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MORPHOBIOLOGICAL CHARACTERISTICS OF WHEAT (TRITICUM AESTIVUM L.) GENETIC RESOURCES AND THEIR BREEDING SIGNIFICANCE

Abstract. *This article presents a comprehensive study of the morphobiological characteristics of wheat (Triticum aestivum L.) genetic resources and their breeding significance. The research was conducted in 2024–2025 and included 384 collection samples obtained from various geographical regions (Central Asia, Russia, Africa, America, and Asian countries). Key agronomically valuable traits such as phenological stages (emergence, heading, maturation), plant height, spike structure, and thousand kernel weight were thoroughly analyzed. The results revealed significant phenotypic variability among the genotypes. The thousand kernel weight ranged from 46 to 56 g, with an average value of 50.7 g, indicating high stability of this trait. In addition, considerable differences were identified among the samples in terms of resistance to yellow rust, with some genotypes demonstrating high resistance, making them valuable donors for breeding programs. The most promising results were observed in samples belonging to the Lutescens, Erythrospermum, and Aestivum groups. These samples are characterized by large grain size, high productivity, and adaptability to environmental conditions. The obtained results provide an important scientific and practical basis for the effective utilization of wheat gene pool, conservation of genetic diversity, and development of new high-yielding varieties resistant to stress factors under climate change conditions.*

Keywords: *genetic resources, wheat (Triticum aestivum L.), gene pool, genotype, morphobiological traits, breeding, spike structure, grain, thousand kernel weight, phenological traits.*

Introduction. Wheat (Triticum aestivum L.) is one of the most important strategic grain crops, ensuring food security for the world's population. In this context, the effective use of genetic resources in the development of high-yielding, environmentally adaptable, and resilient varieties takes on particular significance.

Wheat genetic resources have a wide range of geographical origins, biological and economically valuable traits, and serve as valuable source material in the breeding process. In particular, an in-depth study of morphobiological characteristics is an important factor in determining the productive potential, adaptability, and economic value of genotypes.

Under these conditions, the effective use of genetic resources in the creation of highly productive, ecologically adaptable, and resistant varieties takes on particular importance, as the increasing complexity of agroecological factors has a significant impact on the stability of wheat yields.

The aim of this study is to evaluate the morphobiological properties of wheat genetic resources, determine their genetic diversity, and select promising samples for breeding; this process has practical and scientific relevance.

The main wheat-producing countries are the United States and Canada. The average yield in these regions is 30-40 cwt/ha. Russia, France, Germany, and Ukraine are also leading wheat-producing countries, with average yields reaching 50-80 cwt/ha. In China and India, the world's largest wheat producers, the average yield is 50-60 cwt/ha. The average yield in Kazakhstan and Uzbekistan is approximately 40-60 cwt/ha [13, 14].

The United States, Canada, Russia, France, Germany, and Ukraine lead the global market in wheat exports. These countries account for the bulk of global grain trade and play a significant role in the international food market. At the same time, China and India are among the leading countries in terms of wheat production due to their large populations and high levels of domestic consumption [13, 15].

According to FAO data, wheat is one of the most widely cultivated grain crops in the world and accounts for a significant portion of global grain production [13]. At the same time, the wheat production system faces a number of global challenges.

Climate change, extreme temperatures, droughts, and changes in precipitation patterns have a significant impact on the stability of wheat yields. According to research, rising temperatures and reduced water resources are among the main factors reducing grain yields [16].

Soil degradation, salinization, and erosion are also factors that limit the productivity of agroecosystems [17].

The decline in genetic diversity must be regarded as a serious problem in the breeding process. A narrow genetic base can reduce the resistance of new varieties to diseases and abiotic stresses. Therefore, the conservation and enrichment of the wheat gene pool is an important prerequisite for improving the efficiency of breeding [17].

Advances in molecular genetics and genomics enable in-depth studies of genotypes and the development of high-yielding and stress-tolerant varieties [18].

Therefore, a comprehensive study of genetic resources for the sustainable development of wheat production, ensuring food security, and creating adaptive varieties under conditions of global climate change is a relevant area of scientific research.

Conditions and methods of research. The research was conducted in 2024–2025 at experimental plots of the Research Institute of Plant Genetic Resources, located in the Kibrai District of the Tashkent Region. The area is characterized by typical irrigated gray soils and has favorable agroecological conditions for wheat cultivation.

Samples from a collection of 384 wheat varieties of various geographical origins (Triticum aestivum L.) were studied. The samples were brought from countries in Central Asia, the Russian Federation, Africa, the Americas, and Asia through introductions and expeditions, reflecting genetic diversity.

Field trials were organized based on standard agronomic practices. The experiments were conducted using a randomized block design in 2-3 replications. The plot area for each treatment was 1 m².

During the growing season, the morphobiological characteristics of the wheat samples were studied. In particular, observations and measurements of important agronomic traits, such as phenological stages (emergence, heading, ripening), plant height, spike structure, and 1,000-kernel weight, were conducted regularly.

Statistical analysis of the obtained data was performed using the method of B.A. Dospekhov (1985). Descriptive statistics, mean values, variance, and the coefficient of variation (V, %) were calculated. These methods allowed us to assess the degree of differences between genotypes and identify promising samples.

Research results and discussion. Field experiments were conducted in accordance with generally accepted standard agricultural practices. Plots were arranged in 2-3 replicates using a randomized block design. The plot size for each treatment was 1 m². Phenological observations, morphobiological measurements, and phytopathological assessments were conducted throughout the growing season.

The study included 384 wheat accessions of various geographical origins. In particular, introduction and expedition samples from Egypt, Eritrea, Djibouti, Mexico, Chile, Japan, India, ICARDA, CIMMIT-ICARDA, Turkey, the Russian Federation, Armenia, Tajikistan, Kazakhstan, and Uzbekistan were analyzed.

The collection materials were grouped by subspecies, and their areas of origin were assessed, as well as traits valuable for breeding – phenological indicators, awn structure, 1,000-grain weight, and resistance to yellow rust (Table 1). The results obtained made it possible to determine the botanical and geographical diversity of the gene pool, as well as its potential for use in the breeding process.

Table 1.

Places of origin of the 384 wheat samples studied

№	Geographical origin	Names of countries	Type and quantity, pcs.	As a percentage of the total
1.	Central Asia	Uzbekistan, Kazakhstan, Tajikistan, Turkey	69	18
2.	South Asia	India	1	0,3
3.	South and North America	Mexico, Chile	3	0,9
4.	Eastern Europe	Russian Federation	124	32
5.	East Asia	Japan	1	0,3
6.	South Caucasus	Armenia	3	0,9
7.	North and East Africa	Egypt, Eritrea, Djibouti, IKARDA, SIMMYT-IKARDA	183	47,6
	Total		384	100

Of the 384 samples tested, 382 germinated completely; 2 samples – specifically, seeds from samples coded 10642 (Egypt) and 3106 (Mexico) – did not germinate, which may, of course, be due to seed damage or loss of viability.

Of the 382 samples that germinated, 114 (29.8%) belonged to the “Aestivum” subspecies of soft wheat, 58 (15.9%) to the “Milturum” subspecies, 47 (12.3%) to the “Erythrosperm” subspecies, 33 (8.6%) samples belong to the “Compactum” subspecies, 28 (7.3%) samples belong to the “Vulgare” subspecies, 23 (6.0%) samples belong to the “Lutescens” subspecies, 7 (1.8%) samples belong to the “Albidum” subspecies, 7 (1.8%) samples belong to the “Deficiens” subspecies, 5 (1.3%) samples belong to the “Spelta” subspecies, 2 (0.5%) samples belong to the “Muticum” subspecies, 2 samples (0.5%) were identified as belonging to the “Turgidum” subspecies, and 56 samples (14.7%) were identified as belonging to the “Durum” subspecies of durum wheat.

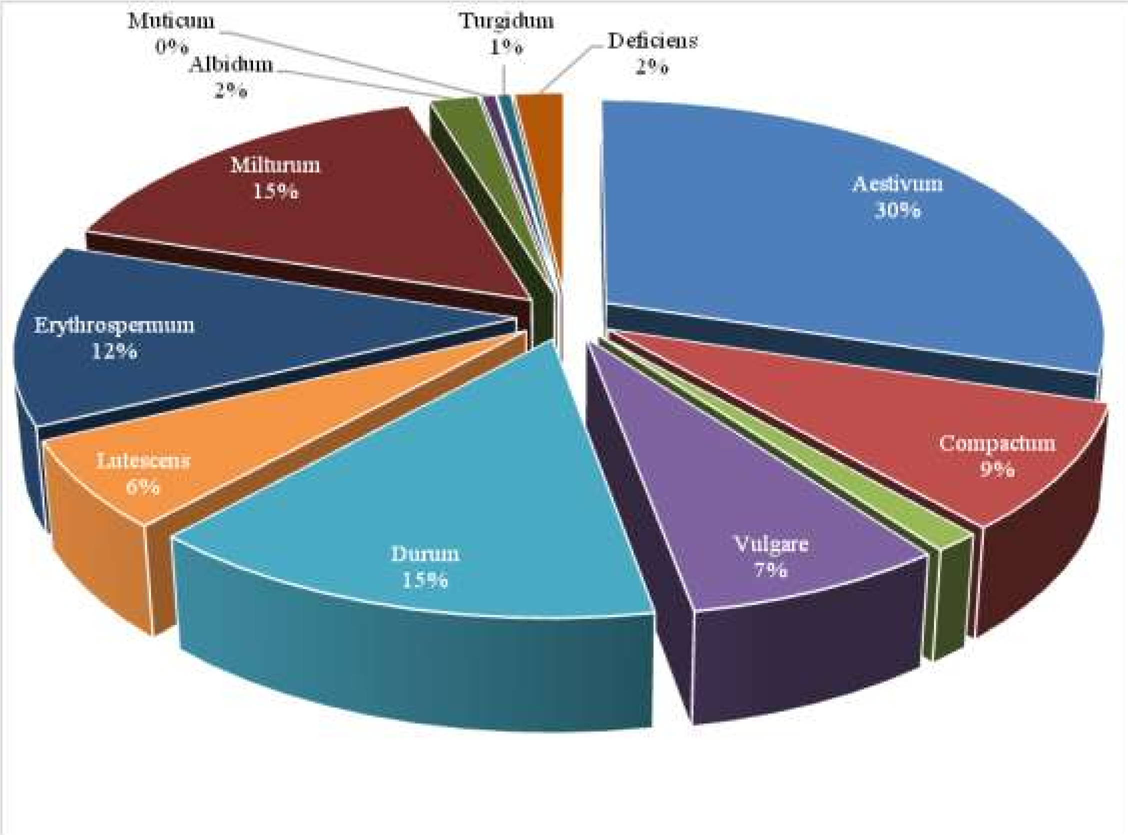

Figure 1. Distribution of the studied wheat samples by subspecies

Resistance and Severity of Rust Infection in Collection Samples. The study evaluated the resistance of winter wheat collection samples to rust under natural infection conditions in the field. Throughout the growing season, the progression of the disease was regularly monitored, and significant differences between genotypes were identified.

Rust disease mainly developed during the booting and heading stages, with maximum infection observed during the milk ripeness stage. Meteorological conditions (humidity and moderate temperatures) during the study year were favorable for pathogen development, which allowed for a clear, differentiated assessment of the genotypes’ resistance levels.

The analysis results showed that the incidence rate ranged from 0% to 80%. That is, in genotypes resistant to rust diseases (R, Mr), infection did not exceed 5-10%, while in moderately resistant (Mr-MS) samples, infection was 20-30%, and in susceptible (MS) genotypes, it was 40-60%. In the most susceptible (S) samples, infection reached 70-80%. When studying the relationship between the distribution of subspecies and rust infection, it was found that the subspecies was unevenly distributed among the 382 samples. That is, specimens belonging to the Aestivum subspecies were numerically predominant (29.8%), followed by specimens of the milturum (15.2%), durum (14.7%), and jythrospermum (12.3%) subspecies. but that the subspecies was unevenly distributed among the 382 samples. That is, specimens belonging to the Aestivum subspecies were numerically predominant (29.8%), followed by specimens of the milturum subspecies (15.2%), durum (14.7%), and jythrospermum (12.3%).

A chi-square test confirmed a significant deviation from uniform distribution ($\chi^2 = 379.9$; df = 11; $p < 0.001$).

Studies have shown that samples of this species are an important resource for creating new wheat varieties adapted to the arid climatic conditions of Uzbekistan, with high protein content and high-quality grain.

Subspecies Lutescens. T. lutescens – (23 samples, 6.0%) belongs to the group of medium-maturing soft wheats with golden ears and originates from Russia, ICARDA, and Uzbekistan. Its main characteristics include yellowish-golden spikelets, fully spiked, with large yellowish-white grains, high yield, and moderate resistance to drought and cold. This subspecies is widely used as the primary breeding line in intensive wheat breeding programs.

Subspecies Erythrospermum. T. erythrospermum – (47 specimens, 12.3%) is a red-grained, mid-season subspecies adapted to climate change; the majority originate from the Russian Federation, as well as from ICARDA and, to a lesser extent, from Uzbekistan. Morphological characteristics: spikes are long, smooth, and dense; grain color is reddish-brown (erythron – red); grain surface is harder; flour quality is high; suitable for baking; frost- and heat-tolerant. This is the most recently described species.

In the context of Uzbekistan, it serves as an important subspecies reference for developing lines resistant to stress factors (water scarcity, heat).

The Milturum subspecies (T. milturum) – (58 samples, 15.2%) includes forms with shorter, yellowish or light brown awns and harder grains. In terms of origin, this subspecies consists of sources from Russia, ICARDA, ICARDA-SIMMYT, and Uzbekistan. Key characteristics: compact, firm spikes that turn completely yellow upon ripening; the grain is large, smooth, dense, and colorful, rich in protein, resistant to dehydration, suitable for mechanical harvesting, non-shattering, and a convenient type for breeding work as intermediate “hard-soft” forms with stable yields.

Subspecies Albidum. T. albidum – (7 samples, 1.8%) – a light whitish, loosely structured form of wheat, originating from sources in Russia, Uzbekistan, and ICARDA. Morphological characteristics: grains are smooth, whitish, with soft endosperm; spikes are of medium length; yield is average, but flour quality is high. This species is the most important genetic source for breeding white-grain varieties, as well as for the production of white flour.

In addition, among the samples studied in the research was Triticum aestivum L., which belongs to a subtype originating from Mexico, Armenia, Kyrgyzstan, Tajikistan, Turkey, India, Afghanistan, Japan, and Chile, as well as from T. compactum and durum wheat. There are also species of Collicia namulari belonging to the Durum subtype.

Among the studied samples in the collection, it should be noted that the Compactum species, with their frost resistance, play an important role in breeding efforts to create new hybrids, while the Durum forms are particularly valuable species samples, resistant to heat and drought, and possessing high-quality flour properties.

The best results by species were obtained when 1,000 grains were identified in the collection samples studied in the research, specifically those from the Ikaridi sources and collection samples 10322 and 10440, i.e., Triticum aestivum subsp. In the Aestivum subspecies, it amounted to 54.0 g, and in the Triticum turgidum subsp. In the Durum subspecies, it amounted to 52.0 g. Also, from the collection samples with the highest grain weight per 1,000 grains, originating from the Russian Federation-samples 10570, 10576, 10584, 10601, 10643, and 10679, i.e., Triticum aestivum L. 52 g in collection sample 10470, belonging to the subtype Triticum turgidum, Triticum aestivum L. var. In samples 10570 and 10576, belonging to the lutescens group, it amounted to 54.0 and 52 g, respectively. Also, 52.0 and 56.0 g in samples 10584 and 10601, belonging to the Erythrospermum group, Triticum aestivum ssp. Compactum and Triticum aestivum ssp. It was found that samples 10643 and 10679, belonging to the Aestivum group, weighed 54.0 and 52.0 g, respectively.

The results obtained show that, when determining the 1,000-kernel weight in the wheat samples studied, a significant difference was observed between genotypes. This parameter is an important criterion in the selection process as one of the factors reflecting grain size, fullness, and yield.

High results were obtained among samples belonging to IKARDA sources. In particular, Triticum aestivum subsp. aestivum (sample 10322) showed 54.0 g, while Triticum turgidum subsp. aestivum (sample 10440) recorded 52.0 g. These genotypes are characterized by larger grains and high yield potential.

High values were also observed in collection samples brought from the Russian Federation. Specifically, Triticum aestivum var. lutescens (10570, 10576) – 54.0-52.0 g; Triticum aestivum var. erythrospermum (10584, 10601) – 52.05-6.0 g; Triticum aestivum var. milturum (10470) – 52.0 g; Triticum aestivum subsp. compactum and subsp. aestivum (10643, 10679) – 54.0-52.0 g.

In particular, the result of 56.0 g for sample 10601, belonging to the erythrospermum group, indicates that this genotype is the most promising source of large grain size.

The 1,000-kernel weight of the selected wheat samples ranged from 46.0 to 56.0 g, with an average of 50.7 g. The coefficient of variation was low (CV = 6.1%), indicating high stability of this trait. The highest values were recorded in samples 10601 (56.0 g), 10322, 10570, and 10643 (54.0 g). These genotypes significantly exceeded the population averages and can be considered promising donors for improving grain size and potential yield. Most samples (70%) exhibited medium to high grain weight, confirming the breeding value of the collection.

The results confirm the presence of genetic diversity within the collection. The use of large-grained samples as donors in the breeding process enables the development of new high-yielding varieties.

Conclusion. In general, samples with a 1,000-grain weight of 46 g or higher are recommended for use in breeding programs as valuable donors for developing varieties with large grains, high yields, and an intensive growth habit. The lutescens, erythrospermum, and aestivum groups are particularly effective breeding materials.

In short, high-yielding samples from the genetic resources of IKARDA and Russia, used as parental forms in the hybridization process, represent important breeding material for creating new varieties characterized by high yield, large grain size, and adaptability to climatic conditions.

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БИДАЙДЫҢ (TRITICUM AESTIVUM L.) ГЕНЕТИКАЛЫҚ РЕСУРСТАРЫНЫҢ МОРФОБИОЛОГИЯЛЫҚ ЕРЕКШЕЛІКТЕРІ ЖӘНЕ ОЛАРДЫҢ СЕЛЕКЦИЯЛЫҚ МАҢЫЗЫ

Аннотация. Бұл ғылыми мақалада бидайдың (Triticum aestivum L.) генетикалық ресурстарының морфобиологиялық ерекшеліктері мен олардың селекциялық маңызы кешенді түрде зерттелген. Зерттеу жұмыстары 2024–2025 жылдары жүргізіліп, әртүрлі географиялық аймақтардан (Орталық Азия, Ресей, Африка, Америка және Азия елдері) алынған 384 коллекциялық үлгі қамтылды. Үлгілердің фенологиялық даму кезеңдері (көктеу, масақтану, пісу), өсімдік биіктігі, масақ құрылымы, сондай-ақ 1000 дәннің массасы сияқты негізгі шаруашылыққа құнды белгілері жан-жақты талданды. Зерттеу нәтижелері генотиптер арасында айқын фенотиптік әртүрліліктің бар екенін көрсетті. 1000 дәннің массасы 46–56 г аралығында өзгеріп, орташа көрсеткіш 50,7 г құрады, бұл белгінің тұрақтылығы жоғары екенін дәлелдейді. Сонымен қатар, сары тат ауруына төзімділік деңгейі бойынша үлгілер арасында елеулі айырмашылықтар анықталып, кейбір генотиптердің жоғары төзімділігі белгіленді. Бұл олардың селекцияда құнды донор бола алатынын көрсетеді. Ең перспективалы нәтижелер Lutescens, Erythrospermum және Aestivum топтарына жататын үлгілерден байқалды. Аталған үлгілер ірі дәнділігімен, жоғары өнімділігімен және қоршаған орта жағдайларына бейімділігімен ерекшеленеді. Зерттеу қорытындылары бидай генофондын тиімді пайдалану, генетикалық әртүрлілікті сақтау және климаттың өзгеру жағдайында жоғары өнімді, стресс-факторларға төзімді жаңа сорттарды шығару үшін маңызды ғылыми және практикалық негіз болып табылады.
Түйін сөздер: генетикалық ресурстар, бидай (Triticum aestivum L.), генофонд, генотип, морфобиологиялық ерекшеліктері, селекциясы, масақ құрылымы, дәні, 1000 дән салмағы, фенологиялық көрсеткіштері.

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МОРФОБИОЛОГИЧЕСКИЕ ОСОБЕННОСТИ ГЕНЕТИЧЕСКИХ РЕСУРСОВ ПШЕНИЦЫ (TRITICUM AESTIVUM L.) И ИХ СЕЛЕКЦИОННОЕ ЗНАЧЕНИЕ

Аннотация. В данной статье комплексно исследованы морфобиологические особенности генетических ресурсов пшеницы (Triticum aestivum L.) и их селекционное значение. Исследования проводились в 2024–2025 годах и охватывали 384 коллекционных образца, полученных из различных географических регионов (Центральная Азия, Россия, Африка, Америка и страны Азии). Были всесторонне проанализированы основные хозяйственно ценные признаки, такие как фенологические фазы развития (всходы, колошение, созревание), высота растений, структура колоса, а также масса 1000 зерен. Результаты исследования показали наличие выраженного фенотипического разнообразия между генотипами. Масса 1000 зерен варьировала в пределах 46–56 г, при среднем значении 50,7 г, что свидетельствует о высокой стабильности данного признака. Кроме того, выявлены существенные различия между образцами по степени устойчивости к желтой ржавчине, при этом некоторые генотипы продемонстрировали высокую устойчивость, что позволяет рассматривать их в качестве ценных доноров в селекционном процессе. Наиболее перспективные результаты были получены у образцов, относящихся к группам Lutescens, Erythrospermum и Aestivum. Данные образцы характеризуются крупным зерном, высокой урожайностью и адаптивностью к условиям окружающей среды. Полученные результаты являются важной научной и практической основой для эффективного использования генофонда пшеницы, сохранения генетического разнообразия и создания новых высокопродуктивных сортов, устойчивых к стрессовым факторам в условиях изменения климата.

Ключевые слова: генетические ресурсы, пшеница (Triticum aestivum L.), генофонд, генотип, морфобиологические особенности, селекция, структура колоса, зерно, масса 1000 зёрен, фенологические показатели.

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