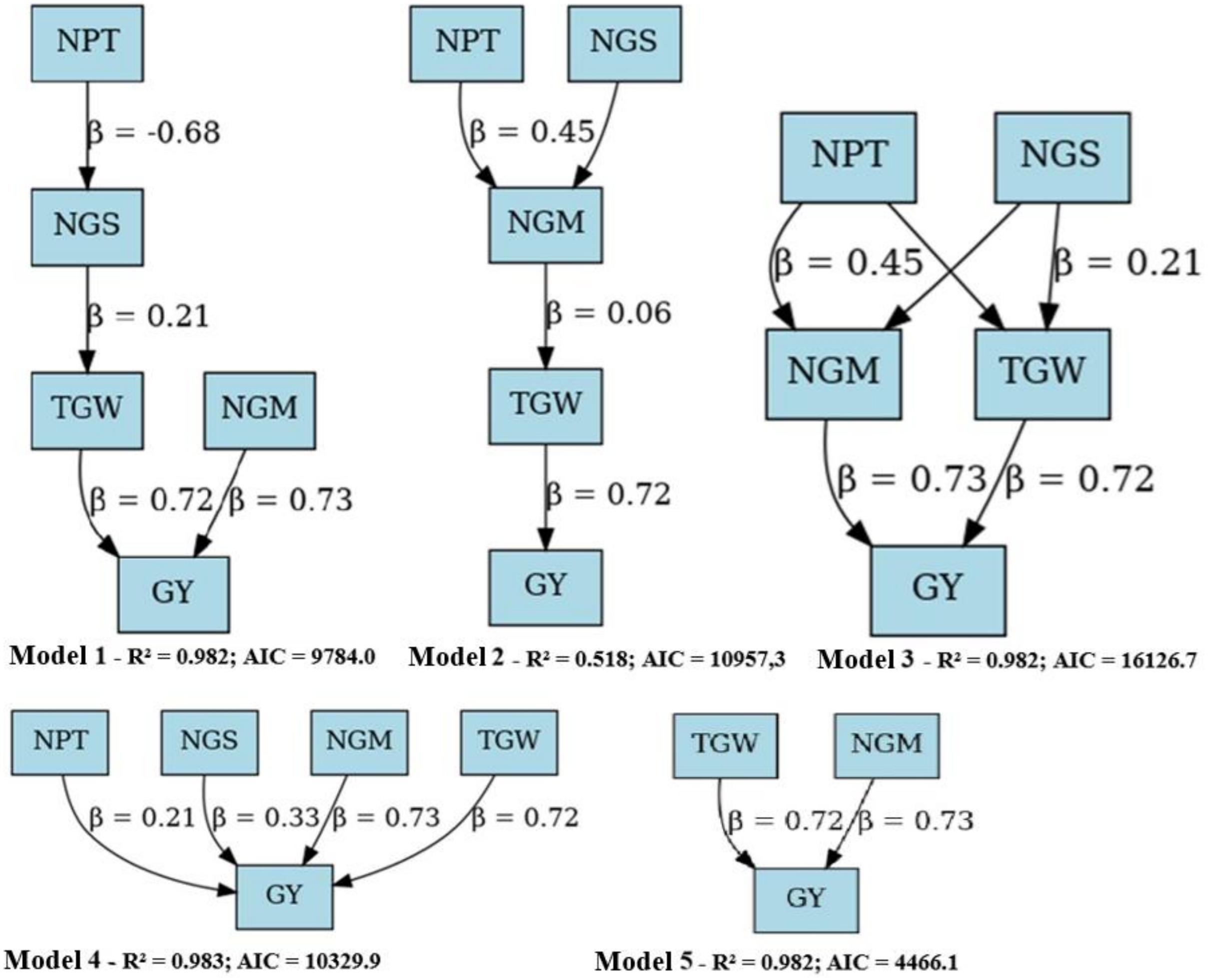
Table 6. Standardized SEM coefficients among yield components and grain yield

Path	Standardized coefficient (β)	p-value
NGM between NPT	0.450	0.0000
NGM between NGS	0.293	0.0000
NGM between TGW	0.063	0.0390
NGM between GY	0.726	0.0000
TGW between NPT	-0.155	0.0000
TGW between NGS	0.213	0.0000
TGW between GY	0.719	0.0000
NPT between GY	0.212	0.0000
NPT between NGS	-0.684	0.0000
NGS between GY	0.331	0.0000

SEM – Structural Equation Modeling; NGM – number of grains per square meter; TGW – thousand-grain weight; NPT – number of productive tillers; NGS – number of grains per spike; GY – grain yield; β – standardized coefficient; p – level of statistical significance.

SEM confirms the conclusions derived from LMM and RF, demonstrating that NGM and TGW occupy central positions in the yield structure, whereas NPT and NGS exert secondary and compensatory effects.

Among the five tested SEM configurations shown in Figure 3, Model 5, which includes only NGM and TGW, proved to be the most parsimonious. It explains 98.2 percent of the yield variation and is associated with the lowest AIC value, which makes it statistically optimal but biologically minimalistic according to Grace (2006). In contrast, Model 4, which incorporates all traits as direct determinants of grain yield, achieves a slightly higher explanatory power with R^2 equal to 0.983, but this improvement is obtained at the expense of increased model complexity and a higher risk of overfitting. Model 2 shows the weakest overall performance and does not provide meaningful practical value for breeding applications.



Model 1 - $R^2 = 0.982$; AIC = 9784.0 **Model 2** - $R^2 = 0.518$; AIC = 10957,3 **Model 3** - $R^2 = 0.982$; AIC = 16126.7

Model 4 - $R^2 = 0.983$; AIC = 10329.9 **Model 5** - $R^2 = 0.982$; AIC = 4466.1

Figure 3. Structural equation models (SEM) explaining grain yield (GY)

The primary focus is on Model 1 and Model 3, which exhibit comparable explanatory power ($R^2 = 0.982$) but differ in structural complexity. Model 3 incorporates parallel and indirect pathways among all traits, reflecting greater biological realism, albeit with a higher AIC (16,126). Model 1, by contrast, is more parsimonious and interpretable (AIC = 9,784), while retaining nearly identical predictive performance.

Thus, the two models should be regarded as complementary. Model 1 is preferable when clarity and parsimony are required, whereas Model 3 is more suitable for capturing complex biological relationships (Grace et al., 2010; Shipley, 2016). Likelihood Ratio Tests (LRT; Table 7) indicate that both Model 1 and Model 3 significantly outperform the simpler Model 5 ($p < 0.001$), while no significant difference exists between Models 1 and 3, confirming their equivalent structural adequacy.

Table 7. Comparison of SEM models using Likelihood Ratio Tests (LRT)

Comparison	LR χ^2	df	p-value
Model 1 vs. Model 5	16.57	2.0	0.0003
Model 3 vs. Model 5	16.57	2.0	0.0003
Model 1 vs. Model 3	0.0	0.0	-

SEM – Structural Equation Modeling; LRT – Likelihood Ratio Test; LR χ^2 – chi-square value from the Likelihood Ratio Test; df – degrees of freedom; p – level of statistical significance.

In summary, Model 1 is optimal from the perspective of parameter parsimony, whereas Model 3 provides a more biologically comprehensive representation. Both models confirm that NGM is the leading factor determining grain yield, TGW has a secondary but stable contribution, and NPT and NGS operate through indirect compensatory mechanisms.

On this basis, several trends can be outlined. Model 5 is the most parsimonious model; by including only NGM and TGW, it explains more than 98% of the variation in grain yield ($R^2 = 0.982$) and has the lowest AIC value, but it is limited in terms of biological interpretation. Model 4, which includes all variables, is more accurate ($R^2 = 0.983$), but also more prone to overfitting due to its higher AIC values, whereas Model 2 is excluded as the weakest model.

The main emphasis therefore remains on Model 1 and Model 3. The former is more parsimonious and statistically efficient, while the latter is more detailed and reflects the actual biological structure and balance among traits (Olivoto et al., 2019; Pour-Aboughadareh et al., 2025). Consequently, Model 1 is preferred when clarity and minimalism are required, whereas Model 3 is more suitable for the analysis of complex relationships (Grace et al., 2010; Shipley, 2016).

II.4. Cluster Analysis

After the main factors determining grain yield had been identified, the multivariate k-means approach was applied to standardized values of GY, NGM, and TGW. The objective was to delineate groups of genotypes with similar responses to environmental conditions. The optimal number of clusters was determined using the Elbow and Silhouette methods (Kaufman & Rousseeuw, 2009; Rousseeuw, 1987). As shown in Figure 4, both approaches indicated that $k = 3$ achieves a balance between internal homogeneity and cluster separability (Silhouette = 0.393). Higher values of k result in only marginal improvements in accuracy but substantially complicate the interpretation of the results (Everitt et al., 2011).

On this basis, $k = 3$ was accepted as optimal for the subsequent classification of genotypes. This ensures clear separation and good interpretability in the context of grain yield and yield components. Figure 5 presents the distribution of the 118 genotypes in the two-dimensional space defined by mean grain yield (GY) and thousand-grain weight (TGW), clearly visualizing the three clusters obtained through k-means classification. The spatial distribution of the points indicates that the grouping is not random, but rather reflects different strategies of productivity formation.

Cluster 1 is located in the upper part of the graph and is characterized by high TGW values at medium to high yield levels, indicating that productivity in these genotypes is achieved primarily through larger grain size. This profile is typical of breeding materials oriented toward grain size stability and quality potential.

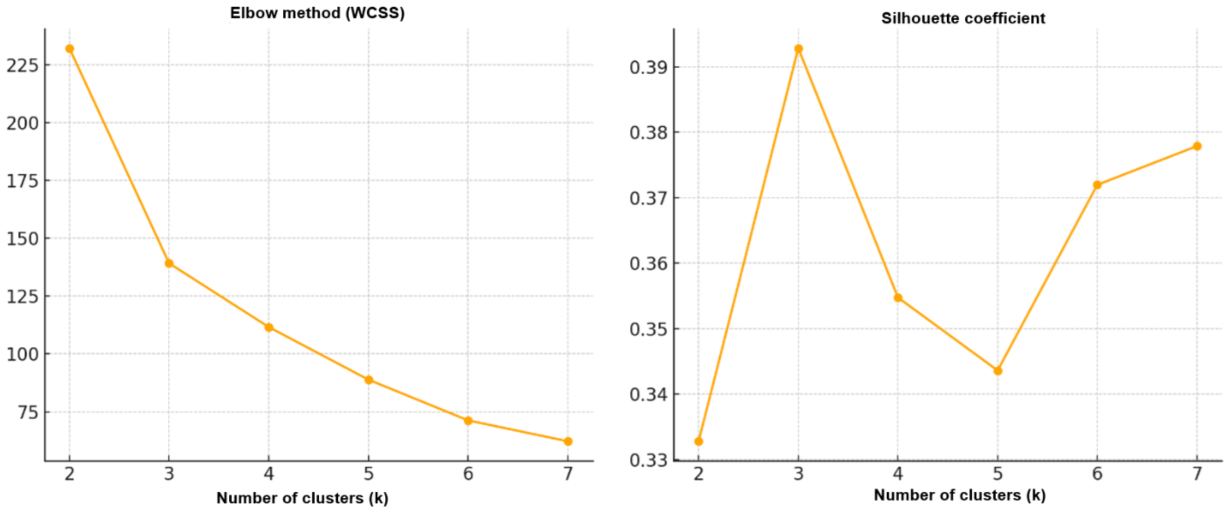


Figure 4. Determination of the optimal number of clusters using the Elbow and Silhouette methods (k = 2–7)

Cluster 2 occupies the lower-left part of the space and is distinguished by lower values of both grain yield and TGW, accompanied by greater variability. This suggests weaker productive realization and higher sensitivity to environmental conditions.

Cluster 3 is concentrated in the right part of the graph and is characterized by high grain yield values combined with moderate grain weight. This indicates that productivity in these genotypes is formed predominantly through other components, most likely related to the number of grains per unit area.

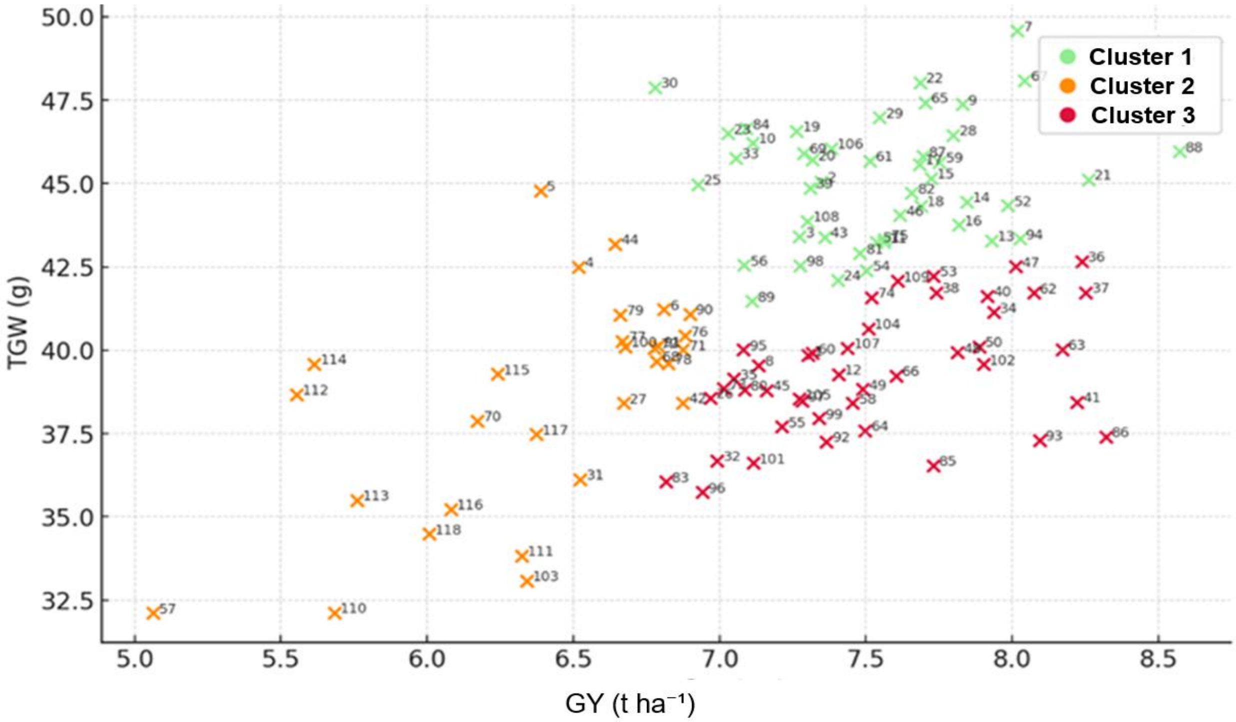


Figure 5. Biplot of clusters in the GY–TGW space

Overall, the figure clearly demonstrates that similar yield levels can be achieved through different combinations of GY and TGW, which confirms the compensatory nature of yield components and justifies the application of cluster-based and multivariate approaches in breeding evaluation.

The data presented in Table 8 show clearly expressed and statistically significant differences among the three clusters with respect to the main yield components. This confirms that the applied k-means classification successfully separated the genotypes into homogeneous groups with specific breeding profiles.

Таблица 8. Средни стойности и стандартни отклонения за трите клъстера.

Cluster	Number of genotypes	Mean yield (t ha⁻¹)	GY, Std	TGW, Mean	TGW, Std	NGM, Mean	NGM, Std
K1	46	7.54^{a}	0.36	$45.04d^{d}$	1.82	16816^{f}	939
K2	29	6.40^{b}	0.48	38.49^{c}	3.25	16642^{f}	1153
K3	43	7.54^{a}	0.42	39.32^{c}	1.85	19279^{e}	1020

GY – grain yield; Std – standard deviation; TGW – thousand-grain weight; NGM – number of grains per square meter. Different superscript letters (a, b, c, d, e, f) indicate significant differences among cluster means according to Tukey's HSD post-hoc test at $p < 0.05$.

Cluster K1, which includes the largest number of genotypes (46), is characterized by a relatively high mean grain yield (7.54 t ha^{-1}), comparable to that of K3, but with the distinctly highest thousand-grain weight (TGW = 45.04 g). The statistically significant differences in TGW compared to the other clusters indicate that productivity in these genotypes is formed primarily through larger grain size, combined with a relatively lower number of grains per unit area (NGM = 16,816 grains m^{-2}). This profile is typical of genotypes with a strong compensatory mechanism, whereby lower fertility is compensated by increased grain weight. Cluster K2 comprises 29 genotypes and is characterized by the lowest mean grain yield (6.40 t ha^{-1}), as well as the lowest TGW values (38.49 g). Although NGM in this cluster does not differ statistically from K1, the lower grain weight results in significantly reduced productivity. The higher standard deviations observed for TGW and GY indicate greater internal variability, suggesting stronger sensitivity of these genotypes to environmental conditions. From a breeding perspective, this cluster represents a group with limited yield potential but possible applicability for specific objectives related to quality or adaptation. Cluster K3 includes 43 genotypes and is characterized by a mean grain yield identical to that of K1 (7.54 t ha^{-1}), but achieved through a fundamentally different mechanism. In this cluster, the highest number of grains per square meter is observed (NGM = 19,279 grains m^{-2}), statistically significantly higher than in K1 and K2, combined with moderate TGW values (39.32 g). This clearly indicates that productivity in this cluster is primarily based on the formation of a large number of grains rather than on grain weight. This profile is typical of genotypes with high productive tillering and spike fertility, which, however, may be more sensitive to water and nutrient stress during critical developmental stages.

II.5. Assessment of Genotypic Stability and Productivity

Stability and productivity are fundamental criteria in the evaluation of genotypes in multi-year trials, as pronounced genotype × environment interaction (GEI) effects may obscure the true yield superiority of genotypes and alter their ranking across years and environments (Annicchiarico, 2002; Pour-Aboughadareh et al., 2025). Contemporary methodological approaches therefore recommend the combined assessment of mean yield and stability using indices based on BLUP or AMMI decomposition (Olivoto et al., 2019), in order to avoid the selection of high-yielding but unstable genotypes.

Mean grain yield serves as a baseline indicator for productivity assessment and as a reference for comparison with stability indices. Higher mean values reflect superior adaptability and consistency of performance across contrasting environments.

As shown in Table 9, the cultivar Midas exhibited the highest mean grain yield (8.57 t·ha⁻¹) over the period 2013–2015, followed by Azimut (8.32 t·ha⁻¹) and Nakhodka (8.26 t·ha⁻¹). The top ten genotypes demonstrated substantially higher yields than the overall mean, identifying them as potential donors of stable productivity. These results provide a reference framework for subsequent stability-index analyses and for the calculation of Spearman rank correlations among indices.

Table 9. Top 10 genotypes based on mean grain yield (2013–2015)

No.	Genotype	Yield 2013 (t·ha⁻¹)	Yield 2014 (t·ha⁻¹)	Yield 2015 (t·ha⁻¹)	Average yield (t·ha⁻¹)	Rank
88	Midas	11.00	6.54	8.18	8.57	1
86	Azimut	10.53	6.69	7.74	8.32	2
21	Nakhodka	11.38	5.14	8.26	8.26	3
37	PKB Rodika	11.53	6.35	6.87	8.25	4
36	PKB Vizelka	11.80	6.25	6.66	8.24	5
41	Kantata	10.47	6.38	7.81	8.22	6
63	Grom	9.93	6.86	7.72	8.17	7
93	Csillag	10.80	6.06	7.42	8.09	8
62	Nota	9.67	6.64	7.91	8.07	9
67	Lut. 601-09	9.38	6.27	8.48	8.04	10

BLUP analysis

Table 10 presents the leading genotypes according to BLUP predictions. Midas (8.291 t·ha⁻¹), Azimut (8.092 t·ha⁻¹), Nakhodka (8.046 t·ha⁻¹), PKB Rodika (8.039 t·ha⁻¹), and PKB Vizelka (8.028 t·ha⁻¹) occupy the top positions. All of these genotypes show positive BLUP effects relative to the overall mean, confirming a stable genetic contribution to yield (e.g., Midas +1.035 t·ha⁻¹, Azimut +0.836 t·ha⁻¹).

The BLUP amplitude distinguishes two major performance profiles. The first profile includes genotypes with high mean yield and moderate amplitude such as Nota, Grom, Lut. 601 09, and Azimut. These genotypes are characterized by predictable performance and good adaptability across environments. The second profile includes Nakhodka, PKB Vizelka, and PKB Rodika, which exhibit higher sensitivity to environmental conditions. This increased sensitivity is likely to reduce their ranking in stability indices such as WAASB and WAASBY.

Table 10. BLUP evaluation of the top 10 genotypes

No.	Genotype	BLUP effect (t·ha⁻¹)	BLUP mean prediction (t·ha⁻¹)	BLUP 2013 (t·ha⁻¹)	BLUP 2014 (t·ha⁻¹)	BLUP 2015 (t·ha⁻¹)	BLUP amplitude (t·ha⁻¹)
88	Midas	1.035	8.291	10.585	6.317	7.97	4.268
86	Azimut	0.836	8.092	10.219	6.433	7.625	3.786
21	Nakhodka	0.790	8.046	10.88	5.223	8.034	5.657
37	PKB Rodika	0.783	8.039	11.002	6.168	6.946	4.834
36	PKB Vizelka	0.772	8.028	11.211	6.092	6.782	5.119
41	Kantata	0.759	8.015	10.17	6.193	7.682	3.977
63	Grom	0.719	7.975	9.748	6.565	7.613	3.183
93	Csillag	0.659	7.915	10.427	5.942	7.377	4.485
62	Nota	0.642	7.898	9.539	6.394	7.762	3.145
67	Lut 601-09	0.618	7.875	9.311	6.103	8.209	3.208

In summary, BLUP predictions provide a corrected and unbiased basis for assessing the genetic yield potential of genotypes and, when combined with stability indices, constitute a robust tool for balanced selection decisions.

WAASB Index

The WAASB (Weighted Average of Absolute Scores from the BLUP matrix) index, proposed by Olivoto et al. (2019), represents an advanced approach for evaluating genotypic stability by integrating genotype × environment interaction (GEI) information with BLUP estimates within a REML/BLUP framework. Unlike classical AMMI models, this approach simultaneously accounts for fixed and random effects, providing a more objective and statistically robust assessment of stability, particularly in multi-year and potentially unbalanced datasets.

Lower WAASB values indicate greater genotypic stability, reflecting smaller absolute IPCA scores and reduced sensitivity to environmental variation. The results of the WAASB analysis are presented in Table 11, where the ten most stable genotypes are ranked according to their stability and mean productivity.

Table 11. Top 10 most stable genotypes according to WAASB

No.	Genotype	Mean yield (t·ha⁻¹)	WAASB	Rank
94	Bohemia	8.03	0.031	1
33	Slaven	7.06	0.039	2
61	Tvorets	7.51	0.042	3
9	Kiara	7.83	0.047	4
25	Niki	6.93	0.056	5
20	Katarzhina	7.32	0.057	6
17	Yanitsa	7.68	0.059	7
66	Mirlena	7.60	0.065	8
2	Pryaspa	7.35	0.073	9
67	Lut 601-09	8.04	0.075	10

The genotype Bohemia exhibited the lowest WAASB value (0.031), combining high mean yield (8.03 t·ha⁻¹) with minimal environmental variation, and was therefore identified as the most stable genotype in the study. The subsequent positions are occupied by Slaven, Tvorets, Kiara, and Yanitsa, all with WAASB values below 0.06 and mean yields exceeding 7.5 t·ha⁻¹, indicating a well-balanced combination of productivity and stability. At the same time, the genotype Lut 601-09, despite its relatively higher WAASB value (0.075), exhibited the highest mean yield among the group (8.04 t·ha⁻¹), demonstrating that high productivity can be achieved even at the expense of moderately reduced stability. This finding further highlights the inherent breeding trade-off between maximum yield potential and environmental stability. Overall, the obtained results confirm the applicability of the WAASB index as a reliable tool for stability assessment in multi-environment trials and its practical value for identifying promising genotypes in cereal crops (Olivoto & Lúcio, 2020; Pour-Aboughadareh et al., 2022).

WAASBY Index

The WAASBY index (Weighted Average of Absolute Scores Based on Yield) represents an integrated selection index that combines information on genotypic stability, quantified by WAASB, and mean productivity, estimated through BLUP, into a single indicator with predefined weights (Olivoto et al., 2019). The main advantage of this index lies in its flexibility, as breeding priorities can be adjusted by modifying the relative weight assigned to stability and yield, making WAASBY particularly suitable for practical selection under conditions of climatic and agroecological variability.

Table 12 presents the top ten genotypes under two selection-weight scenarios: 50:50, where stability and productivity are considered equally important, and 65:35, where greater emphasis is placed on yield. This comparative approach allows an evaluation of the robustness of genotype rankings with respect to changes in breeding priorities.

Table 12. WAASBY index values for the top 10 genotypes

No.	Genotype	Mean yield (t·ha⁻¹)	WAASBY 50:50	WAASBY 65:35	Rank (50:50)	Rank (65:35)
62	Nota	8.07	0.860	0.859	4	3
67	Lut 601-09	8.04	0.886	0.875	2	2
94	Bohemia	8.03	0.922	0.899	1	1
40	Sonata	7.91	0.841	0.832	6	7
9	Kiara	7.83	0.881	0.853	3	5
22	Krasen	7.69	0.820	0.798	10	14
17	Yanitsa	7.68	0.849	0.818	5	10
109	Mv Aprod	7.61	0.820	0.792	9	19
66	Mirlena	7.60	0.832	0.800	8	13
61	Tvorets	7.51	0.840	0.797	7	15

The genotype Bohemia occupies the leading position under both selection scenarios, combining high mean yield (8.03 t·ha⁻¹) with high stability. It is followed by Lut 601-09 and Nota, which also exhibit a favorable balance between productivity and stability, with minimal rank changes between the two weighting schemes. Bulgarian genotypes such as Kiara, Yanitsa, and Krasen are likewise included among the leading positions, demonstrating the strong potential of local breeding programs.

The observed rank shifts following changes in weighting (e.g., Tvorets moving from 7th to 15th position) illustrate the sensitivity of the WAASBY index to breeding priorities and highlight the necessity of carefully balancing yield and stability according to specific agroecological objectives.

YSI Index

The Yield Stability Index (YSI), proposed by Bouslama and Schapaugh (1984), quantifies genotypic tolerance to stress by assessing the ability of genotypes to maintain productivity under unfavorable conditions. In the present study, the index was calculated (Table 13) as the ratio between grain yield in 2014 (stress environment) and 2013 (favorable environment), allowing an evaluation of genotypic responses under contrasting environmental conditions. In this way, the index emphasizes relative stability rather than absolute yield levels.

This approach enables the identification of genotypes that exhibit smaller reductions in productivity under stress, even if they are not among the highest-yielding under favorable conditions. Such an evaluation is particularly valuable in years characterized by pronounced climatic constraints and contributes to a more objective interpretation of genotype × environment responses.

Table 13. Top 10 genotypes according to YSI

No.	Genotype	Yield 2013 ($t \cdot ha^{-1}$)	Yield 2014 ($t \cdot ha^{-1}$)	Yield 2015 ($t \cdot ha^{-1}$)	YSI	Rank
44	Lilyana	6.91	6.29	6.74	0.910	1
83	Avantazh	7.32	6.64	6.48	0.907	2
57	Yunona	6.16	5.46	3.57	0.886	3
55	Tania	7.87	6.7	7.07	0.851	4
65	Jumna	8.93	7.54	6.64	0.844	5
48	Litera	9.27	7.54	6.62	0.813	6
45	F02065G2-204	7.88	6.36	7.23	0.807	7
82	Liman	8.62	6.9	7.45	0.800	8
58	Esaul	8.06	6.42	7.88	0.797	9
84	Apach	7.33	5.82	8.12	0.794	10

YSI – Yield Stability Index, calculated as the ratio between grain yield in the stress environment (2014) and the favorable environment (2013).

The highest YSI values were recorded for Lilyana (0.910), Avantazh (0.907), and Yunona (0.886), identifying these cultivars as highly adaptive under stress conditions. Most of the leading genotypes originate from Romania, Moldova, and southern Ukraine, confirming the importance of geographic origin for stress tolerance.

The YSI index is thus validated as an effective tool for the preliminary assessment of stress tolerance, particularly when combined with other integrative indices such as STI and GMP, which together provide a more comprehensive evaluation of breeding potential (Farshadfar et al., 2012; Mohi-Ud-Din et al., 2025).

Superiority Index (Pi)

The superiority index (Pi), proposed by Lin and Binns (1988), is used for the simultaneous evaluation of mean productivity and stability of genotypes across multiple environments. Essentially, the index measures the deviation of each genotype from the highest yield achieved in each environment, with lower Pi values indicating closer and more consistent performance relative to the optimum across all conditions. The analysis of the results presented in Table 14 shows that the cultivar Midas has the lowest Pi value (0.6918), which indicates exceptionally high and stable productivity across all years of testing.

Table 14. Top 10 genotypes according to the Superiority Index (Pi)

No.	Genotype	Yield 2013 (t·ha⁻¹)	Yield 2014 (t·ha⁻¹)	Yield 2015 (t·ha⁻¹)	Pi	Rank
88	Midas	11.00	6.54	8.18	0.6918	1
86	Azimut	10.53	6.69	7.74	1.1818	2
41	Kantata	10.47	6.38	7.81	1.3918	3
93	Grom	9.93	6.86	7.72	1.7356	4
63	Csillag	10.80	6.06	7.42	1.7379	5
37	PKB Rodika	11.53	6.35	6.87	1.7899	6
62	Nota	9.67	6.64	7.91	2.0706	7
21	Nakhodka	11.38	5.14	8.26	2.0909	8
36	PKB Vizelka	11.80	6.25	6.66	2.1388	9
47	F05190 GP-1	10.21	6.87	6.95	2.1830	10

The next-ranked genotypes, Azimut (1.1818) and Kantata (1.3918), also exhibit yields close to the maximum achieved in each environment and therefore rank among the best-performing genotypes according to this criterion. The presence of Pi values below 1.0 among the leading genotypes is a clear indicator of good adaptation and competitiveness across diverse agroecological conditions. These findings are consistent with previous studies confirming the effectiveness of Pi as a breeding criterion (Lin & Binns, 1988; Cheshkova et al., 2020). Based on Pi, a preliminary selection of genotypes with proven yield potential can be performed regardless of environmental variability.

Kang's Stability Index (KSI)

Kang's Stability Index (KSI), introduced by Kang (1993), is a composite indicator that integrates yield and stability through nonparametric ranking. Each genotype is assigned a separate rank for mean yield and for stability, and genotypes with the lowest KSI values are considered the most productive and stable (Pour-Aboughadareh et al., 2022; Tsenov et al., 2022). As shown in Table 15, Nota ranks first (KSI = 20.0), exhibiting the best combination of high yield (8.07 t·ha⁻¹) and stability. It is followed by Bohemia (24.0), Kantata (30.0), Azimut (32.0), and Grom (35.0), all of which show yields above 8.0 t·ha⁻¹ and stable performance across environments. KSI confirms the importance of combined assessment of productivity and stability.

Table 15. Top 10 genotypes according to KSI values

No.	Genotype	KSI	Mean yield (t·ha⁻¹)	Rank
62	Нота	20	8.07	1
94	Bohemia	24	8.02	2
41	Kantata	30	8.22	3
86	Azimuth	32	8.32	4
63	Grom	35	8.17	5
87	Renan	35	7.69	6
17	Яница	35	7.68	7
9	Киара	35	7.83	8
22	Красен	38	7.68	9
88	Midas	38	8.57	10

Cultivars such as Nota and Azimut, which also rank highly according to Pi, demonstrate high adaptability and stability across diverse environments. These results are consistent with the findings of Tsenov et al. (2022) and Al-Ashkar et al. (2022c), who emphasize the practical value of this index in breeding programs.

II.5.1. Comparative Evaluation of Yield and Stability Indices

A key aspect of breeding is the selection of indices that effectively combine high productivity and stability. Classical indices such as Pi (Lin & Binns, 1988) and WAASB (Olivoto et al., 2019) emphasize predominantly one dimension. Therefore, composite indices such as KSI and WAASBY have been developed to provide a more balanced evaluation (Olivoto & Nardino, 2021).

The correlation analysis (Table 16) indicates that Pi is most strongly associated with yield (r = 0.97), whereas WAASB most accurately reflects stability (r = 1.00). The best overall balance is achieved by WAASBY (50:50), which shows a high correlation with grain yield (r = 0.69), a strong association with WAASB (r = 0.81), the highest geometric mean (0.75), and the smallest deviation from the ideal index (4.2°). KSI also demonstrates good balance (Angle = 1.5°), although with lower combined strength. The WAASBY (65:35) variant shifts the focus toward yield and is therefore more suitable for breeding objectives oriented toward high productivity.

Table 16. Comparative evaluation of yield and stability indices

Index	r(GY)	r(WAASB)	GeomMean(|r|)	MaxiMin(|r|)	Angle_to_Ideal(Â°)
WAASBY,50:50	0.69	0.81	0.75	0.69	4.2
WAASBY,65:35	0.86	0.62	0.73	0.62	9.2
KSI	0.74	0.70	0.72	0.70	1.5
Pi	0.97	0.29	0.53	0.29	28.7
WAASB	0.19	1	0.43	0.19	34.5
YSI	0.16	0.13	0.15	0.13	5.3

The correlation network diagram (Figure 6) further illustrates these relationships, clearly showing the central position of the WAASBY index between Pi and WAASB.

In summary, Pi emerges as the most suitable index for evaluating mean productivity, whereas WAASB remains the leading tool for assessing stability. Positioned between them, WAASBY (50:50) functions as an integrative index that combines the strengths of both approaches and enables simultaneous selection for yield and stability. From a practical standpoint, WAASBY (50:50) should be used as the primary index for final ranking, while WAASB should serve as a control indicator for stability confirmation. This strategy ensures a reliable, reproducible, and methodologically sound selection of genotypes with high and stable yield across diverse growing environments.

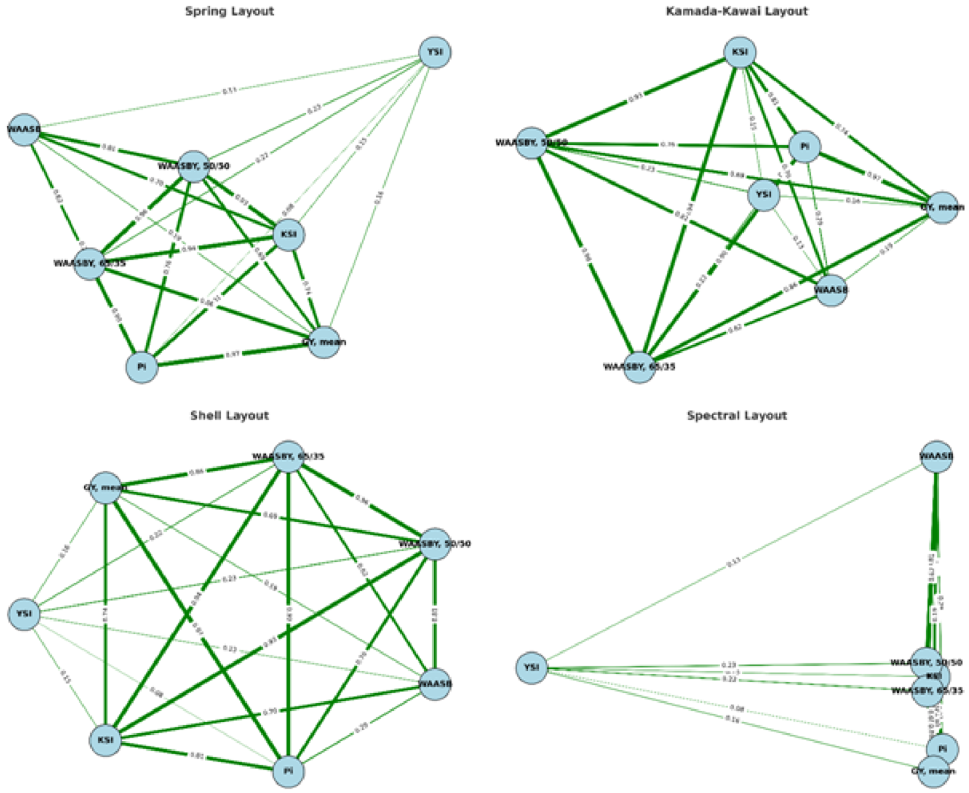


Figure 6. Network diagram of Spearman correlations among yield and stability indices.

II.6. Multi-trait selection indices

The results obtained thus far demonstrated that single indices such as BLUP and WAASB provide reliable but partial evaluations because they address productivity and stability separately. The integrative WAASBY (50:50) has been shown to offer a more balanced approach by combining the two characteristics, yet it remains limited to a single trait, namely grain yield. Previous analyses confirmed that the number of grains per square meter (NGM) is the leading factor determining yield formation, whereas thousand-grain weight (TGW) plays a complementary role. Therefore, the next logical step is the adoption of multi-trait indices that evaluate genotypes simultaneously for GY, NGM, and TGW, providing a more complete and realistic representation of breeding value (Rocha et al., 2018; Olivoto & Nardino, 2020). This approach extends classical methods by integrating productivity, its structural determinants, and stability within a unified framework. In the context of winter wheat, where yield is formed under the influence of complex morphophysiological and climatic drivers, multi-factor evaluation enables the identification of genotypes with consistently high productivity and adaptability (Olivoto et al., 2019). This section is focused on the classification and selection of priority genotypes through the application of multi-trait indices: MGIDI and MTSI, as well as on their comparison with the aim of constructing a consensus list of genotypes with high breeding value (Zuffo et al., 2020).

MTSI index

The assessment of genotypes using the Multi-Trait Stability Index (MTSI) focused on the three leading traits determining grain yield in winter wheat: grain yield (GY), number of grains per m² (NGM), and thousand-grain weight (TGW). All three traits were considered with a desired increase, because higher values reflect superior productivity and breeding value. This is consistent with both the preceding results and the literature confirming the leading role of NGM and the relevance of TGW for yield stability.

The MTSI ranking (Table 17) highlights ten genotypes with the most favorable combination of productivity and stability. Bohemia occupies first position (MTSI = 0.1959) with high mean yield (8.03 t·ha⁻¹), followed by Slaven (rank 2) and Krasen (rank 3). Genotypes such as Katarzhina, Gizda, and Mirlena demonstrate stable performance and favorable NGM values, whereas Kiara and Mv Kikelet combine high TGW and GY, confirming the effectiveness of MTSI in identifying balanced breeding candidates.

Table 17. MTSI values for the top 10 genotypes

No.	Genotype	MTSI value	MTSI rank	TGW (g)	NGM	Mean GY (t·ha⁻¹)
94	Bohemia	0.1959	1	43.34	18461	8.03
33	Slaven	0.2904	2	45.76	15401	7.06
22	Krasen	0.4239	3	48.03	16005	7.69
76	Meleag	0.4831	4	40.43	17191	6.88
20	Katarzhina	0.5373	5	45.71	16188	7.32
32	Gizda	0.6016	6	36.68	19100	6.99
9	Kiara	0.6088	7	47.37	16701	7.83
66	Mirlena	0.6155	8	39.23	19351	7.60
2	Pryaspa	0.6431	9	45.05	16092	7.35
106	Mv Kikelet	0.6912	10	46.06	16333	7.38

Overall, the MTSI analysis clearly identifies genotypes with high values of the major yield components and stability of their expression. These ten lines may serve as a foundation for breeding programs aimed at simultaneously increasing yield and ensuring stable performance across contrasting environments.

MGIDI index

The application of the Multi-trait Genotype–Ideotype Distance Index (MGIDI) to the analyzed genotypes enabled a clear differentiation of genotypes according to their proximity to the defined ideotype. Genotypes with lower index values are those combining high yield and a balanced structure of the main components, namely the number of grains per m² (NGM) and thousand-grain weight (TGW).

The results (Table 18) indicate that the cultivar Midas ranks first (MGIDI = 1.14), demonstrating maximum yield and favorable TGW and NGM values. It is followed by PKB Vizelka and PKB Rodika, which likewise combine high productivity with clearly expressed structural stability. The Bulgarian cultivar Nakhodka (MGIDI = 1.71) stands out with a competitive profile, highlighting the potential of the local genetic base.

Among the top ten are also Nota, Bohemia, and Glosa, which show balance across the three traits. Genotypes such as Grom and Sonata also rank highly due to high NGM values, which compensate for lower TGW values. These results confirm that MGIDI is a reliable tool for comprehensive evaluation, because it integrates productivity and the balance among the main yield components, thereby providing an objective basis for selecting genotypes with an optimal trait combination (Olivoto & Nardino, 2021; Rocha et al., 2018).

Table 18. MGIDI values for genotypes close to the ideotype

No.	Genotype	GY	NGM	TGW	MGIDI	MGIDI, rank
	Идеотип	**8.57**	**21729.83**	**49.58**	**0.00**	
88	Midas	8.57	18605.16	45.96	1.14	1
36	PKB Vizelka	8.24	19363.73	42.66	1.48	2
37	PKB Rodika	8.25	19984.63	41.73	1.53	3
21	Nakhodka	8.26	17810.40	45.12	1.71	4
62	Nota	8.07	19664.09	41.72	1.73	5
47	F05190 GP-1	8.01	19104.17	42.50	1.77	6
94	Bohemia	8.03	18460.56	43.34	1.83	7
52	Glosa	7.98	18245.50	44.34	1.86	8
63	Grom	8.17	20670.53	40.02	1.87	9
40	Sonata	7.91	19239.78	41.62	1.95	10

MGIDI – multi-trait genotype–ideotype distance index (Multi-Trait Genotype–Ideotype Distance Index). GY – grain yield (t·ha $^{-1}$); NGM – number of grains per square meter; TGW – thousand-grain weight.

Comparative ranking of genotypes across indices

For comparison, three independent rankings were applied, namely MGIDI, MTSI, and WAASBY with an equal 50:50 weighting between productivity and stability, in order to evaluate the extent to which the leading genotypes retain their positions irrespective of the index used. The Venn diagram (Figure 7) revealed partial overlap among the rankings and a clear differentiation of their emphases. Only Bohemia appears simultaneously among the top 20 genotypes across all indices, confirming its combination of high productivity, stability, and a balanced multi-trait profile.

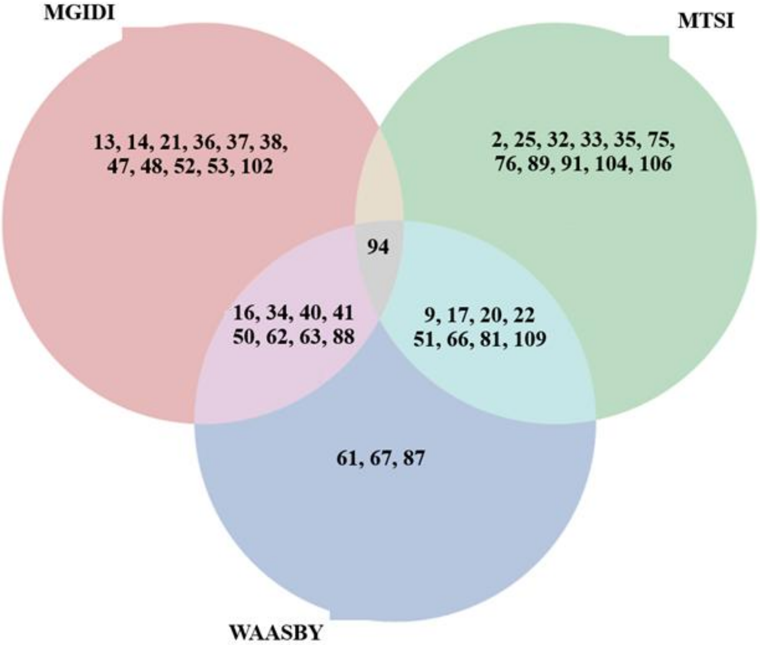


Figure 7. Venn diagram of overlap among the top 20 genotypes according to MGIDI, MTSI, and WAASBY (total: 42 genotypes)

The relationships among indices indicate that eight genotypes are common to MGIDI and WAASBY, and another eight are common to MTSI and WAASBY, positioning WAASBY as an intermediate index between ideotype proximity and stability of expression. The absence of overlap exclusively between MGIDI and MTSI highlights that MGIDI emphasizes proximity to the ideal profile, whereas MTSI is more sensitive to the stability of individual traits.

The overlap between MTSI and WAASBY for the cultivars Kiara, Yanitsa, and Mirlena confirms their stable and productive performance. Similarly, the shared positions of MGIDI and WAASBY for Midas and Grom suggest high potential combined with preserved adaptability and a favorable balance among yield components.

The final ranking (Table 19) includes 24 statistically significant high positions ($p < 0.05$), which are confirmed as priority breeding candidates. These genotypes combine high productivity, stability, and a balanced profile, representing a strategic basis for developing resilient cultivars. Particularly noteworthy are the genotypes Utrish (59), Vesta (74), and Kosara (18), which do not occupy leading positions under individual indices, but rank highly under RRA (ranks 18–21; $p < 0.05$), demonstrating consistent performance across different rankings.

In this context, the application of Robust Rank Aggregation (RRA) made it possible to identify genotypes that consistently occupy leading positions regardless of the index used. The results showed that Bohemia (94), Nota (62), Sonata (40), Mv Aprod (109), Kiara (9), and Mirlena (66) demonstrate stable superiority with high statistical reliability. The presence of Bulgarian cultivars such as Kiara, Krasen, and Zlatitsa among the leading entries emphasizes the competitiveness of the local genetic base.

Table 19. Values and ranks of the three indices for 25 genotypes according to RRA

Номер	Генотип	GY, $t \cdot ha^{-1}$	MTSI	WAASBY	MGIDI	Среден ранг	RRA, ранг	RRA, pV
94	Bohemia	8.03	1	1	7	3	1	0.0002
62	Nota	8.07	27	4	5	12	2	0.0052
40	Sonata	7.91	22	6	10	13	3	0.0065
109	Mv Aprod	7.61	18	9	24	17	4	0.0084
9	Kiara	7.83	7	3	29	13	5	0.0101
34	Elly	7.94	26	13	12	17	6	0.0107
66	Mirlena	7.60	8	8	34	17	7	0.0132
75	Kiriya	7.56	15	22	32	23	8	0.0199
22	Krasen	7.69	3	10	54	22	9	0.0203
51	Boema	7.54	14	14	33	20	10	0.0219
14	Zlatitsa	7.85	34	29	15	26	11	0.0239
88	Midas	8.57	58	18	1	26	12	0.0252
16	Merilin	7.82	35	16	17	22	13	0.0261
104	GK Körös	7.51	19	33	35	29	13	0.0261
63	Grom	8.17	66	12	9	29	15	0.0289
87	Renan	7.70	21	11	37	23	16	0.0308
17	Yanitsa	7.68	16	5	38	19	17	0.0334
59	Utrish	7.75	39	31	26	32	18	0.0361
74	Vesta	7.52	33	40	36	36	19	0.039
81	Livada	7.48	17	15	41	24	20	0.0419
18	Kosara	7.69	43	42	28	38	21	0.0484
33	Slaven	7.06	2	25	88	38	23	0.05
36	PKB Vizelka	8.24	112	94	2	69	23	0.05
67	Lut 601-09	8.04	59	2	22	28	23	0.05
20	Katarzhina	7.32	5	17	68	30	25	0.0563

These results highlight the strength of RRA in capturing not only extreme but also stable trends that often remain hidden in one-sided analyses. The integration of MGIDI, MTSI, and WAASBY (50:50) through RRA provides the most reliable and objective evaluation by minimizing the risk of methodological dependence and ensuring a consensus ranking applicable for final selection decisions.

III. CONCLUSIONS

1. The genotype × environment interaction (GEI) is statistically significant and determines differences in productivity and stability for each of the evaluated genotypes. Genotypes with predictable responses to changing conditions were identified, which facilitates their assessment.

2. The combined use of different statistical approaches (AMMI, REML/BLUP) increases the reliability of GEI analysis by enabling both description of the interaction structure and evaluation of genotypic potential.

3. According to the relative contribution of environmental conditions to the studied traits, they can be classified into two main groups. The first group includes traits predominantly influenced by the environment, namely thousand grain weight (TGW; 65%), grain yield (GY; 60%), and number of productive tillers per m^2 (NPT; 43%). The second group comprises traits for which the magnitude of the environmental effect is comparable to that of the genotype, including number of grains per spike (NGS; 25%) and number of grains per m^2 (NGM; 22%).

4. Genotype × environment interaction induces variation of approximately 11–16% for most traits, except for the number of grains per m^2 (NGM), where the GEI effect is almost twice as strong (29%).

5. Under substantial changes in growing conditions, thousand grain weight (TGW) exhibits the clearest and most proportional response, indicating a relatively linear dependence on environmental variation. In contrast, the remaining traits display more complex, nonlinear dynamics, as evidenced by the high contribution of the second principal component (PC2). For the number of productive stems and the number of grains per m^2, PC2 accounts for 44–45% of the total variation, approaching the explanatory power of the first principal component.

6. Using several independent statistical approaches, it was established that the number of grains per square meter (NGM) most strongly determines the level of grain yield (GY). Thousand-grain weight (TGW) also makes a substantial, but secondary contribution, which supports attainment of the maximum possible yield in some genotypes.

7. The number of productive tillers (NPT) and the number of grains per spike (NGS) exert an indirect effect on final grain yield, with their influence realized mainly through the formation of NGM, whose positive effect on yield is direct.

8. The applied multivariate evaluation methods enable clear differentiation of genotypes into homogeneous groups, with clusters characterized by specific combinations of grain yield (GY) and key structural traits.

9. Cluster analysis (K-means) identified three statistically distinct groups and outlined two effective strategies for achieving high yield: (1) increasing NGM while

maintaining TGW, or (2) increasing TGW while maintaining the existing NGM level observed in the evaluated cultivars.

10. Classification of genotypes based on multi-trait indices leads to clear differentiation of groups with differing breeding potential, thereby facilitating practical interpretation of the results.

11. The multi-trait indices MGIDI, MTSI, and WAASBY (50:50) capture different breeding aspects, and their combined use enriches the information obtained for each cultivar.

12. Accurate and objective selection requires a combined, simultaneous evaluation of productivity and stability; selection based solely on absolute grain yield carries a risk of favoring specific adaptation.

13. The integration of traditional and modern approaches provides a logically reproducible protocol for comprehensive cultivar evaluation, which becomes a specific cultivar characteristic against the background of the pronounced influence of environmental conditions.

14. Grain yield and its main components are closely associated with thermal accumulation and water balance during the critical winter spring and spring summer phases of the growing season.

15. Cultivars with wide adaptation were identified due to their balanced combination of high productivity and stability, making them suitable for direct recommendation and regional deployment in production.

IV. CONTRIBUTIONS

IV.1. Scientific and theoretical contributions

1. It was demonstrated in a clear and statistically supported manner that, against the background of genotype × environment interaction in the main productivity traits, a multi-layered cultivar evaluation is feasible within a large set of tested genotypes.
2. An integrated methodology for evaluating winter wheat cultivars was introduced, combining multifactor statistical analysis (ANOVA, AMMI, REML), yield component analysis, and multi-trait integration (MGIDI, MTSI, WAASBY 50:50), synthesized through robust rank aggregation (RRA).
3. The leading role of NGM for stable high productivity across diverse environments was demonstrated.
4. Three fundamentally distinct but complementary statistical approaches for objective evaluation were defined; these can serve as a basis for targeted cultivar assessment within a group, depending on the specific objective.
5. A protocol was developed whose logical stepwise reproduction, even under changes in specific parameters, leads to similar rankings of the analyzed cultivars.
6. Grouping genotypes based on combinations of their specific trait levels provides a substantially more precise evaluation than approaches based solely on grain yield or on a single trait directly affecting yield.

IV.2. Scientific and applied contributions

1. Genotypes with high productivity and stability were identified as suitable both for deployment and for use as parental material in breeding crosses.
2. Specific guidance for breeding decisions was provided, based on prioritizing NGM while maintaining TGW, which optimizes selection across different environments.
3. A transparent and easily reproducible evaluation protocol was developed, reducing data-processing time and increasing reproducibility in breeding practice.
4. A specific statistical approach for balanced evaluation through combining productivity and stability was clearly indicated.
5. The application of integrated indices results in a different ranking of genotypes compared with classification based only on mean yield; this re-ranking reflects the real impact of genotype × environment interaction.

V. PUBLICATIONS RELATED TO THE DISSERTATION WORK

Raykov, G., Chamurliyski, P., Doneva, S., Penchev, E., Tsenov, N., 2016, Productivity performance of bread winter wheat genotypes of local and foreign origin. *Agricultural Science and Technology, 8*(4), 276–279, DOI:10.15547/ast.2016.04.052.

Raykov, G., 2025, Number of grains per square meter as a key predictor of yield potential in winter wheat. *Agricultural Science and Technology, 17*(2), 30–39. DOI: 10.15547/ast.2025.02.017