as the most stable genotype because of its minimal environmental sensitivity. When productivity and stability were considered jointly, LG Orlis, CHIKO, and LG Kvadrant appeared to be the most valuable broadly adapted cultivars.

At the same time, the results revealed clear zonal differentiation in adaptation. In the Steppe, the most favorable performers were CHIKO, LG Orlis, and Khvylia Dnipra. In the Forest-Steppe, Bosporus, Khvylia Dnipra, LG Orlis, and CHIKO showed the greatest suitability. In Polissia, the leading cultivars were LG Orlis, CHIKO, and Bosporus. In addition, several varieties, including Khvylia Dnipra, Tika Taka, Tenor, LG Litopys, Bosporus, and MIP Nika, displayed pronounced specific adaptation to particular environmental conditions. Such genotypes should not be overlooked merely because they are less universal; rather, they should be considered important material for zone-specific recommendations and targeted breeding strategies.

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YIELD VARIATION OF NEW WINTER WHEAT VARIETIES UNDER DIFFERENCE ENVIRONMENTAL CONDITIONS

A range of statistical tools is used in plant breeding to quantify genotype × environment interaction and to assess the stability of yield expression. These methods include regression-based models, nonparametric approaches, and multivariate techniques. Regression procedures are useful for describing the way a genotype responds to environmental change through the slope of its response curve and the magnitude of deviation from that trend. Nonparametric methods are particularly valuable when the assumptions required for classical parametric statistics, such as normality of distribution or homogeneity of variance, are not fully satisfied. At the same time, multivariate approaches offer a broader analytical perspective, because they are able to reveal complex interaction structures that cannot be adequately represented by a single statistic, especially when many test environments are included.

According to the average productivity background, the most favorable environments in the present trial were Chernivtsi, Ternopil, Lviv, Rivne and Vinnytsia. However, productivity alone was not sufficient to characterize the analytical role of these environments. When evaluated by vector length in the IPC1–IPC2 space, the most representative sites were Volyn, Zakarpattia, Ternopil, Kharkiv and Lviv, because their shorter vectors indicated a closer approximation to the average response of the genotype set. By contrast, Dnipropetrovsk, Khmelnytskyi, Sumy, Vinnytsia and Kirovohrad showed the greatest discriminating capacity, indicating stronger ability to differentiate among genotypes. This pattern highlights the importance of maintaining both reference-type and strongly contrasting environments within the cultivar testing network.

The zonal structure of the results was especially informative. Within the Steppe, no single dominant variety was observed across all locations. DARYNA ranked first in Dnipropetrovsk, ZU Shamal in Kirovohrad, and HIMALAYA in Odesa. Such variation among only three Steppe sites demonstrates that even within one natural zone, environmental contrasts are sufficiently strong to alter varietal ranking. This makes local recommendation particularly important in the Steppe, where cultivar superiority cannot be generalized without reservation.

The Forest-Steppe showed an intermediate pattern between the highly contrasting Steppe and the more consistent Polissia zone. In this group of environments, STK21G, Zoloto Stepu, Atrybut, and ZU Willem appeared more frequently among the leaders, although their exact ranking differed considerably from one region to another. This indicates that the Forest-Steppe combines relatively high productivity with substantial internal heterogeneity, meaning that the specific agroecological background of each testing point must be taken into account when interpreting varietal performance.

In Polissia, the results were characterized by a greater recurrence of the same leading genotypes. Pamiati Horlacha ranked first four times, while STK21G, Atrybut, Dnistrianka Odeska, and ZU Willem repeatedly appeared among the top three. Compared with the Steppe, this suggests a somewhat more homogeneous environmental pattern and a more predictable response of the genotypes. At the same time, the presence of some contrasting sites shows that even within Polissia, local differentiation remains relevant.

For breeding practice, several practical conclusions follow from these results. First, no single environment can replace a properly constructed multi-location network, because different sites perform different analytical functions. Some are valuable for obtaining a generalized estimate of cultivar response, while others are essential for exposing specific adaptation. Second, varieties that repeatedly appear among the top-ranked entries across different zones should be treated as material with broad adaptive value and as sources of favorable stability components. Third, genotypes that dominate only in individual environments should not be underestimated, because their local superiority may reflect useful specific adaptation to particular agroecological backgrounds. Therefore, the most effective breeding strategy is not to search for one universally best genotype, but to assemble a differentiated set of varieties suited to different zones and production scenarios.

When genotypes were compared by mean productivity, the leading varieties were Pamiati Horlacha, ZU Willem, BHV20GV0009, ZU Shamal, and Slava Unavy. However, the picture changed when stability was considered. According to the stability criterion, HIATSYNT was clearly the strongest genotype. This contrast demonstrates that varietal evaluation should not be based on yield alone. A reliable assessment requires the joint consideration of mean performance, ASV, YSI, and the graphical interpretation provided by AMMI biplots.

Additional evidence from the ranking structure and the genotype positions relative to the ideal type suggests that STK21G, Kvitoslava, and Dnistrianka Odeska should be regarded among the most balanced forms in the dataset. At the same time, HIMALAYA, STK21G, Dnistrianka Odeska, and ZU Willem expressed pronounced specific adaptation and may therefore be more suitable for targeted zonal use than for indiscriminate wide deployment. In this respect, STK21G appears particularly interesting, because it combines a strong ability to exploit favorable environments with relatively moderate variation in response, which supports its interpretation as one of the most versatile genotypes in the studied set.

Overall, the combined analysis of varietal ranking, productivity background, environmental representativeness, and discriminating ability provides an integrated picture of the adaptive structure of the tested material. The results clearly show that a well-designed testing system must include environments that differ not only in average productivity but also in their capacity to reveal genotype contrasts. Likewise, recommendations for varietal deployment should not rely solely on mean yield values. They must also account for the specific way in which each genotype interacts with ecological conditions, because it is this interaction that ultimately determines whether a variety will be broadly reliable or only locally superior.

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ASSESSMENT OF POSITIVE VARIATION IN WINTER WHEAT VARIETIES INDUCED BY DAB

Agricultural crops are increasingly exposed to unstable and frequently adverse environmental conditions, which makes adaptive capacity a central requirement for modern breeding. Ongoing climate change has intensified this challenge by altering precipitation patterns, increasing air temperatures, raising the frequency of extreme weather events, and modifying the epidemiological background of pests and diseases. Under such circumstances, the creation of plant material capable of maintaining useful agronomic performance under stress has become one of the major priorities of crop improvement programs.

The present study was undertaken to characterize the patterns of induced hereditary variability in winter wheat and to determine how genotype × mutagen interaction influences the frequency and diversity of useful mutations. Particular attention was given to the occurrence of favorable changes that may be of value for breeding practice.

Eight winter wheat genotypes (*Triticum aestivum* L.) were used as source material: Perspektyva Odeska, Sonata Poltavska, Shpalivka, MIP Lada, Farell, NE 12443, Ronin, and Seilor. For each treatment variant, 1000 seeds with a moisture content of 14% were exposed to DAB (1,4-bisdiazoacetylbutane) at concentrations of 0.1, 0.2, and 0.3%.

Induced changes were evaluated in the M_2 and M_3 generations, where visible mutations were recorded and inheritance patterns were followed. Depending on the year of the study, plot area varied from 5 to 10 m², and the field experiments were conducted with one or two replications. Standard control varieties were inserted after every twentieth plot. Grain protein content was measured using a Spektra RT device. Glutenin and gliadin fractions were quantified by reverse-phase high-performance liquid chromatography (RP-HPLC). The concentrations of essential microelements in grain, namely Mg, Mn, Zn, Mo, Co, and Cu, were determined using an Agilent 5110 inductively coupled plasma atomic emission spectrometer (ICP-AES), with wavelength calibration based on Agilent multi-element standard solutions.

Treatment effects were assessed statistically by analysis of variance (ANOVA). To broaden interpretation of the data structure, discriminant analysis and cluster analysis were also applied, using Euclidean distance and the single-linkage method. Mean comparisons between treatments were carried out using Tukey's HSD test at a significance threshold of $P < 0.05$.

The deliberate induction and exploitation of genetic variability have become indispensable elements of contemporary breeding. Previous studies have shown that mutation-based variability can be successfully used to generate original breeding material with improved manageability, higher reliability, and more predictable expression of economically important traits. In this respect, mutagenesis