Received: 04.02.2026 | Revision: 17.02.2026 | Accepted: 18.02.2026 | Published: 25.06.2026

Agriculture. Plant growing

doi: 10.31210/spi2026.29.01.07
UDC 635.615:631.527
ORIGINAL ARTICLE

Scientific Progress & Innovations
ISSN: 2786-8842 (Print)
2786-8850 (Online)

29 (1)
2026

Hermoplasma of common watermelon ((*Citrullus lanatus* (Thumb.) Matsum. et Nakai) in Ukraine as the basis for the selection of new varieties and hybrids

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Article info

Citation: Shabetia, O., & Serhiienko, M. (2026). Hermoplasma of common watermelon ((*Citrullus lanatus* (Thumb.) Matsum. et Nakai) in Ukraine as the basis for the selection of new varieties and hybrids. *Scientific Progress & Innovations*, 29(1), 43–48. doi: 10.31210/spi2026.29.01.07

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This article summarizes current global approaches to the use of watermelon germplasm and analyzes the potential of Ukrainian genetic resources for breeding new varieties and hybrids. The study utilized the gene pool of common watermelon (*Citrullus lanatus* (Thumb.) Matsum. et Nakai) available at the Institute of Vegetable and Melon Growing of the National Academy of Agrarian Sciences of Ukraine. Screening (2023–2025) of 24 homozygous watermelon lines was conducted for phenological, morphological, and economically valuable traits; the data obtained were included in the analysis of the gene pool. Based on the results of the analysis, a description of the general watermelon germplasm population was provided, and the role and significance of Ukrainian collection samples in modern breeding programs were determined. The Ukrainian watermelon gene pool is represented by 645 watermelon samples of various geographical origins. Samples with a monoecious type of female flowers account for 46 %. Based on the results of the phenological study, the general population was divided into maturity groups: early-maturing – 64 %, mid-early – 19 %, mid-maturing – 14 %, and mid-late – 3 %. Twenty-four samples were identified as having the shortest duration of the period from mass emergence to physiological maturity (56–60 days). Yields of samples from the general population of the watermelon gene pool ranged from 5.1 to 74.2 t/ha (*Am* = 69.1), with an average of 29.2 t/ha. Sources were identified that significantly exceeded the standard by 5 to 42% in terms of yield, with yields ranging from 41.1 to 74.2 t/ha. This includes 34 samples. The level of the "marketability" trait ranged from 44 to 100 % (*Am* = 56), with an average trait value in the general population of 94 %. The level of expression of the "average marketable fruit weight" trait in the general population ranged from 2.0 to 6.5 kg (*Am* = 4.4), with an average trait value in the general population of 3.2 kg. Watermelon germplasm is a key factor in the successful breeding of new varieties and hybrids. Ukrainian watermelon genetic resources have high breeding value and can play an important role in the creation of adapted, productive, and competitive varieties and hybrids. Research on the comprehensive evaluation and selection of watermelon breeding material has allowed for the identification of genotypes that correspond to the modeled traits, and their inclusion in the breeding process to create varieties and hybrids with high adaptability will increase the efficiency of breeding efforts, thereby contributing to ensuring food security in Ukraine.

Keywords: watermelon, germplasm, gene pool, selection, morphological traits, biological traits, valuable economic traits.

Гермоплазма кавуна звичайного ((*Citrullus lanatus* (Thumb.) Matsum. et Nakai) в Україні як основа селекції нових сортів і гібридів

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У статті узагальнено сучасні світові підходи до використання гермоплазми кавуна та надано аналіз потенціалу українських генетичних ресурсів для селекції нових сортів і гібридів. Об'єктом слугував генофонд кавуна звичайного (*Citrullus lanatus* (Thumb.) Matsum. et Nakai), наявний в Інституті овочівництва і баштанництва НААН. Проведено скринінг (2023–2025 рр) 24 гомозиготних ліній кавуна за фенологічними, морфологічними, господарсько-цінними ознаками, отримані дані включені для аналізу генофонду. За результатами узагальнення надана характеристика генеральної сукупності гермоплазми кавуна, визначено місце та значення українських колекційних зразків у сучасних селекційних програмах. Український генофонд кавуна представлений 645 зразками кавуна різного географічного походження. Зразків, що мають моноеційний тип жіночих квіток складають 46 %. За результатами фенологічного дослідження генеральна сукупність розподілена на групи стиглості: ранньостиглі – 64 %, середньоранні – 19 %, середньостиглі – 14 %, середньопізні – 3 %. З найкоротшою тривалістю періоду від масових сходів до фізіологічної стиглості (56–60 діб) були виділені 24 зразки. Урожайність зразків генеральної сукупності генофонду кавуна варіювала в межах 5,1…74,2 т/га (*Am* = 69,1) при середній 29,2 т/га. Визначено джерела, які за урожайністю достовірно перевищували стандарт від 5 до 42 % урожайність яких становила 41,1…74,2 т/га. Це 34 зразки. Рівень ознаки „товарність" мав значення від 44 до 100 % (*Am* = 56), при середньому значенні ознаки у генеральній сукупності 94 %. Рівень прояву ознаки „середня маса товарного плоду" генеральної сукупності мав значення від 2,0 до 6,5 кг (*Am* = 4,4), при середньому значенні ознаки у генеральній сукупності 3,2 кг. Гермоплазма кавуна є ключовим чинником успішної селекції нових сортів і гібридів. Українські генетичні ресурси кавуна мають високу селекційну цінність і можуть відігравати важливу роль у створенні адаптованих, продуктивних і конкурентоспроможних сортів і гібридів. Дослідження з комплексної оцінки і добору вихідного матеріалу кавуна дозволили виділити генотипи які відповідають модельованим ознакам, а залучення їх у селекційний процес зі створення сортів та гібридів з високою адаптивною здатністю дозволить підвищити ефективність селекційної роботи що сприятиме забезпеченню продовольчої безпеки України.

Ключові слова: кавун, гермоплазма, генофонд, селекція, морфологічні ознаки, біологічні ознаки, цінні господарські ознаки.

Бібліографічний опис для цитування: *Шабетя О. М., Сергієнко М. Б.* Гермоплазма кавуна звичайного ((*Citrullus lanatus* (Thumb.) Matsum. et Nakai) в Україні як основа селекції нових сортів і гібридів. *Scientific Progress & Innovations*. 2026. № 29 (1). С. 43–48.

Introduction

Watermelon (*Citrullus lanatus* (Thunb.) Matsum. et Nakai) is one of the leading melon crops in the world and is of great economic importance for Ukraine. In the context of climate change, growing market demands for product quality, and the need to increase the resistance of varieties to abiotic and biotic factors, the use of a diverse genetic base in breeding programs is becoming particularly relevant. The germplasm of watermelon – the totality of the genetic resources of the crop – is the strategic basis for creating new varieties and hybrids with specified economically valuable traits. The most valuable source of starting material for heterotic breeding is and remains the global gene pool of watermelon collections. Ukrainian researchers [1, 2] believe that studying the global genetic potential of watermelon using a comprehensive approach to identifying stable sources of breeding traits can significantly increase the effectiveness of heterosis breeding of this crop.

Africa is considered to be the center of origin of watermelon, where the greatest diversity of wild forms of the *Citrullus* genus is concentrated. The world germplasm includes wild species, semi-wild forms, local populations (landraces), old varieties, and modern breeding lines. Wild and primitive forms are of particular value as they are sources of resistance to drought, high temperatures, soil salinity, and disease pathogens. The common watermelon (*Citrullus lanatus* (Thunb.) Matsum. et Nakai) is a well-studied crop species that is interesting for genetic research due to its small genome size and many available mutants. The size of the watermelon genome is 424 million base pairs. Sixty genes have been identified in watermelon that control morphological traits and resistance. Genes for the following morphological and physiological traits: fruit – 19 genes, leaf – 8, flower – 1, seed – 9, stem – 1, plant habit – 4, as well as genes that determine sex expression – 2, male sterility – 5, resistance to biotic factors – 10, resistance to abiotic factors – 1 [3, 4].

In terms of watermelon breeding, according to Sych [5], the problem of insufficient realization of yield potential to provide valuable vitamin products remains relevant. This problem can be solved by creating new competitive heterozygous hybrids with a complex of valuable economic traits using the existing germplasm of this crop.

Leading breeding centers around the world (the USA, China, Japan, Spain, Turkey) actively use watermelon germplasm to create hybrids with higher yields, improved taste, and longer shelf life. Considerable attention is paid to the involvement of wild species as donors of genes resistant to biotic factors [6]. In modern breeding, marker-assisted selection and genomic analysis methods are widely used, which allows for more efficient use of global germplasm collections [7].

The main areas of application for watermelon germplasm are the selection of sources of early maturity, high sugar content, intense flesh coloration, and resistance to major diseases and stress factors [8]. The combination of Ukrainian adapted forms with foreign high-yielding lines opens up wide opportunities for the creation of a new generation of hybrids.

In the State Register of Plant Varieties Suitable for Distribution in Ukraine, the foreign watermelon market is represented by watermelon hybrids by 50 % [9]. The world leader in the creation of heterozygous watermelon hybrids is the Dutch company “Nuemens Zaden”, which annually offers new competitive hybrids, such as: Krisbi, Trofi, Ledi Dumara, Red Komet, Red Star, Dzhonik, and others. The transnational company Seminis is also actively working in this direction, having created the hybrids Krimson Hlori, Madera, Pata nehra, Roial medzhesti, Roial Svit, Red Svit, and others. Breeders in Hungary, China, Japan, and the United States are working intensively on the creation of heterozygous watermelon hybrids [10].

The country's wealth and national heritage include valuable genetic resources, thanks to which we are able to compete with foreign breeding organizations in creating new varieties and hybrids of agricultural crops. As is well known, the global gene pool of watermelon collections is the most valuable source for creating new high-yielding genotypes that combine resistance to biotic and abiotic environmental factors with other economically valuable traits. Studying the global genetic potential of watermelon using a comprehensive approach to identifying stable sources of various traits, incorporating them into hybridization, and then using analytical breeding methods allows us to create diverse source material and use it effectively in varietal and heterosis breeding of this crop [11, 12]. The growing popularity of melons and gourds in private farms has stimulated increased demand for early-maturing heterozygous hybrids, which are characterized by high yields, excellent fruit quality, simultaneous ripening, and attractive appearance. Consumers want new, earlier maturing, and cold-resistant hybrids that not only have excellent taste properties but also a long shelf life and disease resistance. The effectiveness of commercial hybrid breeding largely depends on the availability of diverse source material, which allows for a rapid response to changes in the market situation. Hybrids play a key role in increasing yields, as they combine valuable economic traits and ensure the scientific novelty of breeding developments. Hybrid breeding promotes active interaction between seed producers and breeders, which has a positive impact on the improvement of cultivation technologies and the dissemination of the latest domestic varieties in farms of various forms of ownership [13].

That is why the research was aimed at a comprehensive assessment of the watermelon gene pool, analysis of the potential of Ukrainian genetic resources, and selection of source material for breeding new varieties and hybrids.

The aim of the study

To summarize current global approaches to the use of watermelon germplasm and analyze the potential of Ukrainian genetic resources for breeding new varieties and hybrids.

Materials and methods

Methods: general scientific, measurement and weighing, calculation, statistical. Screening of 24 homozygous lines of common watermelon (*Citrullus *lanatus* (Thumb.) Matsum. et Nakai) was carried out for phenological, morphological, economically valuable traits and resistance of lines to abiotic and biotic factors. The data obtained were included for analysis of the watermelon gene pool. Experimental studies were conducted on the experimental fields of the breeding crop rotation of the Institute of Vegetable and Melon Growing of the National Academy of Agrarian Sciences of Ukraine, located in the Left-Bank Forest-Steppe of Ukraine in the central moderately humid region of the Kharkiv district, Kharkiv region. The climate of the research area is temperate continental. The experiments were conducted in open ground under natural infectious conditions. The object of the research was collection samples of the gene pool of common watermelon (*Citrullus lanatus* (Thumb.) Matsum. et Nakai). The area of the plot was 19.6 m^2. The experiment was repeated twice. A comprehensive assessment of the samples was carried out according to phenological, morphological, economically valuable characteristics, and resistance to abiotic and biotic factors. The research was conducted in accordance with generally accepted methods [14–17]. Statistical processing of the research results was performed using statistical methods in biology [18]. The mathematical processing of the obtained research results was carried out using the Statistica 6 program. The watermelon cultivation technology corresponded to the generally accepted technologies for this soil and climatic zone [15, 19].

Results and discussion

Research work on the formation of the gene pool of common watermelon began in 2007. Every year, new introduced samples were screened to form the gene pool and to identify sources of valuable traits of common watermelon (*Citrullus lanatus* (Thumb.) Matsum. et Nakai) based on phenological, morphological, economically valuable traits, and resistance to abiotic and biotic factors. Based on the results of many years of research, a comprehensive assessment of 645 watermelon samples was carried out, including 24 new lines created at the IOB NAAS in 2023–2025. The data obtained were included in the analysis of the watermelon gene pool. The Ukrainian watermelon gene pool is represented by samples of various geographical origins: Ukraine, Japan, China, Korea, Poland, the Czech Republic, the Netherlands, France, the USA, Mongolia, and Romania. The samples were evaluated according to a number of valuable breeding characteristics: sex type, ripeness group, yield components, resistance to biotic and abiotic factors, and fruit quality.

A significant number of samples have a common valuable trait for creating female lines for heterosis breeding – monoecious female flowers (46 %). Based on the results of their study, a number of samples with high indicators and other economically valuable characteristics were selected: De la Reina, Kyt 100326, Kyt 100322, Kyt 10061, LMS 1 Pr, Kyt 10080, Slavutych, Yuzh, Dub, Kyt 100324, Kyt 100327, Line 39, Misiats i zirky, Kodata cream, Nishiki jamato, Chumak, Klen, Mistsevyi Khakasiia, Leshchyna, Wm 14 D 1/1, Wm 16 D 2, Wm 18 D 4, Wm 19 D 5, Wm 20 D 6, K 104135, Dub, Form 4, Form 4 ts, Uslad, Semik, No. 5 F, Pershyi, K 104916, k 107633a, Symaryn, Klonoline.

To determine the duration of the growing season, watermelon samples were divided into maturity groups: early maturing (up to 80 days) – 64 %; medium early (81–85 days) – 19 %; medium maturing (86–95 days) – 14 %; mid-late (96–105 days) – 3 %; and late-ripening (more than 105 days) – 0 %. ***Figure 1*** shows the distribution of the general population of watermelon samples by ripeness groups.

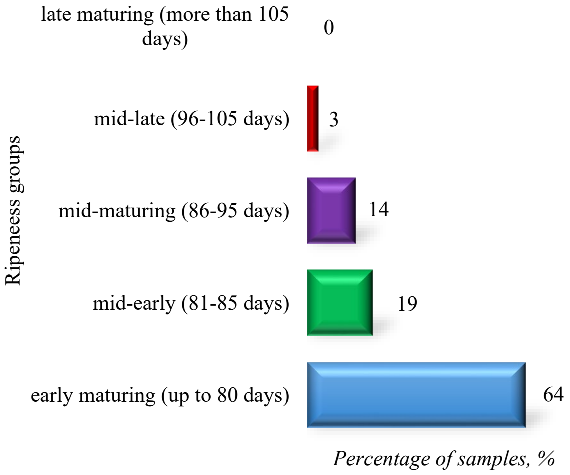

Fig. 1. Distribution of watermelon samples by ripeness groups (average for three years of study for each sample), 2007–2025

A significant number of samples studied belong to the early maturity group. Early samples were selected for early ripening, which during the three-year study consistently had a “germination-ripening” period of less than 60 days: KS 9333 (52 days), Kyt 100329/00 (54 days), Kyt 100329/97, Kyt 100329/98, Kyt 100329/99, Kyt 100329/01, Kyt 10080/11, Kyt 103328/30, Kyt 103328/33, LMS/1 pr, Kyt 100659/97, Ledy 104447, Kyt 100328/32, L Slava, Kyt K 104992, Kyt 10061/08, K 100327/29, 105026/26 (55 days); Kyt 10061/10, Kyt 100326/23, (58 days). To confirm the statistical dependence of the “length of the growing season” trait on environmental factors, the sample was ranked according to the “length of the sprouting-maturation period” trait. The calculated Spearman's rank correlation coefficient was $\rho = 0.69$, which, according to the Chaddock scale, indicates a significant correlation. Samples with the shortest individual interphase periods were also selected, which are suitable for use in obtaining maternal or paternal lines in the selection process when creating early-maturing heterozygous hybrids.

In 2023–2025, 24 new homozygous watermelon lines were comprehensively evaluated and included in the general watermelon gene pool. Based on the results of phenological studies, the samples were divided into groups according to ripeness: early ripening – 12 samples, medium early ripening – 8 samples, medium ripening – 4 samples. The most numerous group was the early ripening samples – 50 %. The samples with the shortest period from mass germination to physiological ripeness (56–60 days) were: Shar, Skarbnytsia, Mia-19, and VO-19.

The watermelon gene pool was evaluated based on the yield of samples, with each sample undergoing a three year evaluation between 2007 and 2025.

***Figure* 2** shows the distribution of watermelon samples by yield into three groups according to the mean value of the trait and its standard deviation separately for each year of the study.

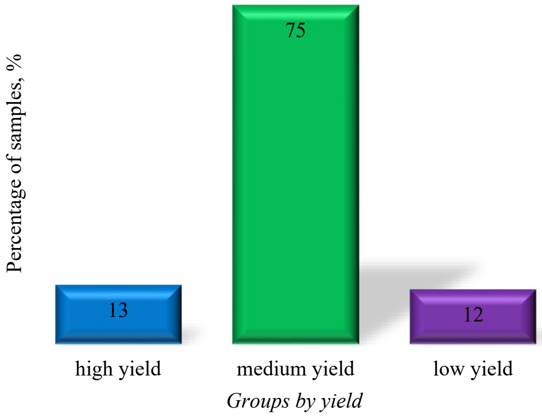

Fig. 2. Distribution of watermelon gene pool samples by yield, 2007–2025

Note: Groups 1-3 by yield: 1 – high yield; 2 – medium yield; 3 – low yield

The yield of samples from the general population of the watermelon gene pool varied between 5.1 and 74.2 t/ha (Am = 69.1) with an average of 29.2 t/ha. Sources that significantly exceeded the standard by 5 to 42 % in terms of yield were identified: Kyt 10061, Lms 1Pr, Leshchyna, Chumak, Kyt 10080, Yuzh, Dub, Krymson svyt, Charly, Asar, Liniia 46, Misiats i zirky, Monholiia, Line 39, Monholiia 2, Sample from China, No. 5F, No. 543, Semik, Lad, A-14 Tur, Yatum 2, Yatum, Lypa, Yasen, LS-1665F1, Tsilnolystnyi, Mak), Zoria, Ket Br-19, Rada and No. 5 F, with yields ranging from 36.6 to 74.2 t/ha.

The total yield of samples evaluated in 2023–2025 and included in the watermelon gene pool varied between 16.6–62.4 t/ha in 2023; 18.9–40.8 in 2024; and 16.1–29.9 in 2025 (***Table 1***).

The level of the “marketability” trait ranged from 44 to 100 % (Am = 56), with an average value of 94 % in the general population. The level of the “marketability” trait in samples evaluated in 2023–2025 ranged from 94.1 to 98.2 %. The following samples had a marketability level of 100 % during the three-year trial: Lms 1Pr, ShRB 2, Slavutych, Yuzh, Dub, Charly, Misiats i zirky, Monholiia, Konho, and Suika Swet, which were identified as sources of high marketability.

The level of manifestation of the trait “average weight of marketable fruit” in the general population ranged from 2.0 to 6.5 kg (Am = 4.4), with an average value of 3.2 kg in the general population. The sources were determined by large fruit size – samples with an average fruit weight of 3.2 to 6.2 kg: Line 39 (6.2 kg), Misiats i zirky (4.6 kg), Charly (4.5 kg), Chumak L (4.2 kg), Line No. 46 (4.0 kg), Asar (4.1 kg), Zhyzel (3.5 kg), Yasen (3.6 kg), Yuzh and Dub (3.8 kg), Sample from China (3.3 kg), Konho, De la Reina, and Monholiia 2 (3.2 kg). In studies conducted in 2023–2025, the average weight of marketable fruit from collection samples ranged from 1.5 to 6.5 kg. The average weight of marketable fruit of the Maks Plius standard was 3.3 kg. The highest average weight of marketable fruit over the three years of research was recorded for the following samples: LP-19 – 4.3 kg and Zorya 3.5 kg.

Table 1

Characteristics of samples evaluated in 2023–2025 and included in the watermelon gene pool, by yield components

Catalog No. Description	Linear output material	Total yield, t/ha				Marketability, %	Average weight of marketable fruit, kg			
		2023	2024	2025	average		2023	2024	2025	average
DN	Maks Plius st	40.6	35.7	26.8	34.4	96.5	3.3	3.7	2.8	3,3
109508	Mak	55.1	26.5	22.5	34.7	95.8	3.9	3.4	2.6	3,3
109511	Shar	33.0	28.6	21.5	27.7	95.2	2.7	2.0	1.5	2,1
109450	Bor	34.9	23.5	18.8	25.7	96.4	2.8	2.3	1.7	2,3
109502	Lypa	41.6	24.5	20.8	29.0	97.5	3.5	3.2	2.4	3,0
109512	Metiu	27.6	27.7	20.7	25.3	94.4	2.6	3.0	2.3	2,6
107631	Rada	36.5	41.8	31.4	36.6	96.5	3.2	2.8	2.1	2,7
107717	Skarbnytsia	31.6	30.6	23.0	28.4	96.8	3.2	2.3	1.7	2,4
106779	Zoria	53.3	34.7	26.0	38.0	97.6	3.5	4.0	3.0	3,5
107630	Ket Br -19	53.8	39.8	29.9	41.2	96.7	3.2	3.7	2.8	3,2
109505	Leshyna	24.2	20.4	15.3	20.0	94.7	2.3	2.2	1.7	2,1
104944	ChB -19	43.1	18.9	16.1	26.0	95.9	2.7	2.3	1.7	2,2
105465	Miia-19	36.2	28.6	21.5	28.8	97.2	2.5	2.0	1.5	2,0
105454	VO -19	32.1	36.7	27.5	32.1	97.6	2.6	2.3	1.7	2,2
104315	GA -48-19	44.9	27.6	20.7	31.1	95.5	2.9	2.8	2.1	2,6
104946	D56B-19	46.0	33.7	25.3	35.0	98.2	3.1	3.2	2.4	2,9
104927	Kira	30.1	22.4	20.2	24.2	96.6	2.7	2.7	2.0	2,5
107935 a	Sich	47.3	32.7	27.8	35.9	97.8	3.1	3.4	2.6	3,0
106033	LPB 44-19	34.7	35.7	27.5	32.6	97.1	2.8	3.0	2.3	2,7
104907	Fantaziia	31.1	27.6	20.7	26.5	95.9	3.3	2.8	2.1	2,7
104752	YuZh	16.6	23.5	20.0	20.0	96.9	2.3	2.4	1.8	2,2
104134	Taniusha	31.9	29.6	22.2	27.9	96.0	2.7	2.3	1.7	2,2
104072	Lenok	21.6	20.4	18.4	20.1	94.1	2.3	2.0	1.5	1,9
107636	LP-19	32.4	22.4	17.9	24.2	94.5	2.6	6.5	3.9	4,3
107935	No. 5F	62.4	30.6	26.0	40.0	98.2	3.6	3.6	2.7	3,3
	Lim	16,6-62,4	18.9-40.8	16.1-29.9	20.0-41.2	94.1-98.2	2.3-3.9	2.0-6.5	1.5-3.9	1.9-4.3
	Am	45,8	21.9	13.8	21.2	4.1	1.6	4.5	2.4	2.4

The level of solar insolation during fruit formation determined the dry soluble matter content in watermelon samples and ranged from 5.0 to 12.0 %. The proportion of samples with dry soluble matter content in fruits ranging from 8.0 to 13.0 % was 75 %. Based on the dry soluble matter content in the fruit, the samples were divided into three groups: low dry soluble matter content (<8.0 %) – 25 %; medium (8.0–10.0 %) – 52 %; and high (>10.0 %) – 23 %.

The sources with the highest dry soluble matter content in fruits have been identified: Klon and Yemen (13.0 %), Maks Plius (12.0 %), Chumak, Kyt 10080, GA-48, Dub, Zhyzel, Charly (11.0 %); Kyt 10059, Misiats i zirky, Yasen, Krymson svyt, Hrybovskyi, Kyt 10061, and Leshchyna (10.0 %).

The results of the research have determined the genotypic diversity according to valuable selection traits: the duration of the growing season, the components of its interphase periods, the components of yield, and the chemical composition of the fruit. About 400 sources of valuable breeding traits have been identified: yield, early maturity, high marketability, monoecy, and high fruit quality. The identified sources of valuable economic traits have been included in breeding programs to create new genotypes with specified parameters.

Ukraine has developed a unique watermelon gene pool, which includes local varieties, breeding lines, and introduced material of various ecological and geographical origins. Domestic germplasm is characterized by high adaptability to the conditions of the Steppe and Forest-Steppe, drought resistance, and the ability to form stable yields under limited moisture conditions. Ukrainian samples are a valuable source material for the creation of competitive varieties and hybrids aimed at both domestic and foreign markets. Recently, significant progress has been made in the development of breeding in Ukraine in the creation of high-yielding varieties and hybrids of watermelon. Research by leading scientists in the field of special genetics, biotechnology, and heterosis genetics is of great importance for the development of a modern theoretical basis for varietal and heterotic watermelon breeding and its practical application for the creation of competitive varieties and hybrids that would be widespread in production [20].

Serhiienkoet al. [21] pay much attention to the development of a theory of selection of parental components for hybridization, criteria for evaluating breeding material and its selection, methods of genetic control of breeding traits and their inheritance and resistance to biotic and abiotic factors. Lymar et al., [17] noted the importance and peculiarities of heterotic selection of watermelon in the breeding process with melon crops using morphologically identified source forms as parental components of heterotic F_1 hybrids.

Global experience in watermelon breeding shows that the key factor in creating competitive varieties and hybrids is the widespread use of genetic resources of different ecological and geographical origins. In the US and China, considerable attention is paid to pre-breeding programs using wild relatives *Citrullus amarus*, *C. colocynthis*, and local landraces as donors of genes for resistance to fusarium wilt, anthracnose, viruses, and abiotic stresses [22]. In EU countries (Spain, Italy, France), germplasm is actively used to improve fruit quality, transportability, and suitability for long-term storage [23].

Modern breeding programs increasingly combine classical hybridization methods with molecular genetic approaches, including marker-assisted selection (MAS), SNP-based genotyping, and genomic studies of germplasm collections. This makes it possible to identify valuable alleles and integrate them more effectively into the breeding process. Against this backdrop, Ukrainian watermelon germplasm, formed in the arid climate of the south, has high potential as a source of adaptability and yield stability.

Accelerating the breeding process remains extremely relevant today. To this end, it is necessary to use existing methods, improve them, and develop new effective methods for evaluating and accelerating the creation and selection of source material at various stages of breeding work [12]. It is particularly important to emphasize the practical significance of national genetic resources. Their targeted use, combined with global achievements in breeding science, can become the basis for the creation of domestic watermelon hybrids that are competitive on the international market.

Conclusions

Watermelon germplasm is a key factor in the successful breeding of new varieties and hybrids. Ukrainian watermelon genetic resources have high breeding value and can play an important role in the creation of adapted, productive, and competitive varieties in combination with global achievements in breeding science. Research on the comprehensive assessment and selection of watermelon source material has made it possible to identify genotypes that correspond to the modeled traits, and their involvement in the breeding process to create varieties and hybrids with high adaptive capacity will increase the effectiveness of breeding work, which will contribute to ensuring food security in Ukraine.

DECLARATIONS

Ethical Statement

Not applicable.

Funding

This research received no external funding.

Conflict of interest

The authors state that there is no conflict of interest.

Acknowledgements

None.

Declaration of AI and AI-assisted technologies

The authors declare that no artificial intelligence or AI-assisted technologies were used in the preparation of this manuscript.

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