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MYCOBIOME OF PEA SEEDS

Pea (*Pisum sativum* L.) is an indispensable source of plant protein, which is comparable to animal proteins in terms of nutritional value and amino acid composition. It possesses a unique ability to fix nitrogen through symbiosis with nodule-forming bacteria, allowing it to accumulate 60–100 kg/ha of nitrogen in the soil. Peas are considered one of the best preceding crops in a crop rotation, as they improve soil structure and increase yields, particularly of winter wheat. Growing peas contributes to the ecologization of agriculture, allowing for a significant reduction in the use of synthetic mineral fertilizers.

Despite these advantages, pea yield can be limited by various diseases, including seed infections, which lead to a decrease in seed germination, rotting of roots and sprouts, and stunted plant growth, as a result, thinning of the crops.

The aim of this study was to investigate the species composition and structure of the pea seed mycobiome, determine the prevalence of micromycetes, and assess their impact on the sowing quality of seed material.

The phytopathological examination of pea seeds was conducted at the Problem-Oriented Research Laboratory of Mycology and Phytopathology of the Department of Phytopathology named after Academician V. F. Peresypkin at the National University of Life and Environmental Sciences of Ukraine. For this purpose, methodologies specified in DSTU 4138-2002 «Seeds of Agricultural Crops. Methods for Determining Quality» were used. Seed samples from the 2025 harvest were obtained from farms in the Kyiv, Odesa, and Khmelnytskyi regions.

A study of seed infection in the pea harvest from the Kyiv region revealed the occurrence frequency of the micromycete *Cladosporium herbarum* (Pers.) Link in the range of 18,5–88,3%. The prevalence of the fungi *Alternaria alternata* (Fr.) Keissl. and *Penicillium* spp. was 2,5–5,0% and 0,7–1,6%, respectively. Additionally, 0.2–3.3% of seeds in the tested samples were found to be infected with *Ascochyta pisi* Lib.

Analysis of seed samples grown in the conditions of the Khmelnytskyi region allowed for the detection of *Fusarium* spp. infection within the range of 2,5–65,5%. The occurrence frequency of *Penicillium* spp. was 3,2–11,5%, *A. alternate* – 4,2–9,0%, and *Sclerotinia sclerotiorum* (Lib.) de Bary – 0,5–3,0%.

Pea seeds from the Odesa region were infected with pathogens causing *Alternaria* spp. – 7,5–24,0%, *Fusarium* spp. – 1,5–18,0%, and *Penicillium* spp. – 0,2–2,5%.

Research on pea seeds grown in the Kyiv, Khmelnytskyi, and Odesa regions confirmed their infection with pathogens, among which the most common are the micromycetes *C. herbarum* (up to 88.3%) and *Fusarium* spp. (up to 65.5%). The level of seed infection by dangerous fungi such as *A. pisi* and *S. sclerotiorum* was established; these pose a significant threat due to a substantial reduction in seed germination and the deterioration of the phytosanitary condition of future crops.

C. herbarum and *A. alternata* are representatives of the mycobiota that colonize the seed surface in field conditions during ripening or during the harvesting process. In our studies, their impact on germination energy and germination was negligible. *Fusarium* spp. in the samples studied were also, in most cases, in the form of surface infection. This means that seed contamination occurred during the pre-harvest period.

Although epiphytes may not directly reduce seed germination, their high concentration is a indicator of growing conditions (e.g., frequent rains during the ripening period), which requires attention when selecting a seed treatment in the future.

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MODERN WINTER WHEAT VARIETIES VARIABILITY DEPENDENT ON ENVIRONMENTAL CONDITIONS

Stable grain production and satisfactory economic returns continue to rank among the principal objectives of both plant breeding and agricultural practice. In the case of winter wheat, modern cultivars are required not only to achieve high yield levels when environmental conditions are favorable, but also to maintain dependable performance under variable and often contrasting production settings. In practical terms, the value of a cultivar is determined not simply by its maximum productivity, but by the extent to which its genetic potential can be realized consistently across diverse combinations of soil properties, climatic conditions, agronomic backgrounds, and year-to-year weather fluctuations. This requirement has become especially important under current conditions of increasing environmental instability.

The present study was designed to determine the extent to which grain yield in winter wheat is influenced by environmental conditions and, on that basis, to identify genotypes that combine high productivity with stable performance under contrasting growing environments. In practical terms, the analysis was aimed not only at estimating the contribution of the major sources of variation to yield formation, but also at clarifying whether varietal differences remain consistent across locations and years or whether their ranking changes substantially depending on the agroecological context.

The experimental design included plots with a net area of 10 m², three replications, and three growing seasons from 2022 to 2024. To study genotype × environment interaction, the AMMI model (Additive Main Effects and Multiplicative Interaction) was applied. This method combines the advantages of analysis of variance for partitioning the additive main effects of genotype and environment with principal component analysis for decomposing the multiplicative interaction component. Such an approach is particularly suitable for multi-environment data, because it allows both quantification and interpretation of the differential responses of genotypes across testing conditions.

The trial network consisted of 17 environments and included locations representing the major agroecological zones of Ukraine: the Steppe, Forest-Steppe, and Polissia. Within such a framework, each environment performs two analytically distinct functions. First, it creates a general productivity background, that is, it determines how fully the yield potential of the tested cultivars can be expressed. Second, it serves as a differentiating factor, either enhancing varietal contrasts or, conversely, smoothing them and thereby reducing the clarity of cultivar ranking. Accordingly, evaluation of the testing environments themselves is not merely auxiliary; it is central both for correct interpretation of cultivar performance and for improvement of the testing network as a whole.

The results demonstrated that the environments with the highest average productivity formed a pattern that was consistent with agroecological zoning. Within the Steppe, the highest mean productivity background was observed in Odesa region. Within the Forest-Steppe, the highest mean yields were recorded in Sumy, Cherkasy, Kharkiv, and Vinnytsia regions. This distribution is broadly consistent with the known suitability of these areas for winter wheat production, where favorable moisture supply during critical developmental phases, comparatively fertile soils, and a more stable thermal regime often promote better realization of yield potential. Environments of this type are particularly important because they reveal the upper productivity ceiling of the tested genotypes.

However, high average productivity should not be equated automatically with representativeness. An environment may provide a favorable yield background while simultaneously exerting a strong differential effect on cultivars, thereby altering their relative ranking. In other words, a highly productive site may still be highly specific in terms of GEI. For that reason, representativeness is better evaluated using the vector length of each environment in AMMI2 space, calculated as $\sqrt{(IPC1^2 + IPC2^2)}$. A shorter vector indicates a weaker contribution to specific interaction effects and therefore a more neutral or representative role within the network. Environments located close to the origin of the AMMI2 plot can thus be interpreted as more suitable for general cultivar assessment.

On this basis, the most representative environments were identified as Chernihiv, Khmelnytskyi, Lviv, Chernivtsi, and Volyn. These sites may be regarded as locations where varietal performance is expressed in a more balanced and less distorted manner, allowing a more objective assessment of baseline productivity. Among them, Chernihiv had the shortest vector and may therefore be considered especially suitable as a reference environment for primary comparison of cultivars. Such locations are valuable because they provide a comparatively averaged expression of genotype response rather than emphasizing narrow local contrasts.

In contrast, some environments played a more strongly discriminating role. Kirovohrad was identified as the most discriminating site, followed by Dnipropetrovsk, Kharkiv, Cherkasy, and Kyiv. These environments are especially useful for revealing specific adaptation, because they accentuate varietal differences and expose the extent to which individual genotypes respond to particular environmental profiles. Although they are less suitable for broad generalization, they are indispensable for identifying narrowly adapted but potentially highly valuable breeding material. In this sense, highly discriminating locations serve not as universal benchmarks, but as filters for detecting adaptive specialization.

Taken together, these findings show that the interpretation of winter wheat performance cannot rely solely on average yield. The same genotype may appear highly promising under one type of environment and much less competitive under another. Therefore, an effective breeding strategy must combine assessment of productivity with assessment of stability and environmental responsiveness. The AMMI approach is particularly valuable in this regard, because it makes it possible to distinguish broadly adapted cultivars from specifically adapted ones while simultaneously evaluating the analytical role of each testing environment. As a result, it supports not only more accurate identification of promising genotypes, but also more rational design of testing networks and more reliable development of region-specific variety recommendations.