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**Evaluation of durum wheat of the KASIB network (Kazakhstan - Siberia) and
identification of genes influencing economically valuable traits**

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NORMATIVE REFERENCES

This dissertation uses references to the following standards:

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GOST 2.105-95 Unified system of design documentation. General requirements for text documents.

GOST 2.11 – 68 Unified system of design documentation. Standard control.

GOST 6.38 – 90 Unified documentation systems. System of organizational and administrative documentation. Documentation requirements.

GOST 7.32-2001 Interstate standard. Report on scientific research work. Structure and design rules.

GOST 2003 Bibliographic record. Bibliographic description. General requirements and drafting rules.

Rules for conducting variety testing of agricultural plants Order of the Minister of Agriculture of the Republic of Kazakhstan dated July 2, 2015 No. 4-2/602 No. 11879

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Law of the Republic of Kazakhstan “On Grain” dated January 19, 2001 No. 143-II

Law of the Republic of Kazakhstan “On Science” dated February 18, 2011 No. 407-IV.

State register of breeding achievements recommended for use in the Republic of Kazakhstan, and the List of promising varieties of agricultural plants. Order of the Minister of Agriculture of the Republic of Kazakhstan dated July 30, 2009 No. 434. Registered with the Ministry of Justice of the Republic of Kazakhstan on August 28, 2009 No. 5759

DEFINITIONS

A **bi-plot** (or density histogram) is a graphical representation of the probability distribution of a continuous random variable. It is constructed by dividing the range of values of a variable into equal intervals and counting the number of observations that fall within each interval. Each interval is then represented as a column whose height corresponds to the number of observations in the interval.

A **cluster** is a group of objects that have similar characteristics or properties and can be grouped together based on certain criteria.

Adaptability is the ability of plants to adapt to changing environmental conditions and survive in them.

A **gene** is a structural and functional unit of heredity that controls the development of a specific trait or properties.

A **marker** is any genetic or phenotypic trait that can be used to identify, classify, or track a specific organism or group of organisms. (e.g., nucleotide polymorphisms, microsatellites, SNPs)

A **pixel** is the smallest image element on a screen or digital image. The word "pixel" comes from the English "picture element".

A **primer** is a short, single-stranded nucleotide fragment that is used in the polymerase chain reaction (PCR) process to increase the amount of a specific piece of DNA or RNA.

Art. (St) – standard, the best variety released in a given zone, which is included in all types of variety testing or experiments as a standard.

A **subpopulation** is a group of individuals within the general population that differ in some way, such as genetic makeup, behavior, or physiology.

A **variety** is a group of cultivated plants obtained as a result of selection within the lowest known botanical taxon and possessing a certain set of characteristics (useful or ornamental) that distinguishes this group of plants from other plants of the same species.

Coefficient of Variation (CV) is the ratio of the standard deviation to the mean, expressed as a percentage. It is used to measure the degree of variability (variation) in data.

Correlation is a statistical measure that describes the degree of relationship between two variables. It shows how strongly and in what direction two variables are related to each other.

Genetic distance is a measure of the difference between the genetic compositions of two populations or species based on genetic markers.

Genetic diversity is the difference in genotypes (sets of genes) between individuals of the same species.

Genomics is the broad study of genomes, that is, the complete set of genes (and their interactions) in an organism or virus, a discipline of science that includes the study of the structure, function, evolution and regulation of genomes.

Genotype is the totality of all the genes of an organism localized in chromosomes, its hereditary material basis. The genotype determines the norm of the

body's reaction in changing environmental conditions, based on interaction with the latter, forming the phenotype of the individual.

High-throughput phenotyping is the process of assessing and characterizing an organism's phenotypic properties (such as morphological, physiological, biochemical and behavioral) with high accuracy using modern technologies and methods.

Molecular markers are a type of marker that is based on the analysis of DNA or RNA molecules. They are used to identify and distinguish genetic differences between organisms or populations.

Originator - the person or organization that originally created the intellectual property - the variety

Plant biomass is the total mass of organic matter contained in plants. It is measured in units of mass (e.g., grams, tons), and can be measured for the entire plant, individual parts (e.g., stem, leaves, roots, flowers), or for a specific part of the plant.

Plasticity is the ability of a population inhabiting a certain area to form new combinations with a certain frequency.

Polymerase chain reaction (PCR) is a method of molecular biology that allows you to achieve a significant increase in small concentrations of certain nucleic acid fragments (DNA or RNA) in biological material (sample).

Population - a collection of individuals of a certain plant species, freely interbreeding with each other, inhabiting a certain territory and in some way isolated from the neighboring population;

Phenomics is a branch of biology and science that studies phenotypes, i.e., observable characteristics and properties of organisms, including their form, structure, function and behavior. Phenotypes can be related to genotypes (genetic information), environment, and their interactions. Phenomics studies how genes and environment influence the formation of organisms' phenotypes.

Phenological observation (phenotyping) is the process of measuring and analyzing the physical and biochemical traits of a plant.

Retrotransposons, or mobile genetic elements of the first type, consist of two subtypes - retrotransposons with long terminal repeats (LTR, long terminal repeats), and retrotransposons without long terminal repeats.

RGB imaging is a technique that uses digital cameras to capture images of plants.

Selection is the science of methods for creating and improving animal breeds, plant varieties, and strains of microorganisms. Selection is also the name given to the branch of agriculture that deals with the development of new varieties and hybrids of crops and animal breeds.

Standard Error of the Mean (SEM) is a measure of the uncertainty of the mean of a sample from a population. SEM measures how closely the sample mean represents the population mean.

The growing season is the time required for a plant to go through the full development cycle: from seed germination to harvesting.

NOTATIONS AND ABBREVIATIONS

% - percentage, SI unit of measurement

°C – degrees Celsius, unit of measurement according to the SI system

Aktobe AES – Aktobe Agricultural Experimental Station

Altai Research Institute of Agriculture (FASCA) - Altai Scientific Research Institute of Agriculture Federal Altai Scientific Center for Agrobiotechnologies.

AMOVA (Analysis of Molecular Variance) is a method for analyzing the genetic structure of populations based on molecular markers. It allows us to determine how significant genetic differences are between and within populations.

a *, **b ***, **u ***, **v *** are color coordinates in the CIELUV color model. They are used to define a color based on its brightness (**L***), hue (**a***) and saturation (**b***). **L*** represents the brightness or lightness of a color, where 0 is black and 100 is white. **a*** and **b*** define hue and saturation: **a*** represents color from green (-) to red (+), and **b*** represents color from blue (-) to yellow (+).

A ton is a metric unit of mass equal to 1000 kilograms

CIMMYT Maize Scanner is a tool developed by the International Maize and Wheat Improvement Center (CIMMYT) to quickly and accurately assess the phenotypic characteristics of maize grains.

cm - centimeter

CSI - Cereal Aging Indices

DH – number of days before heading

DHM – days from heading to maturity

DM – days to maturity, duration of the growing season

DNA - Deoxyribonucleic acid

FAO (United Nations Agricultural Organization) is an international organization created to promote food security, sustainable development and the fight against hunger in the world. She works with governments and organizations around the world to improve food production and distribution, protect biodiversity and improve the livelihoods of rural communities.

Fiji, ImageJ (formerly known as ImageJ) is an image analysis and data processing software. It is developed in Java and can run on various operating systems, including Windows, Mac OS and Linux.

g – gram unit of measurement according to the SI system

g/m² – gram per square meter, SI unit of measurement

GA, GGA, GA m², GGA - m² – green area, greener area, green area per square meter, greener area per square meter.

GenAIEx (Genetic Analysis in Excel) is a program for analyzing genetic data running in the Microsoft environment Excel. It is designed to analyze the genetic structure of populations based on molecular markers.

GD - genetic distance

Ha – hectare, SI unit of measurement

He - genetic diversity

HPT (High - throughput phenotyping) – highly efficient phenotyping

Ht - total gene diversity
I - Shannon information index
iPBS retrotransposons - binding site markers between retrotransposon-based primers
KASIB – Kazakhstan-Siberian network
KazRIAPG – Kazakh Scientific Research Institute of Agriculture and Plant Growing
Karabalyk AES – Karabalyk Agricultural Experimental Station
LLP - limited liability partnership
LSD – least significant difference
M² - square meter
MAX - maximum
Masl – meters above sea level
MCMC - Markov chain Monte Carlo algorithm
MIN - minimum
Million - million
Ne - effective number of alleles
Omsk ASC - Omsk Agrarian Scientific Center
PCA (Principal Coordinates Analysis) is a multidimensional scaling technique used to analyze multidimensional data such as genetic or environmental data. It allows you to transform multidimensional data into two- or three-dimensional space, where each point represents an object (for example, a sample), and the distance between points represents the degree of their similarity.
Pcs - pieces
PH - Plant height
PIC - Polymorphism Information Content
PopGen - program for the analysis of genetic data, designed to analyze the genetic structure of populations based on molecular markers.
R (R Studio) is a programming language and development environment for statistical processing and data visualization. It provides a wide range of functions for statistical analysis, machine learning, graphics, etc. R is free and open source and is widely used in scientific research, data analysis, and business.
RGB stands for red, green and blue, which are the primary colors of light.
Samara RIA branch of the Samara SCRAS - Samara Scientific Research Institute of Agriculture branch of the Samara Scientific Center of the Russian Academy of Sciences
Saratov RI South-East Region (FSBI "FASC of the South-East") - Saratov Scientific Research Institute of the South-East Region (FSBI "FASC of the South-East")
SPC GF named after. A.I. Barayev – Scientific Production Center Grain Farming named after A. I. Barayev
std. dev. is an abbreviation for standard deviation and is a measure of the spread of data around its mean value.
STRUCTURE is genetic data analysis software used to determine the genetic structure of populations based on molecular markers. It uses the MCMC method (Markov Chain

Monte Carlo) to estimate the likelihood of different population structures and genotypes based on molecular marker data.

Th. - thousand

TKW – Thousand (1000) kernel weight

INTRODUCTION

The relevance of research

The continuous growth of the world's population increases the need for food. Currently, the African continent faces the worst hunger, and more than 50% of the population in Asia also suffers from hunger [1]. On the other hand, climate change is also worsening the situation, negatively affecting agricultural productivity. According to Nadeem [2], there is an urgent need to increase global food production to meet the future needs of a growing population.

Durum wheat is a traditional and highly valuable crop, widely grown in Kazakhstan, a country that is one of the largest grain exporters in Central Asia [3]. Durum wheat was grown on an area of up to 3-4 million hectares at its peak in the late 1980s. Durum wheat area in Kazakhstan in 2020 was estimated at 750,000 hectares with the leading regions being North Kazakhstan (300,000 hectares), Kostanay (260,000 hectares) and Akmola (150,000 hectares). The annual production of durum wheat in Kazakhstan reaches up to 500 thousand tons of grain with exports of up to 385 thousand tons [4, 5]. The main region of durum wheat production is Northern and Western Kazakhstan. According to FAO statistics, wheat production in Kazakhstan is 1.3 tons per hectare per year [6]. Due to the above, yield stability and wide adaptation are becoming increasingly important [7].

To obtain high, stable yields, it is necessary to use highly adapted varieties to local conditions [8, 9]. To do this, it is necessary to conduct environmental tests of varieties in different regions [10]. Most varieties grown in Kazakhstan are tall, day-length sensitive material with good drought tolerance and suitable baking quality [11]. Tajibayev et. al. [12] documented that the genotype-environment interaction of Russian varieties is more widely adapted to different growing conditions, and also reported that modern breeding needs new approaches such as phenomics and genomics to improve the wheat program, since it is very important to study and understand wheat genetic diversity through pre-breeding studies.

This includes the study of the gene pool, phenomics, genomics and selection, as well as the association of necessary traits with new varieties [13]. Combining the best traits of agronomic and physiological parameters using genotyping and phenotyping methods in breeding will increase the yield of varieties [14]. In the book *Wheat Physiology*, Reynolds says that targeted research in certain regions undoubtedly increases the yield of wheat, and it also describes making various physiological observations depending on the required parameter and region for wheat improvement [15]. High-throughput phenotyping makes it possible to study complex traits such as plant growth and yield [16]. In turn, this technology allows reducing research time and labor costs while obtaining high-throughput screenings [17].

Marker-assisted selection can be used to characterize germplasm, allowing breeders to develop new genetic variations and use them to select parental lines for further crosses [18]. In plant breeding, successful crossing requires tracking of locus and genome regions; molecular and DNA markers are used for this [19]. To date, a large number of genetic markers have been developed to study many new traits of

crops. To search for the level of polymorphism, codominant DNA markers are needed, which are also highly reproducible and distributed throughout the genome, which makes it possible to study wheat DNA, as described [20]. Calendar et al [21] developed a new marker system called “interprimer binding site (iPBS)”. Due to their general applicability, ease of use, and genotype resolution systems, retrotransposon DNA markers have found widespread use in numerous evolutionary and genetic studies. The iPBS-retrotransposon amplification methodology is very practical and contains a robust DNA detection technology that does not require prior sequence information [22].

In addition to molecular characterization, using iPBS retrotransposon markers, it is possible to study the phylogenetics and evolution of various crop plants [23]. To the best of our knowledge, no studies have yet been carried out on KASIB material using iPBS retrotransposons, with the exception of [24], who used the KASIB-DW nursery and use iPBS retrotransposons in wheat breeding and biotechnology, convenient for use in varietal and intravarietal identification of wheat genotypes. This study aimed to assess the genetic diversity and population structure of durum wheat KASIB germplasm using iPBS retrotransposon markers.

Object of research: Collection of spring durum wheat from the KASIB network, more than 150 samples.

The purpose of the research: to identify genes that influence the manifestation of economically valuable traits of durum wheat in the South-East (Almaty region) and the North (Akmola region) of Kazakhstan and to develop methods for their use in the breeding process using modern genomic approaches and accurate phenotyping.

Research objectives:

1. Study of the main economically valuable characteristics of a collection of more than 150 samples of spring durum wheat KASIB in two regions of Kazakhstan (Almaty region - KazRIAPG and Akmola region SPC GF named after A.I. Baraev). Identification of promising lines/varieties of spring durum wheat for further selection and introduction into production.

2. Phenotyping KASIB-DW using digital methods in the Akmola region. Study of a new promising method of highly efficient phenotyping using a camera and the possibility of its use in breeding.

3. Genotyping KASIB-DW using known functional iPBS retrotransposon population markers to determine genetic diversity and population structure of all samples in the collection according to testing in 2021 and 2022.

Key words: Spring wheat, durum wheat, KASIB, iPBS retrotransposons, phenotyping, genotyping, RGB images.

Scientific novelty.

For the first time, genotyping and phenotyping of durum wheat varieties and lines of the Kazakhstan-Siberian Spring Wheat Improvement Network is being carried out.

Selected high-yielding lines and varieties in the Almaty and Akmola regions from the KASIB nursery will be recommended for transfer to state variety testing.

The results of digital technologies will be recommended for implementation in plant breeding.

iPBS results of retrotransposons will be used to determine genetic diversity, population structure and geographic distribution of genotypes, and effects on agronomic traits will be identified. The use of functional and new markers in the selection of breeding material will significantly increase the efficiency of selection.

Main provisions submitted for defense:

- adaptability of lines and varieties to two regions of the country.
- application of modern digital phenotyping methods.

iPBS retrotransposon genetic markers to determine the genetic population of spring durum wheat

Practical significance of the results obtained:

High-yielding and highly adaptive lines/varieties were selected for two regions of Almaty and Akmola regions. With the best growing season, with the best productivity.

The identified genetic populations are of great importance in durum wheat breeding.

These studies contribute to the transfer of varieties to the SVT by the originators of the varieties.

Relationship of this work with other research works.

The research carried out is a continuation of the Kazakhstan-Siberian network project, which began in 2000 and continues to the present day.

Approbation of work. The main results of the dissertation were reported and discussed at: meetings of the Department of Agronomy of the Kazakh National Agrarian Research University, and at the international conference:

8th International Cereal Nematodes Symposium Abant, Turkey, September 26 to 29, 2022

Publication of research results. Based on the research results, 2 articles were published in Scopus, of which: 1 article is included in the Scopus Q1 database, 1 article is included in the Scopus database Q3.

Scopus database:

Tajibayev, D.; Mukin, K.; Babkenov, A.; Chudinov, V.; Dababat, A.A.; Jiyenbayeva, K.; Kenenbayev, S.; Savin, T.; Shamanin, V.; Tagayev, K.; et al. Exploring the Agronomic Performance and Molecular Characterization of Diverse Spring Durum Wheat Germplasm in Kazakhstan. *Agronomy* 2023, 13, 1955. <https://doi.org/10.3390/agronomy13071955>

Tajibayev D., Yusov VS, Chudinov VA, Mal'chikov PN, Rozova MA, Shamanin VP, Shepelev SS, Sharma R., Tsygankov VI, Morgounov AI Genotype by environmental interactions for spring durum wheat in Kazakhstan and Russia // *Ecological Genetics and Genomics*. – 2021. – T. 21. – S. 100099. <https://doi.org/10.1016/j.egg.2021.100099>

Tajibayev D., Otemissova A., Erginbas-Orakci G., Morgounov A., Dababat AA Evaluation of durum wheat from Kazakhstan and Siberia for nematode (*Heterodera filipjevi*) resistance Proceedings of the 8th International Cereal Nematode Symposium

Dababat AA, Maafi ZT, Muminjanov H, Ozdemir F, Imren M, Smiley RW, Hollaway G, Paulit T, CIMMYT (2022). “Soilborne Nematodes and Fungal Pathogens of Cereals: Advances in Management.” 26-29 September 2022 , Abant , Türkiye . _ Pp 101-107

Recommendations:

Lines of spring durum wheat were recommended for transfer to state variety testing (SVT) in the Akmola and Almaty regions by the corresponding originators.

Highly efficient phenotyping using a digital camera is recommended for implementation in plant breeding.

Scope and structure of the dissertation. The dissertation is written on 101 pages, consists of an introduction, literature review, direction of research, research conditions, research results, conclusions, contains 13 tables, 21 figures, 11 appendices. The list of sources used includes 148 items

MAIN PART

1 CHOOSING A DIRECTION OF RESEARCH

1.1 Durum wheat as an object of research

Durum wheat (*Triticum turgidum* L. subsp. *durum* (Desf.) Husn.) has a tetraploid ($2n = 4x = 28$) AABB genome, which is considered the donor of hexaploid wheat. Durum wheat is one of the most important crops grown in the Mediterranean basin in terms of social importance, and the area under its cultivation is constantly increasing [25]. During 2020-2022, the area under its cultivation in the world amounted to 13.5 million hectares with a total production volume of 33.8 million tons. Kazakhstan, like other countries (Canada, Mexico, USA, Russia and Azerbaijan), is also a large producer of durum wheat [25]. According to Cam Dahl [26], in 2021, Kazakhstan ranked 5th in durum wheat exports to various countries, and Kazakhstan produced 1.97 tons of spring durum wheat.

Durum wheat is a cereal crop that is widely grown throughout the world for its high-quality semolina, which is mainly used for the production of pasta, couscous and traditional foods. Also, a gluten-rich type of wheat, when grown in culture it requires nutritious soils and warmth. Durum wheat is several times superior to bread wheat in product quality [27]. Durum wheat has long been distinguished by its high grain qualities: glassiness, high quality protein, and the special properties of gluten, making it an indispensable product. In developing countries and CIS countries, they continue to produce pasta and cereals from bread wheat grain; their quality is an order of magnitude lower than from durum wheat grain. Durum wheat is intended for the production of high-quality pasta, spaghetti, vermicelli, cereals and confectionery products. That is why it is a unique and priority culture.

Durum wheat is known for its unique nutritional profile, making it a valuable food crop. Several studies have examined the quality of durum wheat. For example, Abdel-Aal [28] reported that durum wheat is a good source of phenolic compounds that have antioxidant properties. Similarly, a year earlier, Chan [29] reported that durum wheat contains high amounts of dietary fiber, which may reduce the risk of chronic diseases. In addition, durum wheat is rich in antioxidants, which may protect against chronic diseases such as cancer and cardiovascular disease [28]. This crop is also grown all over the world for its high-quality semolina. Researchers have made significant progress in understanding the genetics of durum wheat and developing breeding strategies to improve its yield and quality. In addition, durum wheat is a rich source of essential nutrients and is associated with several health benefits, making it a valuable food crop. Consumption of durum wheat has been associated with several health benefits. For example, durum wheat is a rich source of complex carbohydrates, which can provide sustained energy and help regulate blood sugar levels. [30]. Consumption of durum wheat is associated with improved gut health due to its high fiber content [29].

Agriculture around the world faces a major threat from climate change. Rapid temperature fluctuations lead to decreased yields of various crops due to abiotic factors that were previously observed only in certain regions [31]. In Kazakhstan, droughts

also have a negative impact on crop yields, which creates food security problems not only for our country, but also for countries that import agricultural products [32, 33]. Kazakhstan is a zone of risky agriculture due to the sharply continental climate and periodic droughts, characterized by frequent dry winds, which leads to a significant decrease in wheat yield [34]. The northern regions of Kazakhstan are important for wheat cultivation and are also susceptible to climate change and drought [35]. Snowmelt leads to flooding, resulting in excess moisture; heavy rains are possible during the growing season, which leads to lodging of plants [36]. Yield is highly dependent on weather and climatic conditions [37, 38]. Breeding durum wheat is a complex process due to its sensitivity to climate, soil, water and nutritional conditions. However, the use of genetically characterized sources of resistance can speed up the process of creating varieties with increased immunological parameters and adaptive abilities.

The main problems faced by commodity producers in the region are biotic, abiotic and financial. According to various studies, wheat in Kazakhstan has a huge number of diseases and pests. For example, Koishibayev. [39] notes that durum wheat in Kazakhstan faces serious diseases, including leaf spot, brown spot, leaf rust and stem rust. Other studies [40, 41, 42, 43, 44] have shown that 80-90% of cultivated land under wheat is affected by soil-borne diseases such as vascular wilt, rot, damping off, root rot and many others caused by nematodes.

Selection is the most effective and centralized way to increase the size and quality of crops, ensure environmental safety and reliable functioning of agroecosystems, increase their resource and energy efficiency and profitability [45]. To obtain the maximum and stable yield of grain crops, it is necessary to correctly select varieties, taking into account the reaction to the agricultural background and ripeness. It is also necessary to pay special attention to the creation of varieties that would be more agroecologically adapted to different regions and would have increased production capabilities [46]. A review of the varieties included in the list of recommended varieties of the State Variety Test (SVT) shows that they were released between 1957 and 2015. Although these varieties can still produce good yields, there are many newer and more productive varieties that should replace them. In the state register of wheat varieties in various distribution zones, more than half are outdated varieties that are susceptible to diseases and pests, and in modern changing climatic conditions these varieties do not always produce sufficient yield. Of the 84 wheat varieties released into production between 2015 and 2021, 46 were spring bread wheat, 24 were winter bread wheat, 13 were spring durum and 1 was winter durum. Almost half (41) were imported from abroad (22 spring bread wheat, 14 winter bread wheat and 5 spring durum varieties).

Breeding efforts have been aimed at increasing the yield potential, disease resistance, and grain quality of durum wheat varieties [47]. One approach to increasing yield potential is to use hybridization. Several studies have reported successful hybridization of durum wheat using various methods, including in vitro culture methods and traditional crossing methods [48, 49].

In this connection, the Kazakhstan-Siberian spring wheat improvement network was created with the aim of assessing the adaptability of varieties and lines, as well as the exchange of breeding material [50, 51]. Created in 2000, it combines 18 research and breeding programs for spring bread wheat and 10 for durum wheat. The exchange of material is carried out according to the following scheme: every two years, each research institution submits 2-3 varieties/lines for evaluation in all institutes [52]. The results of the test are compiled and distributed to all participants and the nursery is changed. Over the years of evaluation of the nursery, numerous evaluation data have been accumulated on more than 200 durum wheat accessions in the main durum wheat growing regions in Kazakhstan and Russia. Tajibayev et. al. [12] analyzed these data and showed the results of the genotype-environment interaction. Kiryakova [53], assessed adaptability and genotype of environmental interaction in the conditions of the Omsk region. A large number of genotypes from the durum wheat collection of CIMMYT, KASIB and VIR were isolated for the conditions of Western Siberia [54]. Until 2018, trials were coordinated by the International Corn and Wheat Improvement Center in Kazakhstan. In 2018, the main set of KASIB durum wheat was formed, including all the diversity of the nursery over the years of work. Based on the results of research by the Kazakhstan-Siberian network, a large number of works were published on the adaptability of varieties, resistance to diseases of this collection, etc.

Currently, the dependence of agricultural production on the natural and climatic resources of the cultivation zone is becoming increasingly high [55]. The main solution to the problem is to create varieties of agricultural crops that would be adapted to a specific growing zone, would produce high yields at a low level of natural and climatic factors, would not require anthropogenic impact, and would have high consumer properties [56]. The variety as a biological system ensures stability of yield, which is especially important in the context of the diversity of soil, climatic and economic conditions in agriculture. One of the main requirements for a variety is its ability to maintain consistently high yields in various climatic conditions. Newly developed varieties can be used in production only if they produce higher and more sustainable yields than the best existing varieties of a given crop.

The adaptability of a variety to the agroclimatic conditions of different regions is one of the difficult aspects of a breeder's work. Correct selection of varieties is a complex task, the solution of which allows you to maximize the potential of the variety and increase grain yields at the lowest cost [57]. The creation of new highly adaptive varieties resistant to various stress factors is the best way to improve grain quality and increase yield, as well as crop resistance to various pathogens and pests [58]. The introduction of new varieties contributes to better use of natural and anthropogenic resources, increased soil fertility potential and other advances in agriculture [59].

Wheat varieties are an integral part of the global food system, providing a significant portion of the world's diet. The genetic composition of wheat varieties plays a decisive role in determining their productivity, quality and adaptability [60]. Wheat varieties are classified based on their growth habits and genetic composition [61]. Wheat variety selection is critical for optimal wheat production and grain quality, and

it is important to understand the meaning and importance of different wheat varieties [62].

Durum wheat breeding programs are aimed at creating new varieties with improved yield and quality. Many researchers have focused on developing breeding strategies to improve the productivity of durum wheat. For example, Mohammadi [63] developed a strategy to improve the yield and quality of durum wheat by selecting the best genotypes based on their productivity under different conditions. Similarly, Fiedler [64] developed a strategy to select durum wheat varieties with superior yield and disease resistance.

Wheat breeding is a continuous effort to develop new and improved varieties that are better suited to different growing conditions and can meet changing consumer needs [65]. Different wheat varieties have different levels of tolerance to environmental stressors and disease resistance, and have different end uses.

In addition, wheat varieties have implications for the sustainability of the wheat production system. Climate change is a major challenge facing global wheat production, and the development of new wheat varieties that are better suited to changing climate conditions is critical for long-term sustainability [66]. Wheat breeding programs must consider various factors such as water availability, soil quality and temperature conditions when developing new wheat varieties [67].

The value and importance of wheat varieties cannot be overestimated. Wheat variety selection is critical to wheat yield, grain quality, end use, human nutrition and health, and the sustainability of the wheat production system. Therefore, it is vital for farmers, researchers and policy makers to understand the characteristics of different wheat varieties and how they can best be used in different production systems [68].

1.2 High-throughput phenotyping

Phenotyping is an important component of plant breeding, allowing breeders to identify the most promising wheat genotypes based on their traits [69]. High-throughput phenotyping (HTP) is a relatively new approach that uses advanced technologies to collect and analyze data on a large scale [70].

Phenotyping is the process of measuring and analyzing the physical and biochemical traits of a plant [71]. It plays a crucial role in plant breeding as it allows breeders to identify the most desirable genotypes and select them for further breeding. HTP is a relatively new approach that uses advanced technology to collect data on a large scale. HTP is particularly useful in plant breeding because it allows breeders to simultaneously evaluate thousands of plants and collect data on a wide range of traits [72].

In connection with the development of various technologies, it becomes possible to introduce them into plant breeding to conduct various phenological observations. Undoubtedly, training a good breeder is currently a daunting task, and field phenotyping is somewhat limited due to both the variable results of human factors and the difficulty of making observations of plant color differences. In turn, high-throughput RGB- based phenotyping platforms can close this gap. This method was developed by foreign scientists headed by Sean S. Kefauver [72]. This RGB

phenotyping method demonstrates promising results in experiments conducted both on the adaptive potential of various crops and in studies of various diseases. Various studies are also being conducted to compare NDVI indices and RGB phenotyping. This is evidenced by publications based on experiments conducted by various scientists in Spain and Turkey; a study was conducted on predicting diseases and yields of durum wheat using RGB and NDVI indices. [73, 74]. Until recently, the Normalized Difference Vegetation Index (NDVI) was widely used in the world; this multispectral vegetation index was used as an estimate of plant biomass, nitrogen content, wheat yield and much more [75, 76, 77, 78, 79, 80, 81]. The main advantage of RGB phenotyping is its low cost, it eliminates the need to purchase expensive equipment as a method based on optical sensors, such as portable spectrum radiometers (such as GreenSeeker). The second main advantage is that today every person has a pocket camera. These two advantages can overcome the need to purchase expensive equipment, low funding for projects in the country and many other aspects [82, 83, 84]. The technology of high-precision phenotyping using RGB images also has its disadvantages associated with shadows, changes in ambient lighting conditions [85]. The information obtained allows us to study various traits, and first of all, the vigor of plant growth and development, biomass at different stages of plant development, leaf area index, plant aging process, and grain yield [84, 85].

Identifying the key stages of plant development that affect yield will facilitate variety modeling and yield forecasting [85].

Agro-climatic conditions in Kazakhstan are varied, and durum wheat is grown in a variety of environmental conditions, including in arid areas. Research has shown that environmental factors such as temperature, precipitation and soil types play a crucial role in the adaptation and productivity of durum wheat varieties in different regions of Kazakhstan [5, 86].

Kazakhstan has a dynamic agricultural sector, and the introduction of modern technologies and policies has allowed the development of a robust durum wheat breeding program. Research highlights the importance of public-private partnerships, farmer participation and policy support in promoting the development and dissemination of improved durum wheat varieties in Kazakhstan [87, 88]. Durum wheat breeding in Kazakhstan is influenced by environmental, genetic and socio-economic factors. Understanding these factors is critical to developing improved durum wheat varieties that are adapted to local environmental conditions and able to meet the needs of a growing population.

In agriculture, HTP using RGB images can be used for phenotyping plants to improve their genetic characteristics [89]. This approach allows for more efficient and accurate measurement of plant phenotypic characteristics at the population scale.

The cameras capture images of plants in these three colors and the data is processed to provide a wide range of information about the plants. RGB imaging is particularly useful in HTP as it allows breeders to collect data on various traits such as plant height, leaf area and color on a large scale and in a non-destructive manner. For example, the article [89] discusses the use of RGB images for phenotyping crop plants

in the field, and Deery [84] describes approaches to determining and measuring the water-economic efficiency of plants using RGB images.

HTP using RGB images allows us to identify phenotypic characteristics that are usually difficult to measure manually, such as flower color, leaf size and shape, plant height, grain size, and other parameters [90]. This data can be used to analyze and optimize plant genetic characteristics, such as yield, disease and insect resistance, adaptation to different climatic conditions, improving fruit quality, etc. [89, 90]

In addition, HTP using RGB images can be used to create more effective plant breeding strategies. It allows you to reduce the time spent on assessing the phenotypic characteristics of plants and improve the accuracy of the assessment. [90]

For example, HTP can be used to identify plants with the best characteristics in the process of screening a large number of plant genotypes [91]. This can help speed up the selection process for desirable plant characteristics and improve agricultural productivity.

HTP using RGB images can be used to assess the environmental sustainability of plants, such as their ability to adapt to climate change or protection from harmful insects and diseases. This can help plant breeders and farmers develop more resistant plant varieties and improve resource use efficiency [92].

Several studies have demonstrated the feasibility and effectiveness of RGB phenotyping in durum wheat. In a study by Awlia [92], RGB images were used to estimate the cover, height and area of durum wheat plants at different growth stages. The results showed a strong correlation between RGB-derived traits and conventional measurements, demonstrating the potential of RGB imaging for accurate and non-destructive phenotyping of *Arabidopsis thaliana*.

Another study by Nakhforoosh et al [93] used RGB imaging to evaluate the morphological and physiological traits of durum wheat under different water conditions. The researchers found that RGB imaging was effective in identifying differences in traits such as leaf area, biomass and chlorophyll content, indicating the technology's potential for assessing plant responses to environmental stress.

RGB phenotyping has also been used to study the genetic basis of durum wheat traits. In a study by Alemu [94], RGB images were used to estimate the vegetation index, multiple yield indicators of a mapping population of durum wheat. Researchers have identified quantitative trait loci (QTLs) associated with these traits, highlighting the potential of RGB phenotyping to identify genetic markers for desirable traits in durum wheat.

Overall, HTP using RGB images is a powerful tool for plant breeding [95], which can improve the efficiency of the selection process and improve the quality of agricultural products. It is also worth noting that HTP using RGB images can be used to control the quality of agricultural products during their storage and transportation [96]. This technology can detect changes in the color and texture of a product, which may indicate deterioration. This can help identify problems early and take action to maintain product quality.

The use of HTP through RGB images in agriculture has great potential to improve the efficiency and accuracy of breeding processes, as well as improve the

quality of agricultural products. However, to fully realize this potential, it is necessary to continue research in this area and develop appropriate technologies [97].

High-performance phenotyping using RGB images can improve the efficiency of the selection process and improve the quality of agricultural products. However, it is worth noting that this technology also has some limitations: firstly, the use of RGB images does not allow us to fully evaluate all aspects of the plant, such as its structure, biochemical composition and functional characteristics. This requires a more comprehensive approach using other technologies such as spectral scanning and image analysis using infrared photometry [98]. Second, RGB images can be sensitive to changes in lighting, shooting conditions, and camera quality [99]. This can skew the data and make it difficult to compare results between different experiments. Third, although HTP can significantly speed up the selection process, it still requires significant data processing and analysis costs [100]. This may be due to the large volume of data collected and the need to use powerful computing systems.

In any case, HTP with RGB images is a promising direction in the field of plant breeding and can become an important tool for increasing the yield and quality of agricultural products [100].

1.2 Selection of molecular markers

Molecular markers as one of the methods for improving selection have undoubtedly revolutionized breeding activities [2]. The basis for the success of breeding programs is genetic diversity [101]. A decrease in the genetic diversity of wheat varieties during the breeding process can lead to a decrease in yield and loss of disease resistance, which in turn can lead to a crisis [102]. Crossing genetically diverse forms increases yield, adaptability to different regions, and disease resistance [103].

iPBS (intron-containing poly protein of barley stripe mosaic virus) retrotransposons are a family of transposable elements widely distributed in plant genomes.

iPBS retrotransposons are classified as class I transposable elements and are characterized by their long terminal repeats (LTRs) and intron-containing polyprotein structure. The iPBS family has been identified in several plant species, including rice, maize, barley, and wheat. iPBS retrotransposons in wheat have been well studied due to the large genome size and complex genome structure of this crop. There are two types of retrotransposons: LTRs (long terminal repeats found in plant genes) and non-LTR retrotransposons. The iPBS retrotransposon marker system is more reliable than interretrotransposon amplified polymorphism (IRAP) and retrotransposon microsatellite amplified polymorphism (REMAP). The versatility of iPBS retrotransposons lies in the presence of complement tRNA as the reverse transcriptase primer binding site (PBS) in LTR retrotransposons [104].

The ease of working with iPBS retrotransposon markers lies in the fact that the sequence of these genomes in various plants is distributed along the entire length of the chromosomes located in the euchromatic regions; at the same time, they are highly informative under abiotic and biotic stress of plants [105]. Successful studies have been

carried out on crops such as chickpeas, peas, rice, quinoa, adonis, beans and wheat based on retrotransposon interprimer binding site (iPBS) [106].

Several studies have examined the structure and distribution of iPBS retrotransposons in wheat. In a study by Gozukirmizi [107], researchers identified iPBS retrotransposon insertions in the wheat genome and found that most of these elements were clustered in specific regions of the genome. The researchers also identified several families of iPBS retrotransposons that were highly conserved across different wheat cultivars and related species.

Several studies have been conducted to assess the genetic diversity of durum wheat. For example, Oliver [108] analyzed the genetic diversity of durum wheat using molecular markers and identified significant genetic variation among durum wheat accessions. Similarly, Kabbaj et al [109] studied the genetic diversity of durum wheat accessions in Syria using morphological and molecular markers and found significant diversity among the accessions.

The potential role of iPBS retrotransposons in plant genome evolution and regulation was also investigated. In the Juretic study [110], researchers found that iPBS retrotransposons contributed to the evolution of gene structure and expression in rice, and that these elements also played a role in shaping the genome structure of this species.

The iPBS retrotransposons are also involved in plant stress responses. In a study by Arvas [111], researchers found that retrotransposons were activated in response to drought stress in rice, indicating a potential role for these elements in plant adaptation to environmental stress.

Several studies have examined the distribution and abundance of iPBS retrotransposons in the durum wheat genome. Durum wheat is a genetically diverse crop and Kazakhstan has a rich collection of durum wheat germplasm. Studies have shown significant genetic variability in traits of yield, quality and stress resistance of durum wheat samples from Kazakhstan [112, 113, 114]. This genetic diversity gives breeders the opportunity to develop improved varieties with desirable traits. A study by Bariah [115] found evidence for the involvement of transposable elements in chromosomal rearrangements of iPBS retrotransposons in the wheat genome and found that these elements were distributed across all 14 chromosomes. The scientists also identified several families of iPBS retrotransposons that were highly conserved across different durum wheat cultivars.

The potential role of iPBS retrotransposons in the evolution and regulation of the durum wheat genome was also investigated. In a study by Alsaleh [116], researchers found that iPBS retrotransposons contributed to the evolution of durum wheat gene structure and expression, and that these elements also played a role in shaping the genome structure of this species. The scientists also identified several families of iPBS retrotransposons that were associated with genes involved in phenotypic diversity in durum wheat, suggesting a potential role for these elements in partitioning genetic diversity within and between landraces.

The iPBS retrotransposons have also been studied for their potential applications in crop improvement. In a study by Carvalho [117], researchers used iPBS

retrotransposon-based markers to identify genetic diversity in durum wheat germplasm and found that these markers were effective in distinguishing between different cultivars and populations. Similar studies were carried out by Pascual [118], who analyzed the genetic diversity of durum wheat landraces from Spain using iPBS markers and found high levels of genetic diversity with clear differentiation between southern and northern landraces. Similarly, Oliveira [119] used iPBS markers to analyze the genetic diversity of durum wheat accessions from the Iberian Peninsula and found high levels of genetic diversity with clear differentiation between northern and southern accessions. A high level of genetic diversity was found among landraces of Iran and Azerbaijan, with clear differentiation between the two countries [120].

The researchers suggested that these markers could be used in breeding programs to develop new durum wheat varieties with improved agronomic characteristics. Also, the observed population structure may be associated with the adaptation of landraces to different climatic and environmental conditions.

Overall, iPBS retrotransposons represent a diverse family of transposable elements that have the potential to influence the evolution and regulation of the durum wheat genome and contribute to plant adaptation to environmental stress. Further research is needed to fully understand the role of iPBS retrotransposons in durum wheat biology and to develop strategies to use these elements for crop improvement. The studies mentioned above highlight the high level of genetic diversity in durum wheat populations, as well as clear differentiation between different regions or accessions.

Based on the literature review, it is necessary to study the adaptive potential of the existing collection of durum wheat in different regions, to identify highly productive lines/varieties with high yields, to study high-performance phenotyping using RGB images, which can subsequently become one of the cheap tools for increasing the yield of wheat varieties. And with the help of iPBS retrotransposons, it is possible to study the adaptive potential of genotypes and regulate the genetic population.

2 CONDITIONS FOR CONDUCTING RESEARCH

2.1 Soil conditions

Soils Almaty region. The soil cover of the experimental plot of LLP "KazRIAPG" is represented by foothill light chestnut soils. Formed on loess-like loams and having a clearly defined fertile profile. The high carbonate content of these soils is quite clearly visible. Mechanical composition refers to medium loams. The content of coarse dust is 40-45%, physical clay - 40%, and silt fractions decrease along the profile from 13.8 to 8.62%. Mechanical elements are in an aggregated state.

The humus content in the arable horizon is 2.44%, with a sharp decrease down the profile. There is a high content of carbonates (CO₂), as a result of which the reaction of the soil solution is slightly alkaline pH 7.3-7.5. absorption capacity does not exceed 15 mg/eq. In the composition of absorbed bases, the main part is Ca (11.05-13.12 mg/eq), the amount of absorbed Mg is not high (1.97–2.62 mg/eq). In the arable horizon, total nitrogen is 0.15, phosphorus - 0.21%, and a decrease in their amount is also observed from the upper layers of the soil to the lower ones.

Akmola region. The soil of the experimental plot in the LLP "SPC GF n.a. A.I. Baraev" in the arid steppe subzone are represented by carbonate southern chernozems with a fairly high content of organic matter of 3-5%, gradually decreasing with depth. The nitrogen content in the experimental plot in the arable layer reaches 0.31%, and also decreases with depth to 0.06%. The phosphorus content in the soil is 0.12-0.15, in the subsoil layer -0.10-0.11%. Mobile forms of phosphorus are contained in a low amount of 1.2-1.3 mg per 100 g of soil [121]. In terms of mechanical composition, these soils are classified as heavy loamy; the reaction of the soil solution is slightly alkaline pH - 7.3. [122]. Carbonate content occurs throughout the profile, with an average maximum (5-6% carbon dioxide) in the middle part of the profile. Dense fractured, coarsely lumpy illuvial horizon A - 22-24 cm, A+B1 - 35-40 cm, c. [123].

Based on the available indicators, we can conclude that the experiments were conducted on well-cultivated soils.

2.2 Climatic conditions

High productivity, as well as optimal growth and development of field crops, directly depends on the agrometeorological conditions of the region in which the experiment and crop production are carried out. To better understand the growth and development of plants during the growing season, as well as the demands made by plants on the climate, it is necessary to know the quantitative characteristics of the plants' needs for heat and moisture.

In Almaty, as well as in Akmola region, deviations of meteorological conditions from parameters typical for these places are often observed, which leads to a decrease in yields. In this regard, the determination of moisture and temperature conditions when creating highly productive forms of agricultural plants is an integral part.

Analysis of meteorological conditions for 2020-2022. and their influence on the production process of spring durum wheat was carried out according to KazHydroMet data [124]. Meteorological conditions over the years of research were characterized by

great diversity among the months of the growing season and had significant deviations from the long-term average indicators, Figure 1, 2. Monthly data for the growing season of two years are shown in the tables in Appendix A.

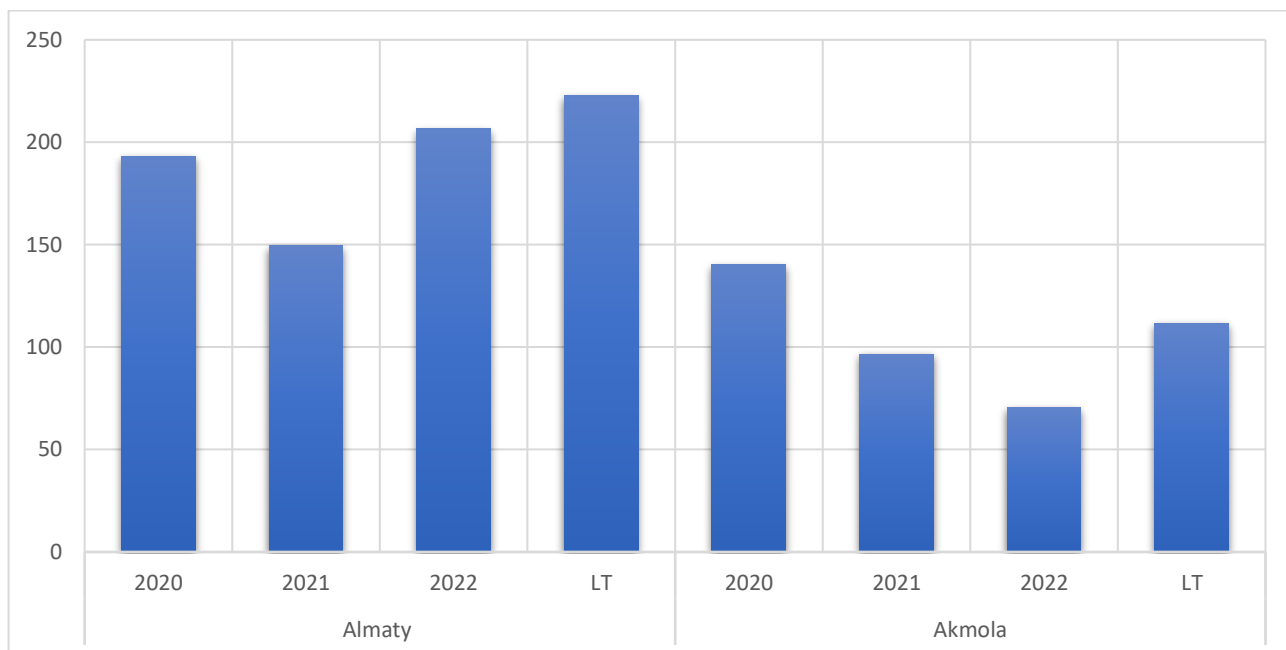


Figure 1 - Average amount of precipitation during the growing season in two regions for 2020 – 2022 (mm)

An analysis of weather data for the growing season of 2020 in the Almaty region showed that the temperature for March – July averaged 17.1 °C. In April, May and June, the average monthly air temperature was 14.0 °C, 18.8 °C and 22.0 °C, respectively (Figure 2). The air temperature in July was 24.3 °C. The amount of precipitation during the growing season in 2020 was 193.1 mm. By month, precipitation was distributed as follows: 25.9 mm fell in March, 69.4 mm in April, 37.2 mm in May, 14.8 mm in June, and 16.1 mm in July. The highest amount of precipitation during the 2020 growing season occurred in April.

In 2021, the temperature regime was presented as follows: in March the average air temperature reached 4.9 °C, in April 12.5 °C, in May 19.5 °C, in June 23.0 °C and in July 27.2 °C. The average temperature for the entire growing season was 17.4 °C. Compared to 2020, the air temperature in 2021 was 2-3 °C higher, while the amount of precipitation was much less compared to the previous year, with a long-term average of 222.7 mm and a record low of 149.5 mm. In March, there was more rainfall of 55.8 mm, in April the rainfall amounted to 26.5 mm, which is almost 25 mm less compared to the previous year, in May, June and July there was also insufficient rainfall of 34.2 mm, 9.7 mm, 11.3 mm respectively. Overall, 2021 was a very dry year, which affected testing.

In 2022, the average temperature for 5 months March - July was 18.4 °C, and the average monthly temperature in March was 5.6 °C, April 16.7 °C, May 19.0 °C, June 24.3 °C and July 26.4 °C. The total precipitation for the entire growing season was very

favorable and amounted to 206.6 mm. By month, precipitation was distributed as follows: 82.9 mm fell in March, 22.4 mm in April, 71.2 mm in May, 17.9 mm in June, and 6.6 mm in July.

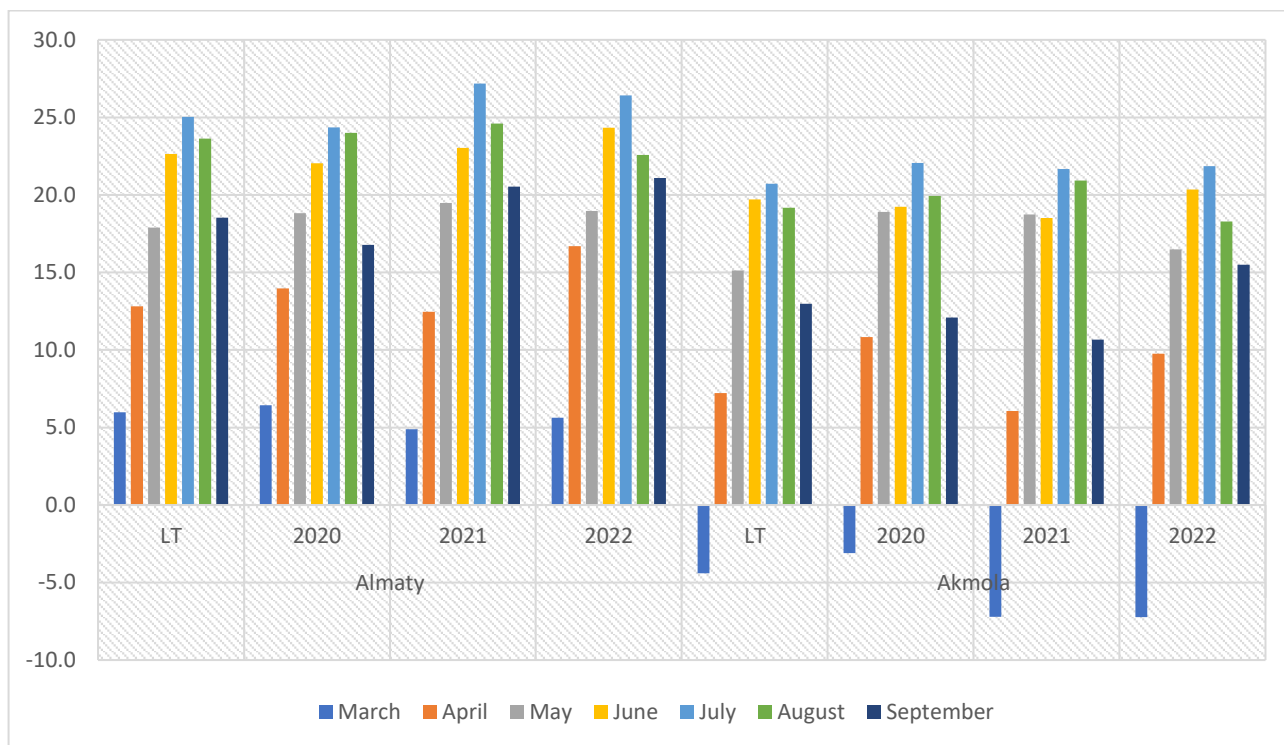


Figure 2 - Temperature regime during the growing season in two regions for 2020-2022 (°C)

The climate of the Akmola region of the Shortandinsky district is sharply continental, characterized by frosty winters, hot summers, with sharp fluctuations in air temperature and fairly low precipitation, with frequent dry winds [123].

Analysis of weather data for the Akmola region showed that this region is drier compared to the Almaty region. So, in 2020, the amount of precipitation during the growing season was 140.4 mm. And the distribution by month was as follows: in May 6.8 mm, in June 48.2 mm, in July 26.4 mm, August 19.4 mm, September 13.7 mm. The average temperature for the entire growing season was 1.0 °C higher and amounted to 18.4 °C. In May, the average air temperature reached 18.9 °C, in June 19.2 °C, in July 22.1 °C, in August 19.9 °C, in September 12.1 °C.

In 2021, the average monthly temperature was as follows: May 18.7 °C, June 18.5 °C, July 21.7 °C, August 20.9 °C, September 10.7 °C. The average temperature during the growing season was at the 2020 level of 18.1 °C. The amount of precipitation during the growing season was 96.6 mm, almost half less than in 2020 and 20 mm from the long-term average, which indicates a dry year in all regions of the country. The distribution of precipitation by month was as follows: 5.4 mm fell in May, 10.8 mm in June, 22.0 mm in July, 3.8 mm in August, 26.3 mm in September.

Analysis of weather data for 2022 in the Akmola region showed that the average monthly temperature was as follows: May 16.5 °C, June 20.4 °C, July 21.9 °C, August 18.3 °C, September 15.5 °C. The average temperature during the growing season was

18.5 °C. The total amount of precipitation during the growing season was 70.5 mm. The distribution of precipitation by month was as follows: May 5.0 mm, June 9.2 mm, July 16.5 mm, August 13.1 mm, September 7.6 mm.

2.3 Materials and methods

2.3.1 Genotypes of spring durum wheat

The object of the study was 151 samples of spring durum wheat from the KASIB nursery, provided by the KASIB network. Samples belong to the following organizations: Aktobe AES (50.3519°N, 57.3928°E; 234 masl) 20 genotypes, Altai RIA (FASCA) (53.4125 °N, 83.5190°E; 169 masl) 20 genotypes, Karabalyk AES (53.854 0°N, 62.1015 °E; 204 masl) 25 genotypes, KazRIAPG (43.1355°N, 76.4209°E, 789 masl) 25 genotypes, SPC GF n.a. A.I. Baraeva (51.4024 °N, 71.0049°E, 369 masl) 14 genotypes, Samara RIA branch of the Samara RCRAS (52.9644°N, 49.4187°E; 45 masl) 14 genotypes, Saratov RI of the South-Eastern Region (FGBNU "FASC of the South-East") (51.3420°N, 45.5952°E, 126 masl) 5 genotypes, Omsk ASC (55.0404 °N, 73.3604 °E; 120 masl) 25 genotypes (Figure 3) a complete list of the collection is given in Appendix B. Varieties were used as standards Nauryz 6, Altyn dala and the Zhemchuzhina Sibiri. The standards in the collection were located after every 20 genotypes. Most of the genotypes in the collection are represented by the varieties Hordeiforme and Leucurum.



Figure 3 - Places of experiments and originators included in the KASIB network (red flags - originators, yellow flags - place of experiments and originators)

The study of lines and varieties in different environments makes it possible to identify genotypes that best suit different agroclimatic conditions. The experiment was carried out from 2020 to 2022 in the Almaty and Akmola regions on the basis of the Kazakh Scientific Research Institute of Agriculture and Plant Growing of the cereals breeding department and the plant gene pool laboratory, as well as on the basis of the Scientific Production Center of Grain Farming named after. A.I. Baraev, Department of Cereal Breeding, Laboratory of Durum Wheat. Each environment presented a unique combination of location, year, and humidity. Trials were designed in randomized complete blocks. The size of the plots was 1–3 m² in two or three repetitions. Sowing was carried out in pure fallow. The sowing dates corresponded to the optimal ones depending on the region, in the Almaty region - the end of March - the beginning of April (from March 20 - April 1), in the Akmola region - the end of May (May 20-25), the seed sowing rate was 400–450 per m². Sowing was carried out manually with a plot size of less than one square meter and with a SSFC seeder with a plot size of more than one square meter, harvesting was carried out with a Wintersteiger breeding harvester, in the phase of full ripeness in the Almaty region - mid-July, in the Akmola region the end of August - the beginning of September.

Phenological observations and censuses were carried out in the field according to the method [125] (Figure 4). The Zadoks scale was used to determine the phenology of wheat growth stages [126]. To determine agronomic indicators, a structural analysis of plants was carried out in a pre-collected sample from plots measuring 0.25 m²: plant height, MT, number of productive spikes, plant biomass, spike length, spike weight, number of spikes in an spike, number of grains in the main spike, grains in a spikelet, the weight of grains from the main spike in grams, the weight of grains from a plant in grams and biometric indicators: the length of the awns in cm, the length of the subspikelet internode and the number of internodes. The weight of 1000 grains were weighed among selected grains of one genotype. The harvest was recorded on a plot-by-plot basis.

2.3.2 Phenological observations using digital technologies

Experiments using digital technologies were carried out in the Akmola region. For each plot, one digital RGB image was taken under natural light conditions on dry, sunny days when the sun was at its zenith between 11:00 and 14:00. Hold the camera at approximately 1.0 m and focus on the center of the plot, above the plant crown in the zenith plane. Photos were taken using a CANON digital SLR camera EOS 2000 D with 24.1-megapixel resolution and 22.3 x 14.9 mm CMOS sensor, in auto mode. All images had a native resolution of 4624 × 2080 pixels and were saved in JPG format using the sRGB color standard (Figure 5).



Almaty region



Akmola region

Figure 4 - Process of harvesting and selecting plants for structural analysis

Measurements were carried out from the booting phase every 10 days until the plants fully matured. The dates for digital measurements are shown in Table 1.

Table 1 - Dates of digital measurements and

No.	2021		2022	
	Date	Development phases	Date	Development phases
1	11 July	Tillering - Piping	-	-
2	July 19	Piping - Heading	the 14 th of July	Piping - Heading
3	July 27	Heading – Milky ripeness	July 23	Heading – Milky ripeness
4	05 August	Milk ripeness – MW ripeness	05 August	Milk ripeness – MW ripeness
5	August 15	MW ripeness – Waxy ripeness	August 16	MW ripeness – Waxy ripeness

To exclude distortion of images or the presence of foreign objects in the photograph, a preliminary assessment of all images was carried out. In order to eliminate distortion of photographs and digital indexes in the results, manual weeding of weeds was carried out both around the plots and inside.

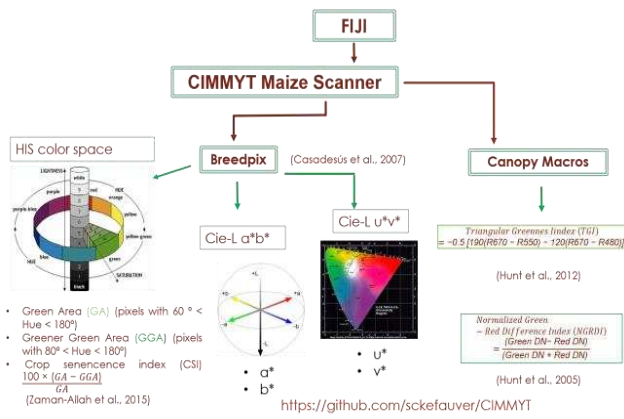


Figure 5 - Images of different genotypes in different growth phases

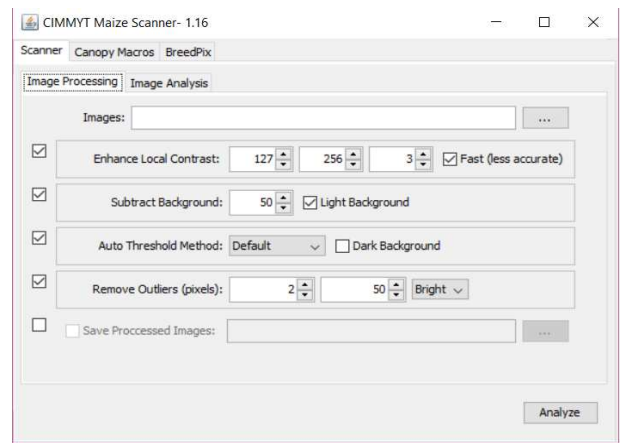
Processing of the resulting images was carried out using the built-in plugin CIMMYT_Maize_Scanner [127] based on the open-source Fiji platform ImageJ for the analysis of biological images (Figure 6). Figure 6 A shows an example of obtaining the digital indices of the green area, the “greener area,” and the coordinates a^* , b^* , and u^* , v^* from RGB images. Fiji uses modern software development techniques to combine powerful software libraries with a wide range of scripting languages to enable rapid prototyping of image processing algorithms [128].

To obtain indicators such as Green Area (GA) and Greener green area (GGA) Pix 4 D calculator was used GSD_Calculator based on MS program office Excel. The images were subsequently analyzed using Breedpix 0.2, an open-source software [129] designed for digital image processing. This software allows you to calculate several RGB vegetation indices based on the different color properties inherent in RGB images.

Conducting phenological observations using a digital camera are shown in Figure 7.



A



B

Figure 6 - CIMMYT _ Maize _ Scanner A - CIMMYT _ Maize _ Scanner image processing scheme, B - CIMMYT _ Maize _ Scanner working window



Figure 7 - conducting digital phenological observations

2.3.3 DNA markers iPBS retrotransposons

DNA extraction. Healthy seeds were sown in germination trays. After germination, fresh, young and healthy leaves were collected for genomic DNA extraction. The CTAB protocol described by Doyle JJ and Doyle JL [130] was used for DNA extraction with minor modifications as described [18]. The isolated DNA was diluted and stored at -20°C. After extraction, the concentration and quality of genomic DNA were measured spectrophotometrically using nanodrop 2000c (Thermal Scientific, USA), and DNA quality was also analyzed using a 0.8% agarose gel.

The photograph shows the selection of spikes for subsequent DNA extraction and transfer to the gene pool laboratory of LLP “KazRIAPG” (Figure 8).



Figure 8 - Selection of spikes for DNA extraction

PCR amplification. The final concentration of genomic DNA was adjusted to 5 ng μl^{-1} using double-distilled water (dd H_2O) and stored at -20°C for polymerase chain reaction (PCR) amplification. Eighty-three iPBS primers were taken from studies Kalander [131] screened on 8 genotypes and selected highly polymorphic primers for further PCR amplification. Information about the selected iPBS-retrotransposon primers, as well as their annealing temperature and sequence are given in Table 2. PCR amplification was performed using a 20 μl mixture containing 2 μl 1X PCR assay buffer (Thermo Scientific), 2 μl dNTP (2 mM) (Thermo Scientific.), 5.6 μl distilled water, 3.2 μl primer (5 mM) and 2 μl MgCl_2 (2 mM), 0.2 μl U Taq DNA polymerase

(Thermo Scientific) and 5 µl (5 ng) genomic DNA. The Kalendar PCR protocol [131] was followed; initial denaturation at 95°C for 3 min; 30 cycles at 95°C for 15 s, annealing temperature from 50 to 65°C (depending on the primer) for 1 min, 68°C for 1 min; and final extension at 72°C for 5 min. PCR products were separated by electrophoresis (Bio-Rad, USA) using a 2% agarose gel in 1× Tris-borate EDTA buffer (TBE) at a constant voltage of 120 V for 2.30 h. The gels were stained with ethidium bromide. The gel image was obtained using a gel documentation system (Bio-Rad, USA).

Table 2 - iPBS retrotransposons used to determine genetic diversity among 151 durum wheat genotypes

Primer name	Subsequence	Annealing temperature (°C)
2228	CATTGGCTCTTGATACCA	53
2074	GCTCTTGATACCA	50
2226	CGGTGACCTTTGATACCA	53
2239	ACCTAGGCTCGGATGCCA	55
2245	GAGGTGGCTCTTATACCA	50
2252	TCATGGCTCATGATACCA	52
2256	GACCTAGCTCTAATACCA	51
2270	ACCTGGCGTGCCCA	55
2271	GGCTCGGATGCCA	55
2389	ACATCCTTCCCA	50

2.3.4 Statistical analysis

Agronomic indicators. The data obtained during the study were analyzed using Dospheov's method [132] in MS Excel and the freely available statistical program R (R Studio) using various packages. Analysis of the main components (Principal component analysis – PCA) was carried out using the FactoMineR package, visualization of the main components of agronomic traits was carried out using the factoextra package [133]. To determine standard errors and standard square deviation in the experiment, the lme4 package was used. The Pearson correlation coefficient was performed using the formula in the statistical program R. Each year and region were calculated separately.

RGB images. At the first stage of data analysis, parameters of little significance were eliminated. During the analysis of photographs obtained using a digital camera in 2021 and 2022 in field areas in the Akmola region, the following parameters were obtained: %Area, Intensity, Hue, Saturation, Lightness, a*, b*, u*, v*, relative parameters GA, GGA, CSI, GAm² GGA m². Light intensity, Hue, Saturation and Lightness are qualitative parameters [134].

BreedPix program automatically converts the original RGB image into numerical color spaces as indicated in Figure 6 and corresponds to the values of the parameters a *, b *, u *, v *.

The a^* and b^* belong to the CIE-Lab color space, being the L^* dimension of luminance, and a^* and b^* the coordinates of opposite colors. Red/green colors are represented by the a^* axis, while the b^* axis represents yellow/blue colors. Likewise, the u^* and v^* indices represent the axes in the chromaticity diagram of the CIE-Luv color space. Thus, the program obtains the average values of these color components for each of the processed images [135].

Relative green area (GA) and relative greener area (GGA) are based on the sum of the histogram class frequencies included in a specific hue range in an image. GA is the percentage of image pixels in the hue range from 60° to 180° , that is, from yellow to bluish-green. On the other hand, GGA is somewhat more stringent, since the range of shades considered by this index is from 80° to 180° , excluding yellowish-green tones, and therefore more accurately describes the amount of photosynthetically active biomass and leaf senescence [136].

Green area (GA m^2) from m^2 and the “greener area” (GGA m^2) from m^2 were calculated in the MS program office Excel .

To understand which parameters of digital images are most closely related to agronomic traits, a correlation analysis was carried out (Figure 11).

The progression of wheat aging when processing digital photograph data was characterized by the area under the progression curve of the cereal aging index, based on the formula for the area under the disease progression curve [137]. The value of the area under the progression curve of the cereal aging index was determined by the midpoint of time between successive measurements of digital photographs for the average value of the assessment of the progression of plant aging.

The iPBS retrotransposons. All clear and distinguishable gel bands were scored, and the presence and absence of a band were reported as 1 and 0, respectively. PopGen software version 1.32 [138] was used to determine genetic parameters such as total gene diversity (Ht), genetic diversity (He), Shannon information index (I), effective number of alleles (Ne) and genetic distance (GD). The polymorphism information content (PIC) was determined using the formula, i.e., $PIC = 2f_i(1 - f_i)$ [139]. Here f_i represents the frequency of molecular marker loci present and $(1 - f_i)$ represents the frequency of missing loci. Principal coordinate analysis (PCA) and analysis of molecular variance (AMOVA) were calculated and analyzed using GenAlExV6.5 software [140]. To accurately determine genetic similarity, 3 independent programs were used STRUCTURE, NJ Tree in the R program, and GenAlExV6.5. To assess the genetic similarity of 151 durum wheat accessions, neighbor-joining tree analysis (NJ Tree) using arithmetic means through cluster analysis using the statistical software R. The program STRUCTURE [141] was run to determine the number of subgroups (K) among the germplasm studied, with K values ranging from 1 to 10 and ten independent runs for each value of K. The Markov chain Monte Carlo (MCMC) algorithm was then adopted to obtain the best-fitting value of K. The initial burn-in period was set to 50,000 with 300,000 iterations of MCMC [142] without prior provenance information. To determine the appropriate number of clusters (number K; number of subpopulations), the STRUCTURE analysis took into account the criteria proposed by Evanno [143].

The best K number was selected using STRUCTURE Harvester online <http://taylor0.biology.ucala.edu/structureHarvester/> based on the largest ΔK value.

3. COMPARATIVE ANALYSIS OF AGRONOMIC INDICATORS OF SPRING DURUM WHEAT IN ALMATY AND AKMOLA REGIONS

3.1 Results of agronomic trials

3.1.1 High-yielding varieties by region

As a result of the experiments carried out in the period 2020 – 2022, the following results were obtained. In 2020, on March 20, seeds of spring durum wheat from the KASIB collection were sown for propagation in the Almaty region at the station of the grain crops department of LLP “KazRIAPG” in an amount of more than 200 samples. Each sample contained from 15 to 52 grains. Phenological observations were carried out. The resulting harvest was distributed over two regions: Almaty region LLP "KazRIAPG" and Akmola region LLP "SPC GF n.a. A.I. Baraev". The average, minimum and maximum values, as well as the coefficient of variation, standard error and standard deviation of the main agronomic traits by year and region are given in Table 3. The average minimum yield among all genotypes was 101 g/m², the average maximum yield was 237 g / m².

According to the results of the experiments, the average yield in the Almaty region was 242 g/m² and the range was from 100 to 436 g/m². The weight of 1000 grains were 39.6 g with a range from 27.9 to 49.5 g. The statistical analysis showed that the coefficient of variation was 0.23%. The smallest significant difference in yield is 12.35%.

The duration of the growing season was 103 days on average and varied from 95 to 112 days. The duration of the period “sprouting – heading” averaged 61 days and varied from 53 to 69 days. The smallest significant difference in the duration of the period “sprouting – heading” was 0.68%. The height of the plants reached 103 cm on average, the height of the short-stem variety reached 77 cm and the high-stem variety 128 cm, the LSD was 1.94%.

The average number of spikes per plant was 1.17. The average length of the spike reached 8.8 cm, the variation ranged from 6.65 cm to 10.92 cm LSD 0.16% with the number of grains being 50 pieces per main spike LSD 1.36%, the weight of which was 2.07 g. LSD 0.06%.

The average yield data obtained from the Akmola region varied from 87 to 286 g/m² and the average was 170 g/m². The smallest significant difference in yield is 8.77%. The minimum weight gain per 1000 grains was 34.9 g, maximum 52.2 g and average 44.0 g, with the least significant difference being 0.73%. For late-ripening varieties, the duration of the growing season was 94 days; mid-ripening varieties ripened within 88 days and early-ripening varieties within 79 days. On average, genotypes emerged 43 days after germination. The maximum duration of the period from germination to heading was 50 days, and the minimum was 35 days LSD 0.63%. The average height of plants in the Akmola region was 72 cm. Tall-stem genotypes reached 89 cm and short-stem genotypes 52 cm, LSD - 1.32%.

The number of spikes per plant is on average 1.5 pieces. The average length of the spike reached 6.18 cm LSD 0.12%, the average number of grains was 24.56 pieces from the main spike with LSD - 0.74% and the weight of grains from the main spike was 1.15 g with LSD - 0.04 %

Table 3 - Statistical analysis of agronomic indicators for 2021-2022 in two regions

Region	Feature	Min	Max	Mean	St Error	St.Dev.	Coefficient var	LSD
	Average yield g/m ²	101	237	168	2.03	24.86	0.15	
Alm	Yield, g/m ²	100	436	242	4.62	56.82	0.23	12.35
Akm	Yield, g/m ²	87	286	170	2.59	31.79	0.19	8.77
Alm	TKW	27.9	49.5	39.6	0.39	4.82	0.12	0.95
Akm	TKW	34.9	52.2	44.0	0.29	3.61	0.08	0.73
Alm	DH	53	69	61	0.28	3.43	0.06	0.68
Akm	DH	35	50	43	0.27	3.29	0.08	0.63
Alm	DM	95	112	103	0.29	3.55	0.03	
Akm	DM	79	94	88	0.25	3.02	0.03	
Alm	DHM	43	59	51	0.26	3.17	0.06	
Akm	DHM	43	48	45	0.09	1.07	0.02	
Alm	PH, cm	77	128	103	0.58	7.16	0.07	1.94
Akm	PH, cm	52	89	72	0.52	6.34	0.09	1.32
Alm	Spikes from plant. pcs	1	3	1.17	0.04	0.44	0.37	
Akm	Spikes from plant. pcs	1	2.3	1.50	0.02	0.27	0.18	
Alm	Spike length, cm	6.65	10.92	8.80	0.07	0.88	0.10	0.16
Akm	Spike length, cm	4.9	7.8	6.18	0.05	0.56	0.09	0.12
Alm	Awn length, cm	0	18.83	11.54	0.15	1.84	0.16	
Akm	Awn length, cm	0	12.05	8.89	0.10	1.21	0.14	
Alm	Grains from main spike, pcs	36.6	70.2	49.91	0.56	6.89	0.14	1.36
Akm	Grains from main spike, pcs	14.1	34.1	24.56	0.28	3.47	0.14	0.74
Alm	Weight of grains from main spike, g	1.19	2.79	2.07	0.02	0.27	0.13	0.06
Akm	Weight of grains from main spike, g	0.69	2.28	1.15	0.02	0.20	0.18	0.04

The genotypes were represented by various varieties, one of the characteristics being the presence of awns, which can be measured. Thus, the length of the awns in the Almaty region was 11.54 cm, and in the Akmola region 8.89 cm. Also, in the collection there was one genotype without awns, Karabalykskaya chernokolosaya.

As a result of a comprehensive assessment, records and observations, high-yielding lines/varieties were identified and presented in Table 4. Among the standards, on average in two regions, the best variety was the Zhemchuzhina Sibiri variety bred by the Omsk ASC with an average yield of 209 g/m². The yield of the Nauryz 6 standard variety bred by LLP “KazRIAPG” on average in two regions was 184 g/m² and Altyn dala 195 g/m² to the selection of the Karabalyk AES. The identified high-yielding varieties on average for two regions were represented by the following originators: Altai Research Institute with the Hordeiforme 924 line and a yield of 237 g/m², LLP “KazRIAPG” variety Ertol with a yield of 236 g/m². Samara RI with the

Leukurum line 1469d-21, Omsk ASC with the line Hordeiforme 91-22-2 and Hordeiforme 95-139-4 with a yield of 223 g/m², 221 g/m², and 219 g/m², respectively, SPC GF n.a. A.I. Baraev with line 250-06-14 with a yield of 219 g/m², Aktobe AES with the Kargala 1540 variety and a yield of 216 g/m², Karabalyk AES with the Hordeiforme 1790 line with a yield of 214 g/m², Samara RI with the Leukurum line 1594d- 3 and a yield of 214 g/m².

Table 4 - Average yield of standout genotypes in Almaty and Akmola regions

Genotype	Originator	MEA N Yield, t/ha	Almaty region						Akmola region					
			Yield, g/m ²	TKW	PH	DH	DM	DHM	Yield, g/m ²	TKW	PH	DH	DM	DHM
Nauryz_6 (St -1)	KazRIAPG	184	169	36.2	108	60	97	53	200	40.6	67	42	89	47
Altyn_Dala (St -2)	Karabalyksaya AES	195	200	44.8	107	62	105	49	190	48.3	75	44	88	44
Zhemchuzhina_Sib iri (St. -3)	Omsk ASC	209	214	41.2	110	61	105	49	204	43.1	70	38	82	44
Hordeiforme_924	Altai RI	237	206	43.9	102	65	107	48	268	49.1	81	47	91	45
Ertol (18104)	KazRIAPG	236	317	49.4	105	61	105	49	156	44.9	71	43	89	46
Leukurum_1469d- 21	Samara RI	223	205	49.0	107	58	100	53	240	51.1	78	41	87	47
Hordeiforme_91- 22-2	Omsk ASC	221	294	44.6	106	54	98	55	147	42.3	72	42	86	44
Hordeiforme_95- 139-4	Omsk ASC	219	196	44.3	101	61	105	49	242	50.6	77	44	89	45
Line_250-06-14	SPC GF n.a. Baraev	219	230	38.6	96	67	107	47	208	44.7	71	50	93	43
Kargala_1540	Aktobe AES	216	216	46.9	104	56	98	54	216	48.1	73	42	89	47
Hordeiforme_1790	Karabalykskay a AES	214	203	37.4	110	64	105	48	225	43.0	80	47	91	44
Leukurum_1594d- 3	Samara RI	214	292	44.8	111	59	100	53	211	46.5	81	44	91	48
Hordeiforme_242- 93	Karabalykskay a AES	211	180	37.2	103	62	105	49	241	46.1	77	45	90	45
Hordeiforme_94- 71	Omsk ASC	206	223	46.0	108	60	102	52	189	46.5	74	42	89	47
Hordeiforme_00- 96-8	Omsk ASC	205	124	28.2	103	69	109	44	286	40.7	74	46	91	45
Line_G1612	Karabalykskay a AES	204	212	34.9	101	62	105	49	197	42.0	76	46	91	45
Kostanayskaya_15	Karabalykskay a AES	203	183	40.0	108	64	105	49	222	44.4	81	48	92	44
Kargala_1538	Aktobe AES	202	192	45.6	98	60	105	49	213	46.3	72	37	82	45
Serke	KazRIAPG	199	231	40.2	105	59	105	50	167	38.5	63	39	84	45
Line_69-08-2	SPC GF n.a. A.I. Baraev	198	193	34.8	111	65	107	47	204	45.6	73	44	88	44
Hordeiforme_91- 102-6	Omsk ASC	197	244	45.4	107	53	98	57	151	42.2	70	39	85	46
Hordeiforme_895	Altai RI	197	180	39.3	120	63	105	49	213	47.1	84	48	92	45
Line_1970d-5	Samara RI	197	247	41.7	101	61	107	48	146	46.7	70	42	86	44
Omskiy_Rubin	Omsk ASC	196	187	35.3	107	64	102	52	206	38.3	75	45	90	45
Kargala_228	Aktobe AES	196	197	48.4	101	58	100	53	194	48.4	75	42	86	44

Hordeiforme_553	Altai RI	195	215	40.2	99	61	103	51	174	44.9	75	44	89	45
Altayskaya_Niva	Altai RI	194	199	43.5	117	56	98	54	189	45.6	81	40	86	46
Damsinskaya_Yantarayana	SPC GF n.a. A.I. Baraev	191	221	35.5	106	64	105	49	162	38.5	70	44	88	44
Zhemchuzhina_Sibiri	Omsk ASC	191	186	42.9	103	56	100	53	195	44.9	67	39	85	45
Hordeiforme_426	Altai RI	190	181	38.7	104	62	105	49	200	39.6	76	45	90	45
383-MC	Aktobe AES	190	193	40.1	92	61	105	49	188	44.0	62	42	89	47
Hordeiforme_113/01	Karabalykskaya AES	189	173	34.9	115	65	112	43	206	44.9	88	48	92	44

The average yield for 2 years of research in the Almaty region of check varieties was as follows, Altyn dala - 200 g/m², Zhemchuzhina Sibiri - 214 g/m², and Nauryz 6 - 169 g/m². The weight of 1000 grains of check varieties were Altyn dala - 44.8 g, Zhemchuzhina Sibiri - 41.2 g, Nauryz 6 - 36.2 g. The average duration of the growing season was 102 days, and the duration of the period from germination to heading of standard varieties was 61 days. The height of plants on average reached 109 cm. High-yielding genotypes were mainly distinguished by high-stem forms of 14 genotypes, 11 genotypes of medium-stem forms, and 6 short-stem forms. The duration of the growing season for the highest-yielding varieties lasted from 95 to 107 days. The highest-yielding variety was the local selection of LLP “KazRIAPG” Ertol with an average yield for 2 years of 317 g/m² and the highest thousand grain weight among high-yielding varieties, plant height reaches 105 cm, the duration of the growing season of this variety is 105 days. In second place among high-yielding lines was Hordeiforme 91-22-2, bred at the Omsk ASC, 294 g/m², its weight of 1000 grains reach 44.6 g, with a plant height of 106 cm, the length of the growing season was 98 days. In third place in terms of yield was the Leukurum 1594d-3 line bred at the Samara RI of Agriculture with 292 g/m², the length of the growing season in the Almaty region was 100 days, and the plant height reached 111 cm. Further in descending order of yield was Line 1970d-5 of the Samara bred. with a yield of 247 g/m², the duration of the growing season was 107 days, TKW was 41.7 g, it had an average stem capacity of 101 cm. Hordeiforme line 91-102-6 of the Omsk ASC yield was 244 g/m², TKW was 45.4 g, plant height was 107 cm and 98 days maturity time.

In the Akmola region, the duration of the growing season for high-yielding varieties ranged from 82 to 93 days. The first three lines in terms of high yield in this region were occupied by varieties of Omsk and Altai selection. The Hordeiforme line 00-96-8 showed a yield of 286 g/m², the duration of the growing season was 91 days, the TKW was 40.7 g, the plant height was 74 cm. The yield of the Hordeiforme 924 line was 268 g/m², the TKW was 49.1 g., Plant height 81 cm, duration of the growing season 91 days. The yield of the Hordeiforme 910 line was 246 g/m², TKW 48.4 g, plant height 74 cm, duration of the growing season 90 days. The collection of nutrients and filling of grain took an average of 45 days. The height of the plants reached 71 cm. The average TKW was 44.0 g. The Hordeiforme 95-139-4 line shows an average yield of 242 g/m², with an TKW of 50.6 g, the duration of the growing season is 89 days and the plant height is 77 cm. Further being inferior in yield to these four lines, the accessions of the Karabalyk AES and the Aktobe AES show high productivity. The

yield of the line Hordeiforme 242-93 selection of the Karabalyk AES reaches 241 g/m², 46.1 g - weight of 1000 grains, plant height reaches 77 cm and the duration of the growing season of this line takes 90 days. Variety Kargala 238 selection of the Aktobe AES produces a yield of 239 g/m², with a TKW of 45.7 g, plant height of 77 cm, and the duration of the growing season is 92 days. The highest weight of 1000 grains were in the Samara selection line Leukurum 1469d-21 51.1g, the yield reaches 240 g/m².

For a more accurate understanding of the influence of all traits among themselves, a heat correlation map was constructed, presented in Figure 9. It visually shows a positive correlation between the traits, the duration of the “heading - maturity” period with a weight of 1000 grains, the correlation coefficient of which is (0.21), duration period “heading – maturity” with awn length (– 0.2). Also, the weight of 1000 grains positively correlate with the weight of grain from one spike; the correlation coefficient is (0.42). The length of the awns positively correlates with the grain weight per spike (0.3). The number of grains positively correlates with the grain weight per spike (0.48). And the grain weight per spike is positively correlated with plant height (0.25). A high negative correlation is manifested in spike weight with the duration of the “heading – maturity” period (-0.03). Yield is positively correlated with the length of plant awns (0.07). There is also a high correlation between yeild and the number of productive spikes per plant (0.08). The highest correlation coefficient was recorded between yield and the number of grains from the main spike (0.16).

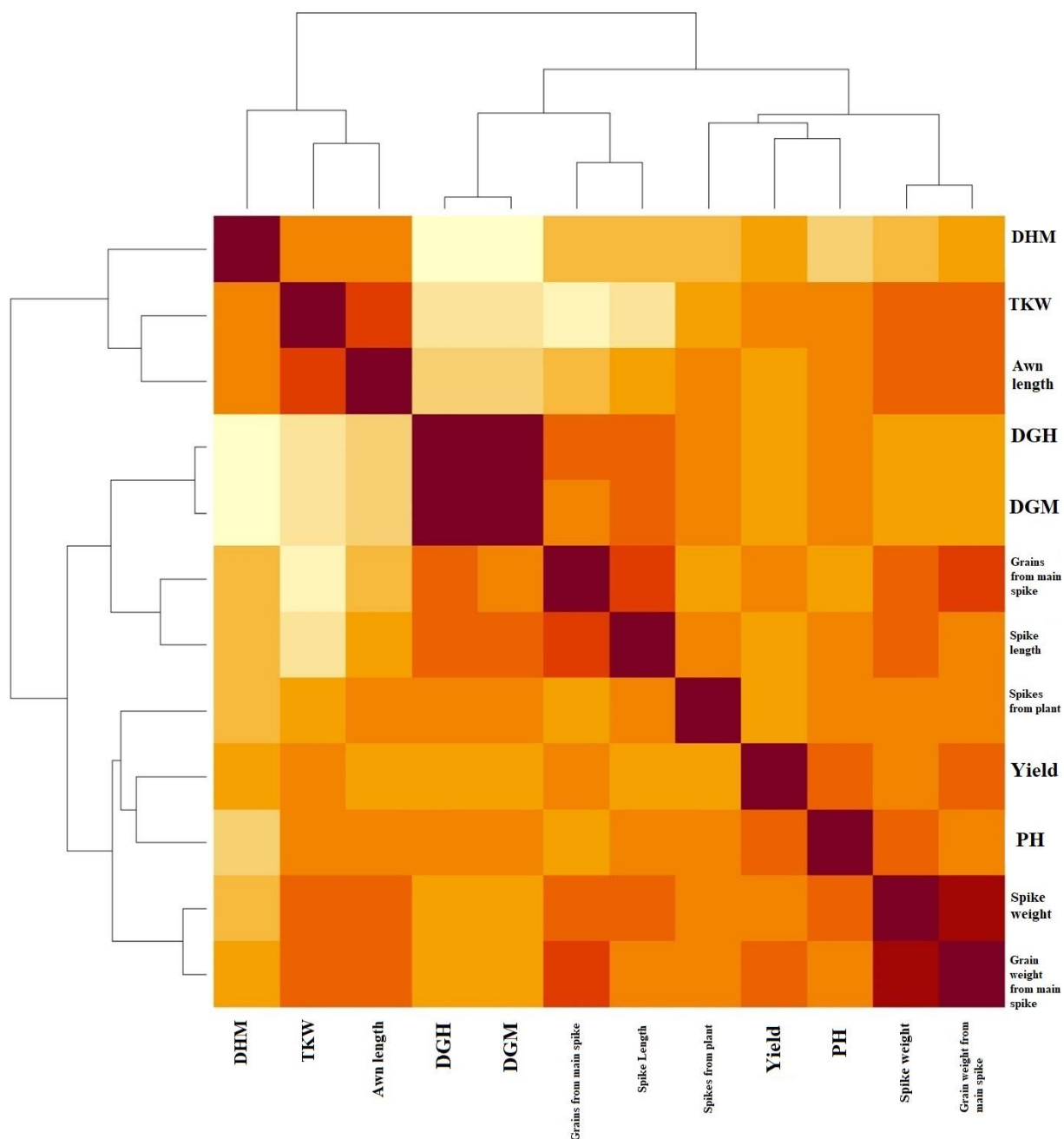


Figure 9 - Heat map of correlation coefficients between all agronomic indicators on average for 2021 – 2022. across two regions.

3.1.2 Agronomic indicators of groups of varieties by originator

A comparison of yields by group of genotypes presented by the originators showed the following results and are presented in Table 5. The genotypes of the Samara and Saratov breeding are combined into one group since they, on average, represent one large region with similar climatic conditions. High yield in the Almaty region is shown by the lines/varieties of the Omsk ASC represented by 25 genotypes - 267 g/m², with a TKW of 38.7 g. The average height of plants of this originator reached 103 cm. The duration of the growing season took 102 days, the duration of the period from

germination to heading was 61 days. In second place in terms of high yield of a group of genotypes from 14 lines of varieties is the SPC GF n.a. A.I. Barayev with a yield of 253 g/m². The TKW was 37.0 g. The duration of the growing season of the genotypes averaged 106 days and the duration of the period from germination to heading was 63 days. The third place is occupied by a group of genotypes of 20 lines and varieties of the Aktobe AES with a yield of 244 g/m², the weight of 1000 grains of which was 42.0 g. The length of the growing season in the Almaty region of the group of genotypes of this originator was 102 days. The duration of the “heading – maturity” period was 51 days and the duration of the period from germination to heading was 60 days. The average yield of a group of 25 genotypes of LLP “KazRIAPG” is 241 g/m², plant height reaches 102 cm, the duration of the growing season was 102 days. The weight of 1000 grains are 38.6 g. The Altai RI with 20 lines/varieties shows a yield of 237 g/m².

Table 5 - Average agronomic indicators of groups of varieties of breeding programs in Kazakhstan and Russia

Originators	No genotypes	Region	DH	DM	DH M	PH	Yield, t/ha	TK W
Local checks	3	Almaty region	61	102	50	109	254	40.7
		Akmola region	41	86	45	71	198	43.9
Aktobe AES	20	Almaty region	60	102	51	102	244	41.9
		Akmola region	41	87	45	71	176	45.1
Karabalykskaya AES	25	Almaty region	62	104	50	107	229	37.6
		Akmola region	44	89	45	76	178	42.5
KazRIAPG	25	Almaty region	59	102	52	102	241	38.6
		Akmola region	42	87	45	69	158	43.1
SPC GF n.a. A.I. Baraev	14	Almaty region	63	106	49	103	253	36.9
		Akmola region	46	91	44	74	161	43.2
Altai RI	20	Almaty region	62	104	50	105	237	41.2
		Akmola region	44	89	45	74	168	45.1
Samara/Saratov	19	Almaty region	58	101	53	98	223	42.4
		Akmola region	41	86	45	68	156	46.9
Omsk ASC	25	Almaty region	61	102	52	103	267	38.7
		Akmola region	43	88	45	71	182	42.8

The average number of days in growing season of these varieties takes 104 days, during this period they form a mass of 1000 grains of 41.2 g, and the plant height reaches an average of 105 cm. The duration of the period from germination to heading of this group of genotypes among all originators reaches 62 days, as well as genotypes of the Karabalyk AES, which form a yield of 229 g/m², their plant height on average reaches 107 cm during the growing season of 104 days, they gain a mass of 1000 grains in 37.6 g. Lines and varieties of Samara and Saratov selection among groups of originating varieties form the lowest yield of 223 g/m². Over the duration of the growing season of 101 days, these samples gain a weight of 1000 grains of 42.4 g.

The fastest maturity among the presented originators in the Almaty region was a group of durum wheat samples from the Samara RI of Agriculture, a branch of the Samara Scientific Center of the Russian Academy of Sciences, and the Saratov Research Institute of the South-Eastern Region (FSBI "FASC of the South-East"), the duration of the growing season of which took an average of 101 days. The highest TKW is also observed in this group of samples and in the Almaty region reaches 42.4 g on average.

In the Akmola region, a group of samples from the Omsk ASC 182 g/m², also stood out for their high yield. The weight of 1000 grains were 42.8 g, the height of the plants reached 71 cm. The average duration of the period from germination to full maturity took 88 days. The duration of the period from germination to heading is 43 days. Also, in this region, a group of varieties selected by the Karabalyk AES and the Aktobe AES distinguished themselves with a yield of 178 and 176 g/m², respectively. The height of plants selected by the Karabalyk AES reaches an average of 76 cm, the Aktobe AES 71 cm. The earliest maturing in this region is the group of varieties of the Samara Research Institute of Agriculture, a branch of the SamRC RAS and the Saratov Research Institute of the South-East Region (FGBNU "FANC of the South-East"), Aktobe AES and KazRIAPG, the duration of the growing season is 86, 87, 87 days, respectively. The yield of a group of samples from the Aktobe AES in this region reaches an average of 176 g/m², and the weight of 1000 grains averages 45.1 g and is one of the highest among originators. The yield of the Altai RI is on average 168 g/m² and the weight of 1000 grains is the same as that of the Aktobe AES - 45.1 g. A group of samples from the SPC GF n.a. A.I. Baraev gains a weight of 1000 grains over the duration of the growing season of 43.3 g and forms a yield of 161 g/m², while the average yield of a group of KazRIAPG samples is 158 g/m², with a weight of 1000 grains of 43.1 g. The average yield of a group of samples Samara and Saratov selection reaches 156 g/m², but with the best weight of 1000 grains at 46.9 g.

3.1.3 Analysis of the main components of agronomic indicators

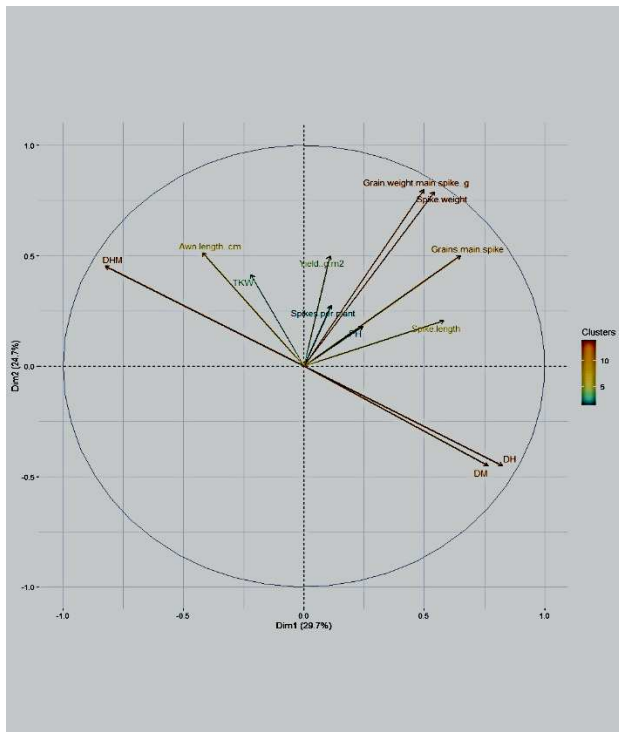
Principal component analysis was conducted separately for each region and year to better understand the relationship between agronomic traits. (Figure 10). This analysis evaluates genotypes based on multiple traits and identifies those that outperform desired variables. Hands-on visualization of this analysis allows the genetic correlation between traits to be determined. The angle between two property vectors approaches the Pearson correlation between them, with an angle less than 90° indicating a positive correlation, an angle greater than 90° a negative correlation, and an angle 90° indicating zero correlation. Additionally, the length of the vector corresponds to the approximate variability of the property. Agronomic indicators for the Almaty region in 2021 were divided into 5 clusters (Figure 10, A). The first cluster included phenological indicators of the growing season of plants and indicators of spike weight, and grain weight from the main spike. There is a positive correlation between the indicators of the mass of the spike and the weight of grain from the main spike; between the indicators of the growing season, that is, the duration of the period from germination to maturity and the duration of the period from germination to heading, a

positive correlation is also observed, while the duration of the period from heading to maturity negatively correlate with all of the above indicators. The second cluster includes the number of grains from the main spike; it also negatively correlates with these characteristics. The third cluster includes two traits: awn length and spike length, which are negatively correlated with each other, but awn length is positively correlated with the weight of 1000 grains, which is classified in the fourth cluster. The fourth cluster also contains Yield. The fifth cluster includes 2 indicators: the number of spikes per plant and plant height. All indicators of plant productivity negatively correlate with indicators of the duration of the growing season, except for the length of awns and the weight of 1000 grains, which positively correlate with the duration of the period from heading to maturity.

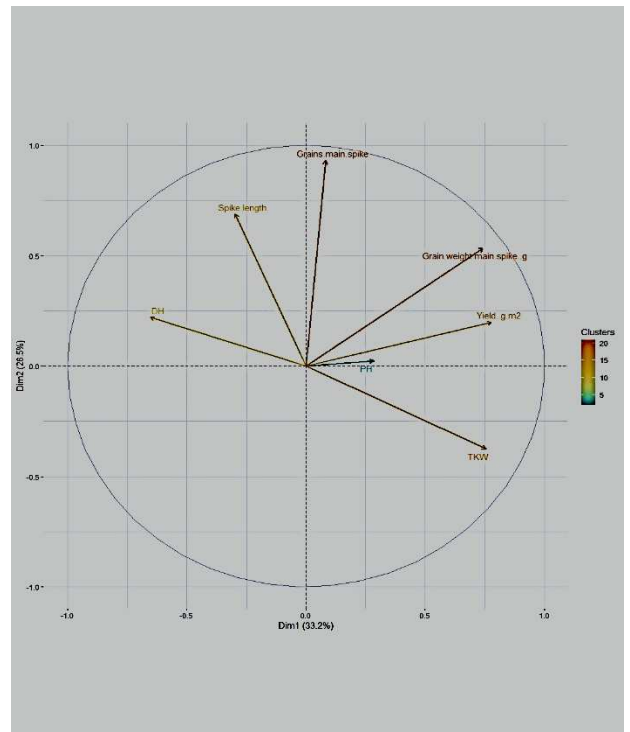
By 2022 (Figure 10, B), the indicators of grain weight from the main spike and the number of grains from the main spike were in the first cluster. The yield indicator and TKW were in the same cluster with indicators of spike length and the duration of the period from germination to heading, while a negative relationship was observed between them. Plant height is included in the third cluster.

The component analysis graph for the Akmola region for 2021 shows similar features as the PCA graph for the Almaty region for 2021 (Figure 10, B). The first cluster includes 3 characteristics: the duration of the period from germination to heading, the weight of the spike, and the weight of grains per spike. The weight of the spike and the weight of grain per spike are negatively correlated with the duration of the period from germination to heading.

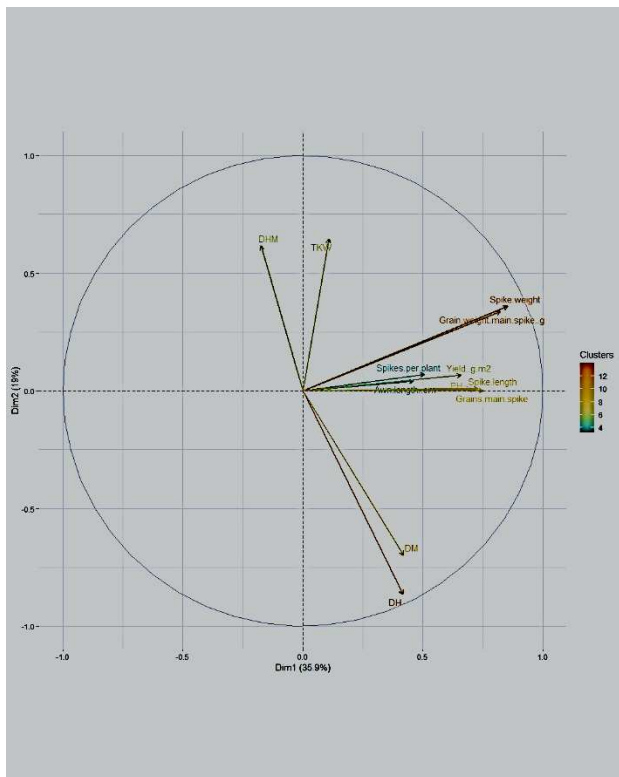
In the second cluster, indicators are highlighted: Spike length, number of grains in the main spike and plant height, all positively correlated with each other, the yield indicator assigned to the third cluster and negatively correlated with the weight of 1000 grains and the duration of the period from heading to maturity. The third cluster included such indicators as Weight of 1000 grains, duration of the period from heading to maturity and yield; TKW is positively correlated with the duration of the period from heading to maturity and both of these indicators are negatively correlated with yield. The fourth cluster contains 2 indicators: the number of spikes per plant and the length of the awns. Positively correlated with each other, with yield, plant height, spike length, number of grains per spike, weight of grains per spike and weight of the spike.



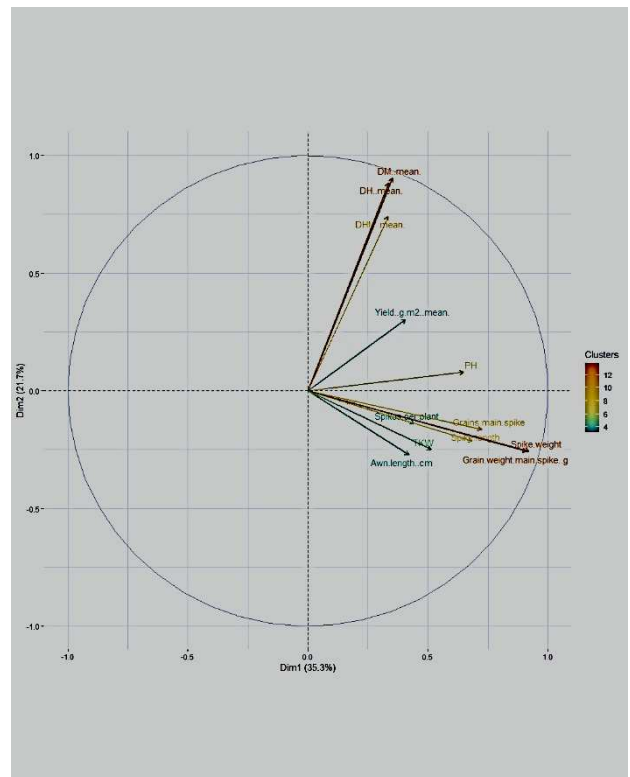
A



B



C



D

Figure 10 - PCA principal component analysis of the main agronomic traits in two regions based on observations in 2020–2022. (A - Almaty region 2021, B - Almaty region 2022, C - Akmola region 2021, D - Akmola region 2022)

Principal component analysis for 2022 for the Akmola region (Figure 10, D) showed that all indicators were divided into 3 clusters. The first cluster included

indicators of spike weight, grain weight from the main spike, the duration of the period from germination to heading and the duration of the period from germination to maturity, the former negatively correlate with the latter. In the second cluster, the characteristics of plant height, the number of grains from the main spike, the length of the spike and the duration of the period from heading to maturity were identified. In the third cluster, yield, number of spikes per plant, length of awns, and weight of 1000 grains were identified.

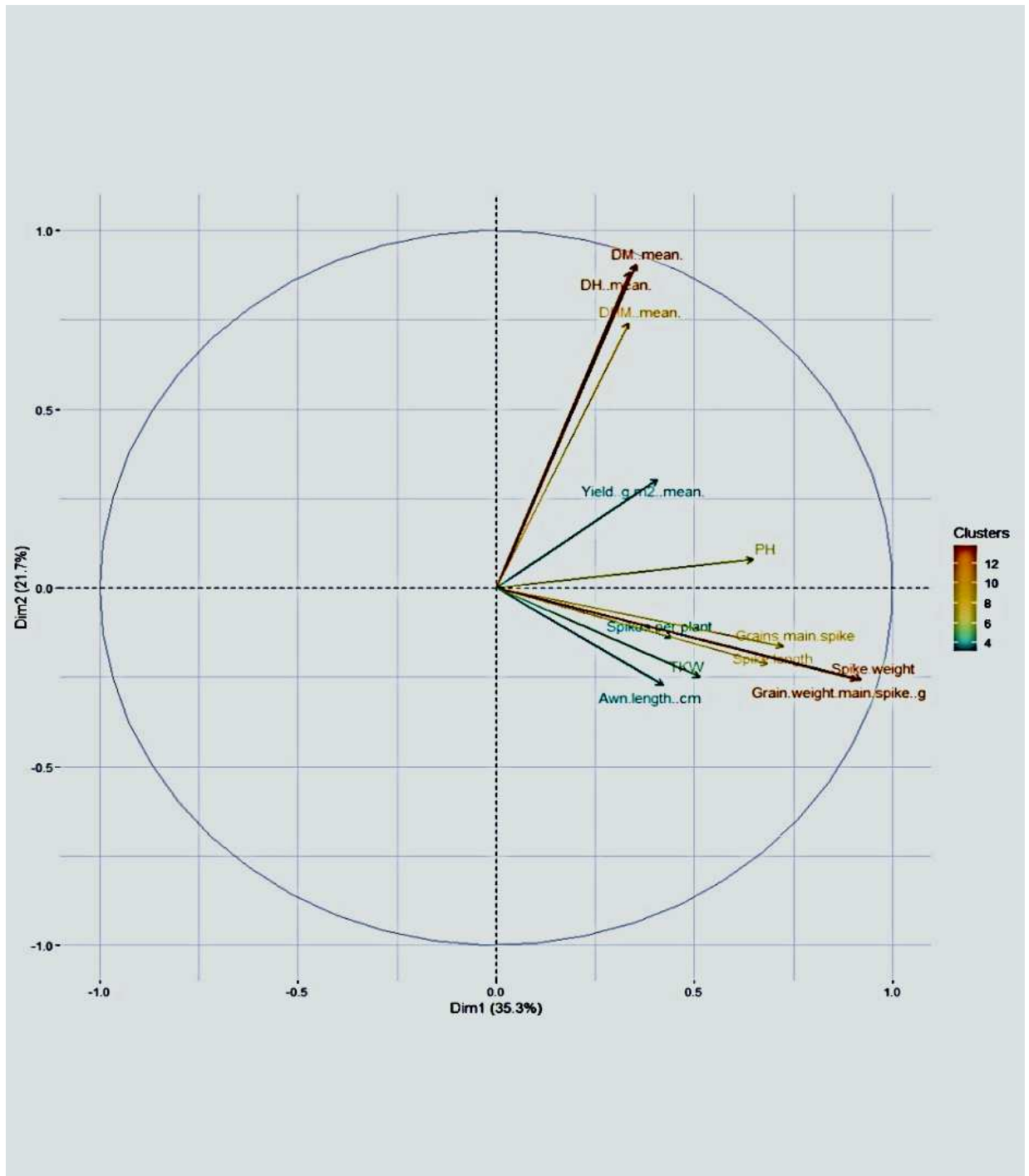


Figure 11 - PCA principal component analysis of main agronomic traits averaged over 2 years for two regions

Analysis of the principal components of average indicators for 2 years and for two regions (Figure 11) showed that all indicators were divided into 3 clusters, as in Figure 10, D. The first cluster included indicators of spike weight, grain weight from the main spike, the duration of the period from germination to heading and the duration of the period from germination to maturity, the former negatively correlate with the latter. In the second cluster, signs of plant height, the number of grains from the main spike, the length of the spike and the duration of the period from heading to maturity were identified. In the third cluster, yield, number of spikes per plant, length of awns, and weight of 1000 grains were highlighted. All biometric parameters, as well as productivity traits, negatively correlate with the growing season.

3.2 Discussion of agronomic results of growing durum spring wheat in the conditions of Almaty and Akmola regions

In this thesis, a pre-breeding study of varieties and lines of spring durum wheat was carried out in two regions - Almaty and Akmola regions of Kazakhstan. The purpose of this study was to prepare samples for further breeding work.

The experiments were carried out according to the methodology of field experiments, and statistical analysis of agronomic indicators showed that the experiments were carried out correctly. The standard error of the mean, standard deviation, and least significant difference were within normal limits.

The analysis of the PCA principal components clearly shows a negative relationship between the length of the growing season and agronomic indicators. In the Akmola region, this is explained by the fact that early ripening varieties go through growth stages faster, which affects their yield. Late-ripening varieties, although they gain a high grain weight and produce more yield, are at risk of early snowfall, which can result in a possible loss of yield and grain quality. Also, the growth and development of plants is strongly influenced by the length of daylight hours in the Akmola region; this period lasts 16 hours 30 minutes, while in the Almaty region the length of daylight hours lasts 15 hours 30 minutes; in addition, the foothill region also shortens the length of daylight hours due to shade. All this increases the duration of the growing season of all genotypes in the Almaty region. Nevertheless, in the lines and varieties there is a hereditary predisposition to early or late ripening, which is clearly visible in the experiments conducted.

Most of the high-yielding genotypes from the spring durum wheat collection of the KASIB network in the Almaty region also show high yields in the Akmola region, 7 out of 15 genotypes.

Russian genotypes of the Omsk ASC are more adaptive to different regions, as can be seen from the group of varieties. From the domestic selection, the genotypes of the originators of the Karabalyk AES, the Aktobe AES in terms of genotype yield and KazRIAPG in terms of early maturity performed well in adaptation, and on average over two years in two regions the Ertol variety is high-yielding. Russian lines/cultivars are also adapted to grow over a wide range, that is, in several different regions.

Significant differences in the passage of growth and development phases between originators were observed. The sets of varieties and lines of the Aktobe AES,

the Karabalyk AES and LLP “KazRIAPG” differ in the length of the growing season from the varieties of the LLP “SPC GF n.a. A.I. Baraev” and the Altai Research Institute of Agriculture, the Samara and Saratov Research Institute of Agriculture and the Omsk ASC in that the passage of development phases during the period from germination to heading of the genotypes of the first three institutions takes a shorter period of several days than the passage of development phases during the period from heading to maturity as in Almaty and Akmola regions. The genotypes of Russian institutions in the Akmola region also go through development phases during the period from germination to heading and from heading to maturity on par with the Aktobe AES, Karabalyk AES, LLP “KazRIAPG”, but in the Almaty region the genotypes of Russian originators take the duration of the period from germination to heading longer than the duration of the period from heading to maturity. Passage of development phases of genotypes of LLP “SPC GF n.a. A.I. Barayev” during the period from germination to heading takes longer than the duration of the period from heading to maturity in both the Akmola region and the Almaty region.

Duration of the growing season of varieties and lines of LLP “SPC GF n.a. A.I. Barayev” is the largest among all originators and accounts for the largest number of days in both the Almaty region and the Akmola region. Thus, the period for the accumulation of nutrients in the grain of the genotypes of the LLP “SPC GF n.a. A.I. Barayev” is the highest in the Almaty region, but in the Akmola region they are not effective because the season there is shorter and maturity occurs later, which significantly affects the quality of the grain and leads to crop losses due to late harvesting.

According to the height of the stem, sets of varieties and lines of the Aktobe Agricultural Society, LLP “KazRIAPG”, LLP “SPC GF n.a. A.I. Baraev”, Altai RIA and Omsk ASC can be classified as medium-stem. The set of varieties from the Samara and Saratov SRIA are the shortest-stemmed among all the originators, while the highest-stemmed varieties were from the Karabalyk AES.

The genotypes of the originators of the Aktobe AES, Altai RIA, Samara and Saratov RIA are the most resistant to various growing conditions and show similar results in terms of weight of 1000 grains. The remaining originators of the group of varieties in the Almaty region show a lower weight of 1000 grains than in the Akmola region, this is caused by different growing conditions and different genetic characteristics of the varieties, which can respond more effectively to certain growing conditions in one region than in another.

Yield reaches the highest values and is stable in various growing conditions at the originators of the Omsk ASC, the Karabalyk AES and the Aktobe AES. Despite the fact that the varieties and lines of LLP “KazRIAPG”, LLP “SPC GF n.a. A.I. Barayev” were adapted to regional conditions, the yield level turned out to be lower than expected, which represents a well-known paradox.

Based on the experiments performed, the results obtained and the above conclusions, a preliminary conclusion can be made. Since the Almaty region has a milder climate and high humidity, which creates ideal conditions for selection for various diseases. Crossbreeding in the Almaty region and further selection of

genotypes for the Akmola region is possible. Taking into account the need to replenish the collection with drought-resistant varieties. Increasing the yield of early and mid-ripening lines/varieties. Regardless of the region of crossing, and in the presented collection of lines and varieties belong to 10 originators from Russia and Kazakhstan, many of the genotypes show high adaptability and yield in two geographically different regions. Lines and varieties of domestic selection, although they show high adaptive potential in one region, but, unfortunately, they do not have adaptability to several different regions. This result can only be achieved through the selection and testing of lines in each region of the country, regardless of the place of crossing. There is a need to expand environmental testing nationwide.

Regarding the duration of the growing season, there is also the question of its optimization; genotypes whose yields were low over the years of research were influenced by weather conditions in specific regions without having time to go through the growth and development phases of plants necessary to obtain high yields and productivity, that is, the adaptation of these plants did not develop best during years of research. Possible need for research to study the timing of sowing durum wheat in these regions.

4 High throughput phenotyping of plant cover of spring durum wheat in field conditions in northern Kazakhstan using a digital camera

4.1 Results of high-throughput phenotyping

Research in the field of digital technologies has advanced very much today. With the latest technologies, it is possible to carry out additional observations without invasive intervention either in the structure of crops or without causing damage to plants throughout the entire growing season. One such method that has been used in research is high-throughput phenotyping with RGB images.

During the 2021–2022 years of research in the Akmola region, a large amount of digital phenotypic data was obtained. Indicators obtained using RGB images varied significantly depending on the year. Phenological variability showed significant differences in the relationships of indicators with yield.

As described in Chapter 3, significant differences in yield were highly dependent on weather conditions. This manifestation of variability in yield and other indicators is also noted in digital indicators.

The signs $GA\ m^2$, $GGA\ m^2$ and CSI obtained from digital images reliably show the accumulation of green mass before plant heading and the beginning of their wilting during the accumulation of nutrients in the grain. (Figure 12).

These indicators are most closely related to plant yield. The period of greatest accumulation of green mass on the graph is marked by a peak on the second date of taking digital indicators and occurs on the 20th of June or during the main phases of plant development - booting and heading. The greenness indicators in 2021 are not significant due to the low amount of precipitation and acute drought this year, while in 2022 these indicators are highly different from 2021 due to the prevailing weather conditions. The green area in 2021, as noted on the graph, appears as a descending line after the date of plant heading. In 2022, this same indicator increases until the date of heading and then sharply falls down according to the marked date of the beginning of necrosis of plant leaves. The graph of greener mass $GGA\ m^2$, as scientists note, is more suitable for monitoring plant photosynthesis, and correlates perfectly with photosynthesis indicators.

The process of plant wilting also begins at this stage of plant development after heading and reaches a peak value on the fourth date of taking digital indicators, which falls on August 4-10 or during the milky and milky-waxy ripeness phases of plants. Unlike green indices, during the process of plant necrosis or wilting, the plant wilting index does not decrease significantly after reaching its peak. As known, wheat begins to wither from the bottom leaf to the very awns, gradually transferring all the nutrients from the green organs to the grain. This is visually evident in this graph based on the recorded stages of wheat development. In 2021, there is a gradual increase in wilting, while in 2022 this indicator appears at a faster pace than 2021, possibly influenced by meteorological conditions.

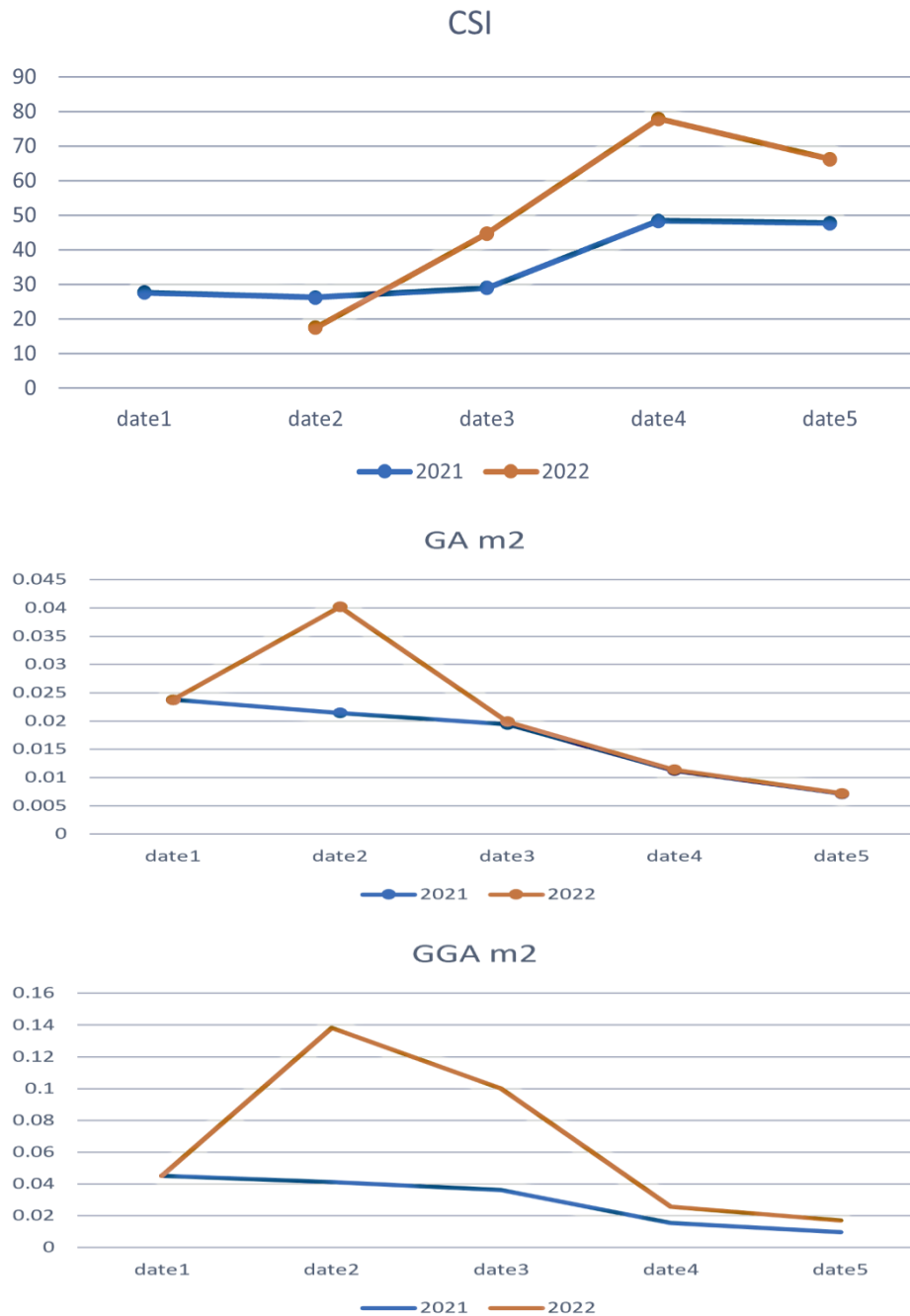


Figure 12 - Indices of aging of grain and green area for the growing season of 2021 and 2022. in Akmola region

According to the results of the correlation analysis, the AUPC value of the variables green pixels a^* , u^* , green area per m^2 , greener area per m^2 and the plant wilting indicator were significantly associated with agronomic traits, which is clearly visible in Figure 13. The value of the period duration correlation coefficient from heading to maturity with green pixels a^* was (0.082), with a green area $GA\ m^2$ and a greener area $GGA\ m^2$, (-0.054) and (-0.023), respectively. Also, a high correlation was noted between the weight of 1000 grains and the indices a^* (0.04), u^* (-0.071), $GA\ m^2$ (-0.023), $GGA\ m^2$ (-0.016) and CSI (-0.068). All biometric parameters were also

correlated with digital parameters. A negative correlation is observed between yield and plant wilting index CSI, the influence of this indicator on the duration of the growing season is significant.

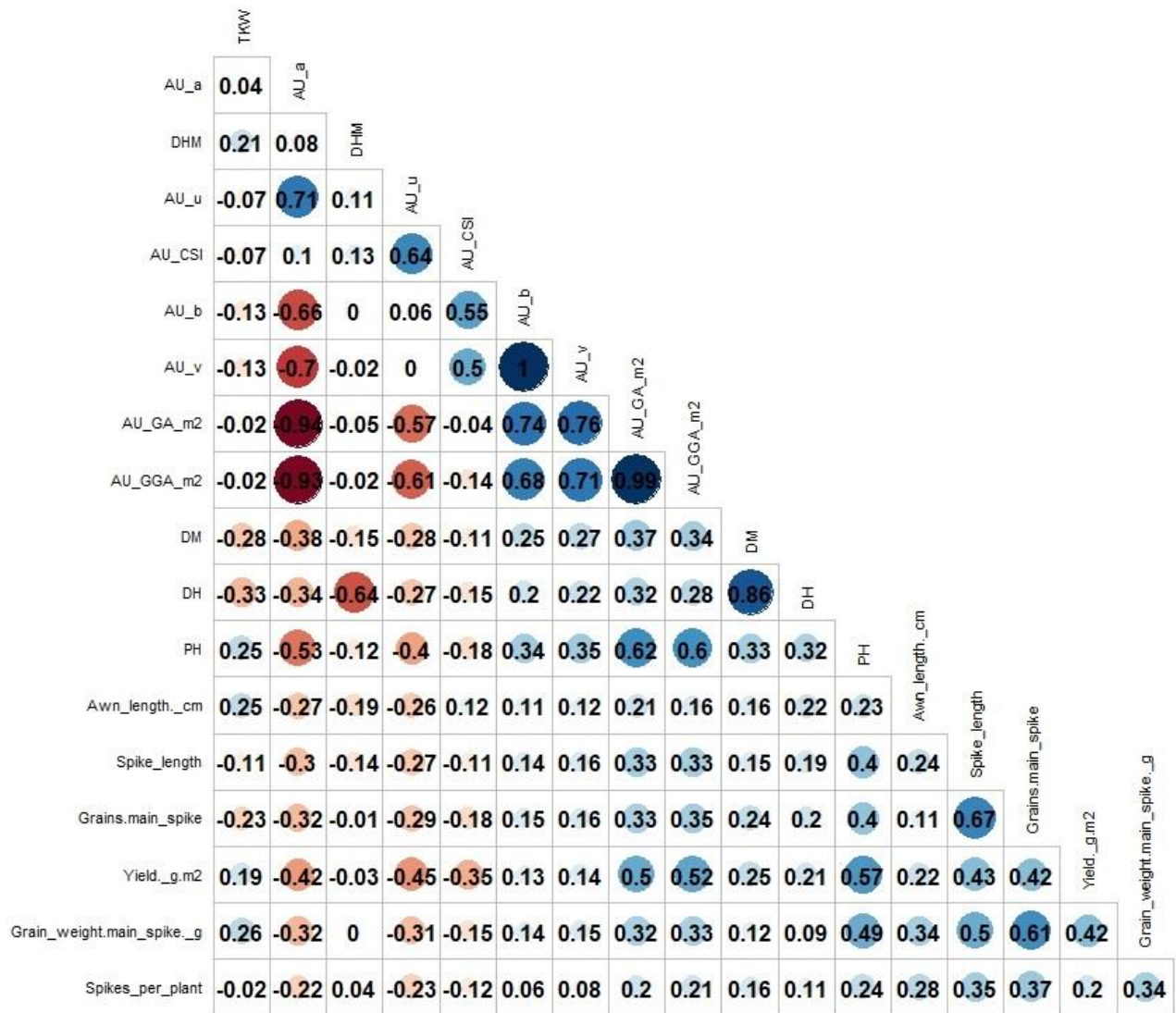


Figure 13 - Heat map of correlation coefficients on average over 2 years for two regions.

The results of the relationships between the characteristics in different years are clearly visible in Figure 14. The bi-plot was divided into 3 clusters according to all characteristics. The first cluster included the following TKW characteristics, Grain weight per spike, Yield, a*, u*, CSI. All these signs refer to the period when the plant is gaining grain mass and the correlation between them is obvious. Thus, the listed agronomic traits positively correlate with the indices a*, u*, CSI and green mass indicators GA m², GGA m². A decrease in the number of green pixels (a*, u*) indicates that during this period the plants are actively gaining nutrients and the transfer of nutrients from the plant to the grains. The second cluster included characteristics of the duration of the period from germination to heading, the duration of the period from

heading to maturity, the duration of the growing season, the number of grains in the spike, GA m², GGA m², plant height and plant biomass.

The correlation shown in Figure 14, A. Agronomic traits Grain weight per spike, Yield, weight of 1000 grains are to a small extent positively correlated with the following digital parameters u*, green area, greener area and plant wilting index. The length of awns and the duration of the period from heading to full ripeness also correlate positively with the digital parameters u*, green area, greener area and plant wilting index, but to a greater extent.

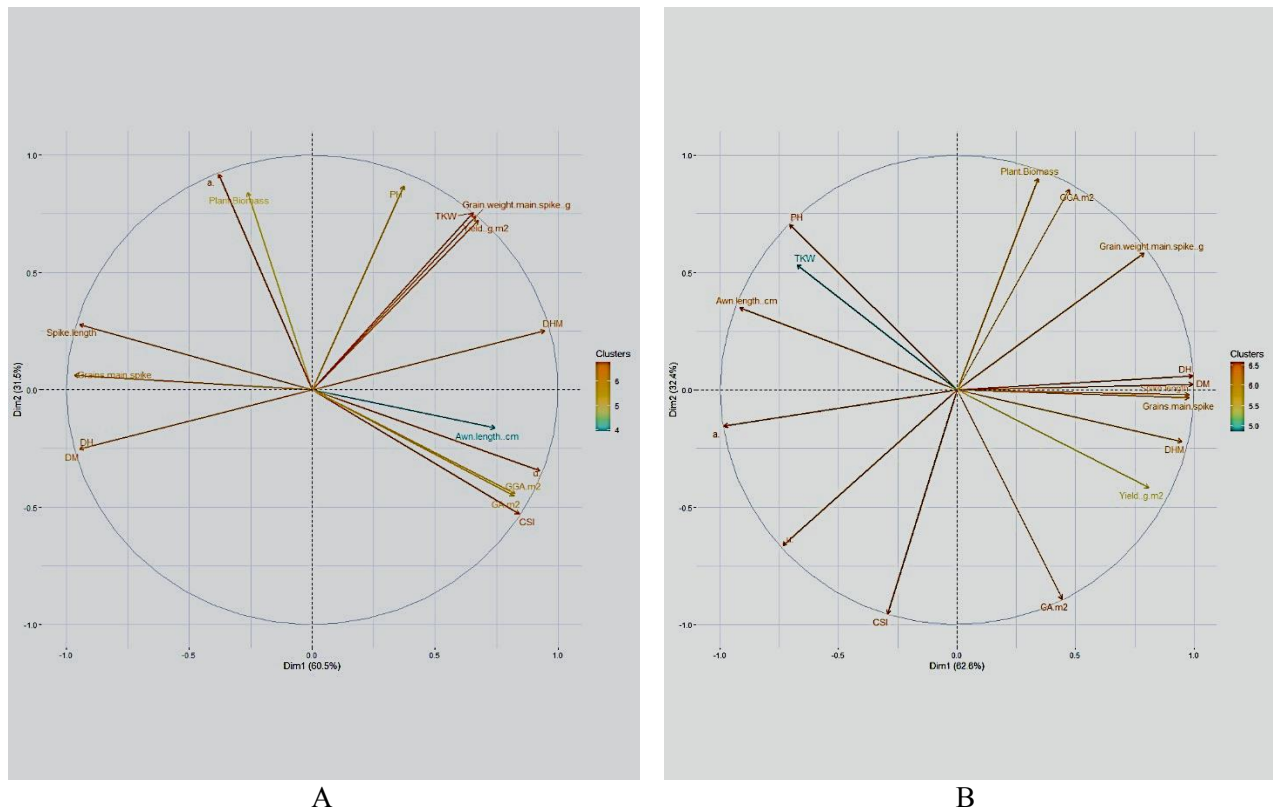


Figure 14 - Bi-plots according to the main agronomic, biometric and digital indicators (A indicators for 2021, B - indicators for 2022)

Plant biomass is positively correlated with the a* coefficient, although they are in different clusters. Only one trait, awn length, was included in the third cluster. But in turn, it negatively correlates with the coefficient of the number of green pixels (a*) and a positive relationship with other digital coefficients is visible. Namely GA m², GGA m², u*, CSI. The awns, in contrast to the whole plant, turn from green to yellow, that is, they fade last, because of this, a high positive correlation can be traced, which in turn leads to the theory that the awns of plants have an important role in plant development, photosynthesis, and recruitment. grain mass, and the accumulation of nutrients, and, consequently, yield.

There is also a negative correlation of phenological traits, the duration of the period from germination to heading and the duration of the growing season, with the digital parameters u*, green area, greener area and plant wilting index. This

relationship between these characteristics is explained by the fact that insufficient precipitation and the time of sowing do not meet the requirements of these varieties.

In 2022, these signs were distributed as follows (Figure 14, B). A positive correlation with yield is manifested in digital indicators: green area, plant wilting index, a small correlation with greener area and a negative correlation of yield with digital indicators: u^* , a^* . The number of grains from the main spike is also positively correlated with green area, greener area and plant wilting index, and a negative correlation is observed with u^* , a^* . The biometric indicator spike length is also highly correlated, as is the number of grains from the main spike. The mass of grains from the main spike, on the contrary, correlates more strongly in a positive direction with a greener area and a negative correlation with all other digital indicators. Plant biomass is more positively correlated with greener area and negatively correlated with other digital indicators. And the length of the awns is more positively correlated with the indicators u^* , a^* and negatively with the green area, greener area, and plant wilting index. The 1000 grain weight is positively correlated with u^* , a^* and greener area, and there is also a negative correlation with plant wilting index and greener area. The height of plants, as well as the weight of 1000 grains, positively correlates with the indicators u^* , a^* , greener area. And negatively with the green area and the plant wilting index, which means taller plants wither more slowly than short-stemmed ones. Phenological indicators - the duration of the period from germination to heading, the duration of the period from heading to maturity and the duration of the growing season - are equally positively correlated with green area and greener area with all other digital indicators is negatively correlated.

An analysis of the principal components of average indicators for 2021 - 2022 is shown in Figure 15. All characteristics were also divided into 3 clusters, the first cluster included such characteristics as: Yield, spike length, plant biomass, plant height, awn length, greener area, a^* , u^* .

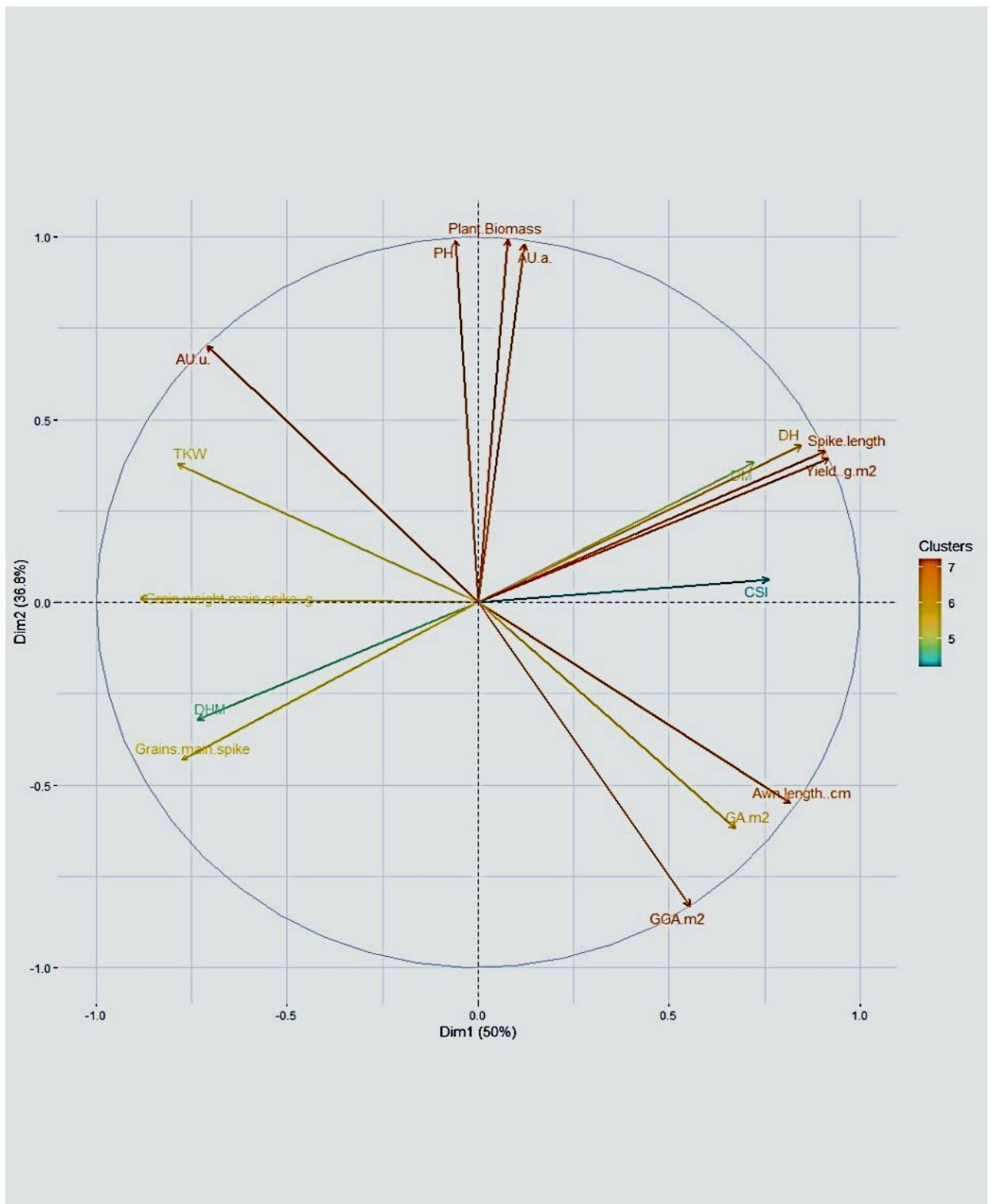


Figure 15 - Analysis of the main components of digital indicators for 2021 – 2022

The second cluster includes indicators: duration of the period from germination to heading, weight of 1000 grains, weight of grains from the main spike, number of grains from the main spike, duration of the period from germination to heading and green area. The third cluster includes the duration of the growing season of plants, the duration of the period from heading to maturity and the index of plant wilting.

There is also a correlation between all the signs. Yield is positively correlated with the plant wilting index, which confirms the accumulation of nutrients in the grain in the post-flowering phase. Also, a positive correlation of yield is observed with indicators of green area and greener area, that is, on average, over two years, these indicators gained optimal green mass, and plant photosynthesis also took place in optimal conditions for these varieties to gain the resulting yield. There is also a positive correlation with the yield and the number of pixels in the photograph a^* , which also confirms the optimal passage of plant development phases to achieve high yields. Yield is negatively correlated with the u^* index which shows the number of green pixels at a later time. Exactly the same correlation is observed in the duration of the period from germination to heading, the growing season and the length of the spike. Biometric indicators such as plant biomass and plant height correlate to a greater extent with the a^* and u^* index, just during the period of plant growth and development, an increase in green pixels is observed in photographs, that is, an increase in plant biomass. There is a negative correlation with other digital indicators, that is, plant height and plant biomass do not directly affect the green area in the photograph. Awn length is highly positively correlated with plant wilting index, green area and greener area. The indicator of the length of the awns remains green until the last and the process of wilting in the awns begins last, which explains the interaction with the wilting index and green area, and for the greener area indicator which shows the photosynthetic activity of plants, it leads to the theory that the awns continue photosynthetic activity and the transfer of nutrients substances into the grains even after the entire plant has withered, additional research is needed to confirm the theory. The mass of 1000 grains are most positively correlated only with the digital indicators a^* , u^* , and the most negative correlation is observed with the digital indicators of green area, greener area and plant wilting index. The number of grains negatively correlates with digital indicators a^* , and the plant wilting index, that is, an increase in grains is not observed during this period, which is natural for plants, this indicator is determined by the genotype and during the flowering period of plants. And with the indicators u^* , green area and greener area there is no correlation at all. The mass of grains from the main spike is positively correlated with the index u^* , which refers to the period after heading, which means the bulk of the grain is gained in the period after heading. There is a clear negative correlation with all other digital indicators; the higher the grain weight per spike, the lower the green area, greener area and plant wilting index.

4.2 Agronomic indicators of high-yielding accessions in comparison with indicators obtained using digital technologies

Table 6 highlights high-yielding varieties in the Akmola region for 2021 in comparison with digital indicators; for 2022, the data is presented in Table 7. Despite the dry conditions in 2021, the yield was higher in 2021 compared to 2022. This is justified by the lack of precipitation during the required period of development of plants.

Table 6 - High-yielding varieties in comparison with digital data for 2021 in Akmola region

Genotypes	Average Yield 2021 - 2022, g/m ²	Yield, g/ m ²	DM	CSI	GA m ²	GGA m ²	a*	u*
Nauryz_6 (LC-1)	200	260	86	1213	0.572	1.034	-15	292
Altyn_Dala (LC-2)	190	227	82	1241	0.718	1.358	-24	264
Zhemchuzhina_Sibiri (LC-3)	204	262	82	1270	0.509	0.910	-101	206
Hordeiforme_00-96-8	286	381	89	1184	0.747	1,393	-21	257
Hordeiforme_924	268	370	89	925	0.724	1,367	-135	177
Hordeiforme_910	246	298	86	996	0.639	1.156	-154	145
Hordeiforme_95-139-4	242	344	86	1060	0.710	1,396	-40	208
Hordeiforme_242-93	241	328	86	1254	0.723	1.355	-77	249
Leucurum_1469d-21	240	337	86	1370	0.665	1,209	-71	254
Kargala_238	239	265	89	1481	0.684	1.163	-105	183
Seymur	235	289	89	1307	0.620	1.116	-90	262
Hordeiforme_1790	225	311	89	894	0.606	1.111	-87	238
Kostanayskaya_15	222	288	89	1074	0.490	0.853	-150	157
Yantarnaya_60	217	277	86	1088	0.469	0.801	-122	203
Kargala_1540	216	296	86	1254	0.688	1,284	-113	188
Hordeiforme_895	213	259	89	1066	0.613	1.067	-122	180
Kargala_1538	213	300	82	1289	0.662	1.228	-117	180
Leucurum_1594d-3	211	309	86	1364	0.776	1.428	-77	242
Line_250-06-14	208	285	89	1042	0.567	0.989	-100	216
Omskiy_Rubin	206	242	88.0	1244	0.712	1.341	-27	222
Hordeiforme_113/01	206	274	89	1436	0.810	1,340	-132	192
Line_69-08-2	204	250	82	1069	0.474	0.815	-102	203
Hordeiforme_94-24-12	202	297	89	1238	0.629	1.155	-35	238
Hordeiforme_426	200	266	89	1274	0.807	1.457	-120	174
Hordeiforme_98-42-1	199	236	86	1404	0.592	1.031	-41	220
Line_G1612	197	246	88	1468	0.664	1.085	-151	172
Zhemchuzhina_Sibiri	195	256	82	1412	0.607	1,041	-49	184
Hordeiforme_59-92	195	252	86	1256	0.640	1.181	-135	204
Kargala_228	194	247	82	1194	0.582	1,063	-123	187
Hordeiforme_127-89	194	241	88	1144	0.806	1.524	-100	230
Bezenchikskaya_139	194	266	86	1366	0.661	1.185	-94	240
Hordeiforme_18585-2	193	233	86	1359	0.621	1,092	-137	197
Orenburgskaya_2	192	244	86	1250	0.700	1.257	-70	264

Table 7 - High-yielding varieties in comparison with digital data for 2022 in Akmola region

Genotypes	Average Yield 2021-2022, g/m ²	Yield, g/m ²	DM	CSI	GA m ²	GGA m ²	a*	u*
Nauryz_6 (LC-1)	200	139	91	1770	0.087	0.883	-127	126
Altyn_Dala (LC-2)	190	154	93	1729	0.090	1,360	-153	150
Zhemchuzhina_Sibiri (LC-3)	204	146	81	2018	0.084	1.149	-87	189
Hordeiforme_00-96-8	286	191	92	1744	0.087	1.322	-142	154
Hordeiforme_924	268	165	93	1813	0.090	1,198	-133	169
Hordeiforme_910	246	195	93	1742	0.087	1.219	-111	209
Hordeiforme_95-139-4	242	140	91	1621	0.097	1.552	-129	164
Hordeiforme_242-93	241	155	93	1689	0.072	1.085	-139	179
Leucurum_1469d-21	240	144	88	1861	0.111	1.261	-221	123
Kargala_238	239	212	94	1959	0.115	1.418	-101	154
Seymur	235	181	97	1794	0.109	1.495	-138	181
Hordeiforme_1790	225	140	92	1692	0.113	1,579	-202	121
Kostanayskaya_15	222	156	95	1832	0.104	1.545	-236	40
Yantarnaya_60	217	157	85	1824	0.105	1,189	-75	266
Kargala_1540	216	136	92	2086	0.118	1.237	-109	191
Hordeiforme_895	213	167	95	1423	0.131	1,760	-119	182
Kargala_1538	213	125	82	1584	0.086	1.428	-128	166
Leucurum_1594d-3	211	114	96	1903	0.118	1,520	-161	130
Line_250-06-14	208	130	96	1905	0.115	1.276	-158	161
Omskiy_Rubin	206	170	91	1703	0.106	1,983	-151	156
Hordeiforme_113/01	206	138	94	1915	0.097	1.216	-178	143
Line_69-08-2	204	157	93	1960	0.089	1.257	-180	132
Hordeiforme_94-24-12	202	107	92	1830	0.081	1,270	-147	137
Hordeiforme_426	200	133	91	2061	0.119	1.236	-73	217
Hordeiforme_98-42-1	199	162	91	1994	0.083	1.057	-199	88
Line_G1612	197	147	93	1771	0.111	1.676	-164	216
Zhemchuzhina_Sibiri	195	134	87	1850	0.087	1,090	-220	77
Hordeiforme_59-92	195	139	92	1630	0.075	1,302	-124	214
Kargala_228	194	142	90	1838	0.077	1.129	-126	199
Hordeiforme_127-89	194	148	93	1890	0.085	0.944	-133	160
Bezenchikskaya_139	194	123	94	2004	0.081	1,083	-161	137
Hordeiforme_18585-2	193	152	92	1709	0.092	1.161	-142	204
Orenburgskaya_2	192	140	87	1809	0.076	1.124	-97	218

First of all, it should be noted that there is a clear difference in digital characteristics between 2021 and 2022. As mentioned above, 2021 turned out to be a dry year, as a result of which the plants did not receive both green mass and harvest,

and all agronomic characteristics showed a negative influence of weather conditions, this difference is also noticeable in digital signs. Thus, the indices of green area m^2 , greener area m^2 in 2021 had a lower indicator compared to 2022. In 2021, the maximum value of green area m^2 was 0.810, and the minimum was 0.268; in 2022, the maximum value of green area m^2 was 0.131, and the minimum was 0.066. The value of greener area m^2 is maximum 1.592 and minimum 0.411, while in 2022 2.018 maximum and minimum 0.789.

In 2021, the highest yield was shown by the Hordeiforme line 00-96-8 - 381 g/m^2 , the plant wilting index was 1184, the green area m^2 was 0.747, the greener area was recorded as 1.393, the green pixel index in the period before heading was 21 and the indicator green pixels in the period after heading 257.

In comparison with standard varieties, the yield of the Hordeiforme 00-96-8 line was higher by more than 100 g/m^2 , the wilting index value was 100 less, and the green area indicator value was the same as the standard variety Altyn Dala. Also, this line exceeded the value of the green area m^2 of the varieties of the Zhemchuzhina Sibiri and Nauryz 6 standards by 0.200. The value of the greener area for the varieties of the Zhemchuzhina Sibiri and Nauryz 6 standards is 0.500 and 0.400 lower than that of the high-yielding line.

In general, in 2021, in high-yielding lines, the plant wilting index formed in the range from 894 to 1200, that is, the process of plant wilting was much slower than in samples whose wilting index exceeded 1300, and the duration of the period from germination to heading in high-yielding lines reached 47 - 50 days. For all these lines, the duration of the growing season was also recorded within 89 - 90 days, which apparently is the optimal number of days of the growing season for the formation of high yields. The remaining samples, which showed lower yields, were earlier ripening than the selected lines and shown in tables 6 and 7. A high greener area with m^2 was also seen in the samples: Karabalykskaya_chernokolosaya, Hordeiforme_127-89, Line - 18987, Hordeiforme_426, Leucurum_1594d-3, Damsinskaya_Yubileynaya, Hordeiforme_95-139-4, Hordeiforme_00-96-8, Lavina, Hordeiforme_924, Shortandinskaya_256, Altyn_Dala (LC -2), Hordeiforme_242-93, Line_e147-z, Omskiy_Rubin, Hordeiforme_113/01, these samples had a greener m^2 area recorded ranging from 1.34 to 1.59 and their yield was 237 g/m^2 , 241 g/m^2 , 204 g/m^2 , 266 g/m^2 , 309 g/m^2 , 202 g/m^2 , 344 g/m^2 , 381 g/m^2 , 193 g/m^2 , 370 g/m^2 , 262 g/m^2 , 227 g/m^2 , 328 g/m^2 , 224 g/m^2 , 242 g/m^2 , 274 g/m^2 , respectively; this list mainly consists of high-yielding lines. This indicator shows the high photosynthetic activity of these plants, which results in high yields. The height of the plants reached from 70 to 80 cm.

In 2022, the plant wilting index formed in the range from 1423 to 2156; this indicator was much higher than in 2021 in proportion to the formed green mass of plants, but unlike 2021, the plant wilting index in high-yielding samples was in the range from 1700 to 1800. Duration of the growing season the period for these samples lasted from 94.7 to 100 days. The duration of the period from germination to heading ranged from 47 days to 52 days. A high greener area in 2022 was observed in samples with a yield of Karabalykskaya_chernokolosaya -132 g/m^2 , Omskiy_Rubin - 170 g/m^2 , Serke - 110 g/m^2 , Hordeiforme_895 - 167 g/m^2 , Kostanayskaya_12 - 154 g/m^2 , Line_G

1612 – 147 g/m², Leucurum_1469-21 – 126 g/m², Angel – 124 g/m², Nauryz_8 – 169 g/m², P - 1409 – 130 g/m², Line_54-02-2 L – 104 g/m², Hordeiforme_97-49-1 – 166 g/m², Hordeiforme_1790 – 140 g/m², Hordeiforme_95-139-4 – 140 g/m², Hordeiforme_01-115-5 – 178 g/m², Kostanayskaya_15 – 156 g/m², The weight of 1000 grains of these samples ranged from 37.9 – 49.8 g.

On average for 2021–2022, the plant wilting index ranged from 1245 to 1783 (Table 8). According to the plant wilting index, most of the high-yielding varieties were in the range from 1245 to 1473. Their growing season lasted from 83 days to 93 days with the lowest 1000 grain weight of 37.93 g and the highest 51.45 g. High greener area m² 1.33 – 1.80 was observed in samples with a yield of Karabalykskaya chernokolosaya - 184 g/m², Omskiy_Rubin - 206 g/m², Hordeiforme_95-139-4 - 242 g/m², Leucurum_1594 d - 3 – 211 g/m², Angel – 179 g/m², Nauryz_8 – 187 g/m², Hordeiforme_895 – 213 g/m², Damsinskaya_Yubileynaya – 166 g/m², Line_G 1612 – 197 g/m², Line_54-02-2 L – 167 g/m², Hordeiforme_553 – 174 g/m², Line_18987 – 165 g/m², Altyn_dala (LC -2) – 190 g/m², Hordeiforme_00-96-8 – 286 g/m², Line_18472-3-2 – 165 g/m², Kargala_24 – 155 g/m², Hordeiforme_426 – 200 g/m², Hordeiforme_1790 – 225 g/m², Kargala_1539 – 161 g/m², Hordeiforme_587 – 155 g/m².

An analysis of agronomic and digital indicators on average by originator and year is shown in Table 8. Thus, standard varieties on average in 2021 showed a yield of 250 g/m², formed a weight of 1000 grains on average of 41.7 g, the duration of the period from germination to heading was 40 days and the total duration of the growing season is 83 days. The plant wilting index was 1241, the green area m² was 0.60 and the greener area m² was 1.10.

In 2022, the indicators of the standard varieties were as follows: yield - 146 g/m², weight of 1000 grains - 46.2 g, duration of the period from germination to heading - 42, duration of the growing season - 89 days, CSI - 1839, green area m² – 0.09, greener area m² – 1.13.

In 2021, the genotypes of the Aktobe AES generated an average yield of 213 g/m², the average weight of 1000 grains were 45.5 g. The set of genotypes went through the main phases of growth and development, the duration of the period from germination to heading in 40 days and the overall duration of the growing season period was 84 days.

Table 8 - Average digital indicators with the main agronomic indicators of groups of varieties of breeding programs of Kazakhstan and Russia

Originators	Year	No genotypes	Yield, g/m ²	TKW	DH	DM	CSI	GA m ²	GGA m ²	a*	u*
Local checks	2021	3	250	41.7	40	83	1241	0.60	1.10	-95	235
	2022		146	46.2	42	89	1839	0.09	1.13	-153	156
Aktobe AES	2021	25	213	45.5	40	84	1264	0.58	1.03	-47	254
	2022		138	44.7	42	89	1771	0.09	1.27	-122	155
Altai RIA	2021	20	197	43.9	43	86	1318	0.58	1.00	-104	208
	2022		138	46.1	45	91	1778	0.10	1.30	-147	152
Karabalykskaya AES	2021	25	219	41.4	43	86	1290	0.63	1.13	-105	225
	2022		137	43.6	45	92	1821	0.09	1.23	-160	159
KazRIAPG	2021	14	179	42.3	40	85	1292	0.53	0.93	-115	202
	2022		138	43.8	43	90	1773	0.09	1.27	-147	162
SPC GF n.a. A.I. Baraev	2021	20	198	41.6	45	87	1297	0.64	1.12	-101	213
	2022		125	44.9	47	94	1885	0.10	1.22	-134	179
Samara/Saratov	2021	19	183	47.7	39	83	1312	0.45	0.75	-82	236
	2022		128	46.0	42	89	1854	0.09	1.31	-159	152
Omsk ASC	2021	25	222	42.1	41	85	1253	0.59	1.06	-51	209
	2022		143	43.5	44	91	1801	0.09	1.26	-153	142

The plant wilting index was 1264, the green area m² was 0.58, and the greener area m² was 1.03. Samples from the Karabalyk AES in 2021 on average produced a yield of 219 g/m², with a weight of 1000 grains of 41.4 g. The duration of the growing season for a set of samples from the Karabalyk AES took 86 days, and the duration of the period from germination to heading was on average 43 days. Plant wilting index 1290, green area 0.63 m², and greener area m² 1.13. The duration of the growing season for a set of LLP “KazRIAPG” samples in 2021 was 85 days, with a duration of the period from germination to heading of 40. The average yield of all varieties was 179 g/m², with a wilting index of 1292, a green area of 0.53 and more green area m² - 0.93. Genotypes of LLP “SPC GF n.a. A.I. Baraev” on average gained a yield of 198 g/m² and a weight of 1000 grains of 41.6 g, for a growing season of 87 days and an average of 45 days for the duration of the period from germination to heading, while the plant wilting index was 1297, green area m² 0.64 and more green area m² - 1.12. The genotypes selected from Samara and Saratov gained a yield of 183 g/m² during a growing season of 83 days with a duration of the period from germination to heading of 39, while the weight of 1000 grains were 47.7 g. The plant wilting index was 1312, the green area m² was 0.45 and more green area m² - 0.75. The genotypes of the Omsk

ASC generated a yield of 222 g/m², with a weight of 1000 grains of 42.1 g, this yield was formed by a set of varieties during a growing season of 85 days and a duration of the period from germination to heading of 41. At the same time, the plant wilting index reached the value in 1253, green area m² - 0.59, and greener area m² - 1.06. Samples from the Altai RIA produced an average yield of 197 g/m² with a weight of 1000 grains of 43.9 g. The plant wilting index was 1318 for a growing season of 86 days, and the duration of the period before heading was 43. The green area m² was 0.58, and the greener area was 1.00.

In 2022, the indicators for originators were as follows. The genotypes of the Aktobe AES on average generated a yield of 146 g/m², the weight of 1000 grains averaged 44.7 g. The duration of the period from germination to heading of this set of genotypes was 42 days and the overall duration of the growing season was 89 days. The plant wilting index was 1771, the green area m² was 0.09, and the greener area m² was 1.27. Samples from the Altai RIA produced an average yield of 138 g/m² with a weight of 1000 grains of 46.1 g. The plant wilting index was 1778 for a growing season of 91 days, and the duration of the period from germination to heading was 45 days. The green area m² was 0.10 and the greener area was 1.30. Samples from the Karabalyk AES on average produced a yield of 137 g/m² with a weight of 1000 grains of 43.6 g. The duration of the growing season for a set of samples from the Karabalyk AES took 92 days, and the duration of the period from germination to heading was on average 45 days. Plant wilting index 1821, green area 0.09 m², and greener area m² 1.23. The duration of the growing season for the collection of LLP "KazRIAPG" samples was 90 days, with the duration of the period from germination to heading 43 days. The average yield of all varieties was 138 g/m², with a wilting index of 1773, a green area of 0.09 and a greener area of 1.27 m². Genotypes of LLP "SPC GF n.a. A.I. Baraev" averaged a yield of 125 g/m² and a weight of 1000 grains of 44.9 g, over a growing season of 94 days and an average of 47 days from germination to heading, while the plant wilting index was 1885, green area m² 0.10 or more green area m² - 1.22. The genotypes selected from Samara and Saratov gained a yield of 128 g/m² during a growing season of 89 days with a duration of the period from germination to heading of 42 days, while the weight of 1000 grains were 46.0 g. The wilting index of plants was 1854, green area m² - 0.09 and more green area m² - 1.31. The genotypes of the Omsk ASC generated a yield of 143 g/m², with a weight of 1000 grains of 43.5 g, this yield was formed by a set of varieties during a growing season of 91 days and the duration of the period from germination to heading of 44 days. At the same time, the plant wilting index reached a value of 1801, the green area m² was 0.09, and the greener area m² was 1.26.

The index of plant wilting in 2021 among the originators that showed the best yield was Omsk ASC 1253, Karabalyk AES - 1290, Aktobe AES - 1264. In 2022, the Omsk ASC 1801, Karabalyk AES - 1821, Aktobe AES - 1771.

4.3 Discussion of high-throughput phenotyping results

Drought (understood as a combination of water stress and heat) and heat stress itself are among the most limiting environmental factors affecting wheat development, causing a variety of biochemical, molecular and physiological changes that affect yield.

With the development of digital technologies, new technologies are increasingly being introduced to improve breeding. The introduction of digital photography technology is no exception. This technology is of particular importance in the study and development of fungal diseases of various crops, as evidenced by the large number of articles described in the literature review. The study of plant adaptability to daylight, as well as their growth and development during the growing season is the most important trait in breeding. RGB images are one of the best tools for understanding the adaptive potential of plants; in comparison with NDVI, it is also the cheapest tool. They also provide a large amount of data, which can be observed in this study. Analysis of RGB data allows you to visualize the growth and development of each individual variety, which in turn gives an idea of the adaptive potential of the variety. Improvement of regionally appropriate heading and flowering time or RGB indicators, additional parameters such as CSI and GGA m^2 will improve yield potential. The larger the leaf area of the plant, the more carbohydrates are formed after heading, which in turn can have a positive effect on the yield. This is due to the fact that a large leaf area contributes to better nutrition of the plant, which affects the number and weight of grains formed during the heading period. Reliable determination of vegetation cover is possible using the indices GA m^2 and GGA m^2 , a^* and u^* . Drought and heat stress significantly reduced the values of RGB image indices, corresponding to a decrease in productivity and the development of plant vegetation. Large leaf area increases the total surface area for photosynthesis and promotes energy storage in plants. This allows you to increase the number of grains and their weight, which has a positive effect on yield.

There are several genotypes for which there is some correlation between CSI, GA, GGA and yield. For example, for the *Hordeiforme_242-93* variety, you can notice that the higher the GGA value, the higher the yield. For the *Kostanayskaya_15* variety, you can notice an inverse correlation between yield and GGA value.

Genotypes with greener area (higher GA and GGA) may have higher yields as this may indicate healthier plants and more productive growth. Among the studied genotypes of spring durum wheat, there are several varieties/lines with high yield (more than 240 g/ m^2), such as *Hordeiforme_00-96-8*, *Hordeiforme_924*, *Hordeiforme_910* and *Seymur* and others, which also have high green area and greener area.

Speaking about the yield and the weight of 1000 grains, a clear connection is visible with the area of green vegetation. During the maturation process, there is a clear connection with a decrease in green area. Thus, it can be assumed that phenotypes that retain green color longer or early necrosis from plant aging, these values can be attributed to certain genotypes and, accordingly, crosses can be carried out to improve yield.

Based on the tests conducted, we can say that the best time to conduct digital research is the transition phase of wheat, the duration of the period from heading to full ripeness, since at this time phenotypic differences between early and late ripening

varieties are noticeable. For green mass, it is better to take measurements during the period from the beginning of germination to heading. This is also confirmed by various studies. The plant wilting index is largely related to the growing season of plants, and there is also a connection with the increase in yield. Green area m^2 and greener area m^2 have a clear relationship with yield, which confirms various studies and the feasibility of using this method in plant breeding. The data analysis also suggested theories for future research on the relationship between greener mass and photosynthetic activity of plants during the growing season.

The high correlation between digital data and agronomic indicators suggests that digital technologies such as remote sensing can be useful for collecting and analyzing data in agriculture. This can help breeders make more accurate and informed decisions regarding improving plant varieties, determining optimal sowing and harvesting times, monitoring plant health, and much more. In addition, a high correlation between numerical data and agronomic indicators can confirm the importance of the latter in assessing crop quality and quantity, identifying potential problems and developing yield improvement strategies.

With the help of highly efficient phenotyping in the field, it was possible to collect data on green mass from a large number of plants and different genotypes, without resorting to heavy physical labor and without losing plants in the plots. The most optimal genotypes were identified according to several criteria simultaneously.

Data obtained through high-throughput phenotyping have enormous potential for optimizing the breeding process and developing new plant varieties. They can also help advance understanding of plant physiology and morphology, as well as their interactions with the environment. Phenotyping can be used to study various aspects of the plant life cycle, including growth, development, flowering, fruiting, resistance to diseases and pests, adaptation to climate change, and others. Such data can significantly speed up the process of developing new plant varieties that can provide higher yields, more efficient use of resources and increased resilience to changing environmental conditions or increase the adaptability of plants to multiple regions and more sustainable yields.

5 GENETIC DIVERSITY AND POPULATION STRUCTURE OF KASIB NURSERY DURMUM WHEAT USING MARKERS BASED ON IPBS-RETROTRANSPOSONS

5.1 Polymorphism of iPBS retrotransposon primers

An integral part in the yield of wheat plants is the yield and adaptability of plants to cultivated conditions, which in turn is determined by the genetic characteristics of genotypes that are transmitted from generation to generation and accumulate in the DNA/chromosomes of plants. [144] Using retrotransposon markers, it is possible to determine the number of genetic populations and determine the approximate place of origin of all studied genotypes. Also, based on the place of origin, an approximate understanding of the adaptive potential of all available material is possible. [145]

All primers used in the study produced bands that were consistent, clear, and quantifiable. A total of 345 bands were obtained from ten primers, 317 of which were highly polymorphic. The number of bands at each locus ranged from 23 (iPBS-2228) to 44 (iPBS-2226), with a mean of 34.5 bands per locus. The percentage of polymorphism found among the primers ranged from 75.00% to 100% with a mean of 91.88%. The highest and lowest polymorphism information content was 0.118 (2389) and 0.308 (2226), respectively, with an average value of 0.251 (Table 9).

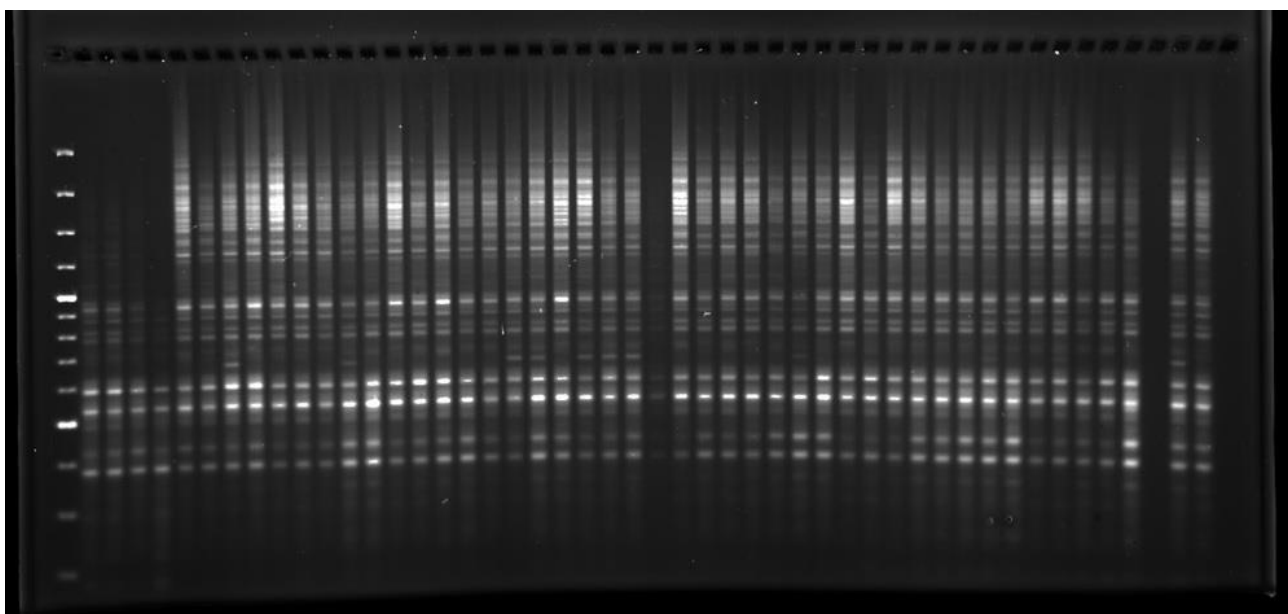


Figure 16 - Part of the PCR results obtained using iPBS retrotransposon markers

Table 9 contains the values for the number of effective alleles (N_e), genetic diversity N_{ei} (h), total gene diversity (h_t) and Shannon information index (I). The range of effective number of alleles (N_e) was from 1.186 (iPBS -2389) to 1.524 (iPBS -2239) with a mean of 1.418. The highest level of gene diversity (0.309) was recorded for iPBS at 2226 and the lowest (0.118) for iPBS at 2389, with a mean of 0.251. The Shannon Information Index ranged from 0.201 (iPBS - 2389) to 0.472 (iPBS - 2239) with a mean of 0.388. The maximum total gene diversity was found in primer 2226

(0.293) and the minimum in primer 2389 (0.056) with a mean of 0.233. Primer 2226 was more informative, as reflected in its high diversity indices, while 2389 was the least informative (Table 9). These results indicate higher genetic variation in the germplasm studied.

The PIC value indicates the resolution of the marker. The mean PIC value obtained in this study was 0.251, which ranged from 0.118 to 0.308. iPBS 2226 with the highest PIC value (0.308) was identified as the best marker for differentiating the presented genotypes.

Several indices were calculated to identify genetic diversity in durum wheat germplasm KASIB (Table 9). Maximizing the number of effective alleles is always beneficial because they demonstrate the presence of more genetic variation. The average effective number of alleles (1.41) found in the present study.

Table 9 - Diversity indices calculated to assess genetic diversity among 151 durum wheat accessions using 10 iPBS retrotransposon primers.

Primer name	TNB	PB	Polymorphism (%)	Ne	h	I	ht	PIC
2228	23	20	86.96	1,248	0.165	0.277	0.165	0.165
2074	36	35	97.22	1.435	0.265	0.412	0.246	0.262
2226	44	44	100.00	1.514	0.309	0.472	0.293	0.308
2239	36	33	91.67	1.524	0.306	0.462	0.270	0.307
2245	32	32	100.00	1,498	0.293	0.446	0.293	0.294
2252	33	32	96.97	1.403	0.251	0.395	0.233	0.251
2256	31	29	93.55	1,407	0.260	0.406	0.260	0.260
2270	36	27	75.00	1,487	0.266	0.385	0.257	0.267
2271	38	33	86.84	1,480	0.280	0.420	0.261	0.281
2389	36	32	88.88	1,186	0.118	0.201	0.056	0.118
Average	345	317	91.88	1,418	0.251	0.388	0.233	0.251

Note Total number of TNB bands, effective number of alleles Ne, polymorphic bands PB, gene diversity h, Shannon information index I, total gene diversity Ht, polymorphism information content PIC

The average gene diversity (0.25) obtained in the study was higher than reported [2] using iPBS retrotransposons to estimate the genetic diversity and population structure of Turkish bread wheat germplasm and thus explains the presence of higher diversity in the studied germplasm. The Shannon information index is an important criterion for recognizing variation because it differentiates genetic diversity in a population by combining abundance and evenness [146]. Average Shannon Information Index (0.40)

The likely reasons for the presence of higher values of the various diversity indices may be due to the high efficiency of the iPBS-retrotransposon marker system

in assessing genetic diversity, or the higher diversity may be due to the nature of the germplasm itself.

To obtain a more accurate idea of the genetic diversity of the studied germplasm, its genetic distance was calculated in three different programs Popgen, STRUCTURE, GenAlex. The average genetic distance of all 151 samples was 0.287. The maximum genetic distance (0.7077) was found between genotypes Seymour_17 and Hordeiforme_430-88, and the minimum genetic distance (0.0384) was found between genotypes Hordeiforme_98-42-1 and Altyn_Shygys (data not shown).

5.2 Determination of the number of populations in the KASIB collection

5.2.1 Constructing genetic populations using the STRUCTURE program

Also, to analyze the genetic structure of populations, an analysis was carried out using STRUCTURE in which two classified populations (K = 2, A and B) and one unclassified population were identified based on $Q \geq 75\%$ of individual origin coefficients. To determine the number of populations, several values of K were run, then an algorithm was used to select the most appropriate value of K, which was based on the probability of the model. This algorithm is called the probability estimation method [147] (Figure 17, 18). The first population (Pop A) consisted of 82 genotypes, including 46 Kazakh and 35 genotypes of Russian samples. Population B included 54 genotypes, including 30 from Kazakhstan, 23 from Russia, and 15 samples were not classified and were located between populations A and B (Figure 18).

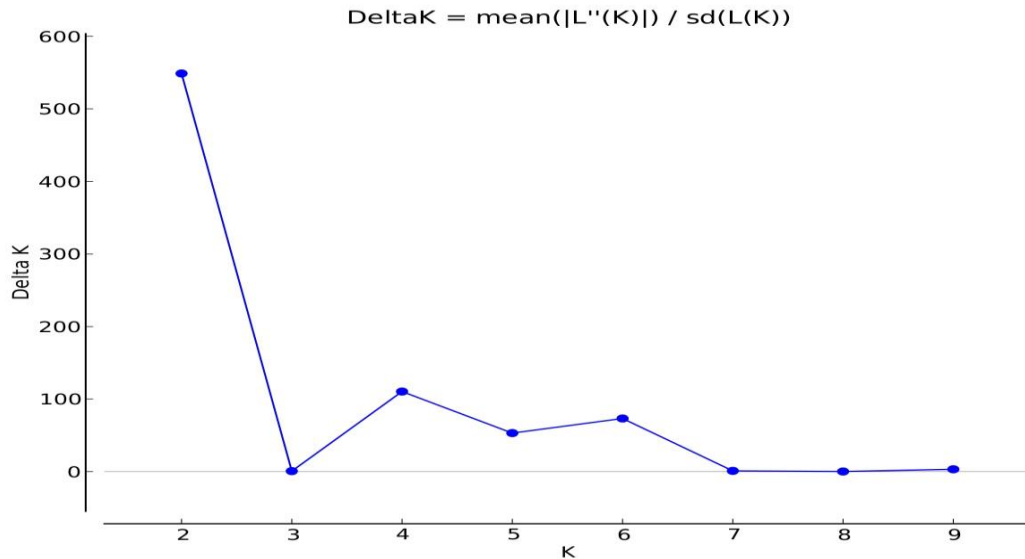


Figure 17 - Delta value K, suggesting the presence of two germplasm populations of durum wheat KASIB using the iPBS retrotransposon marker system.

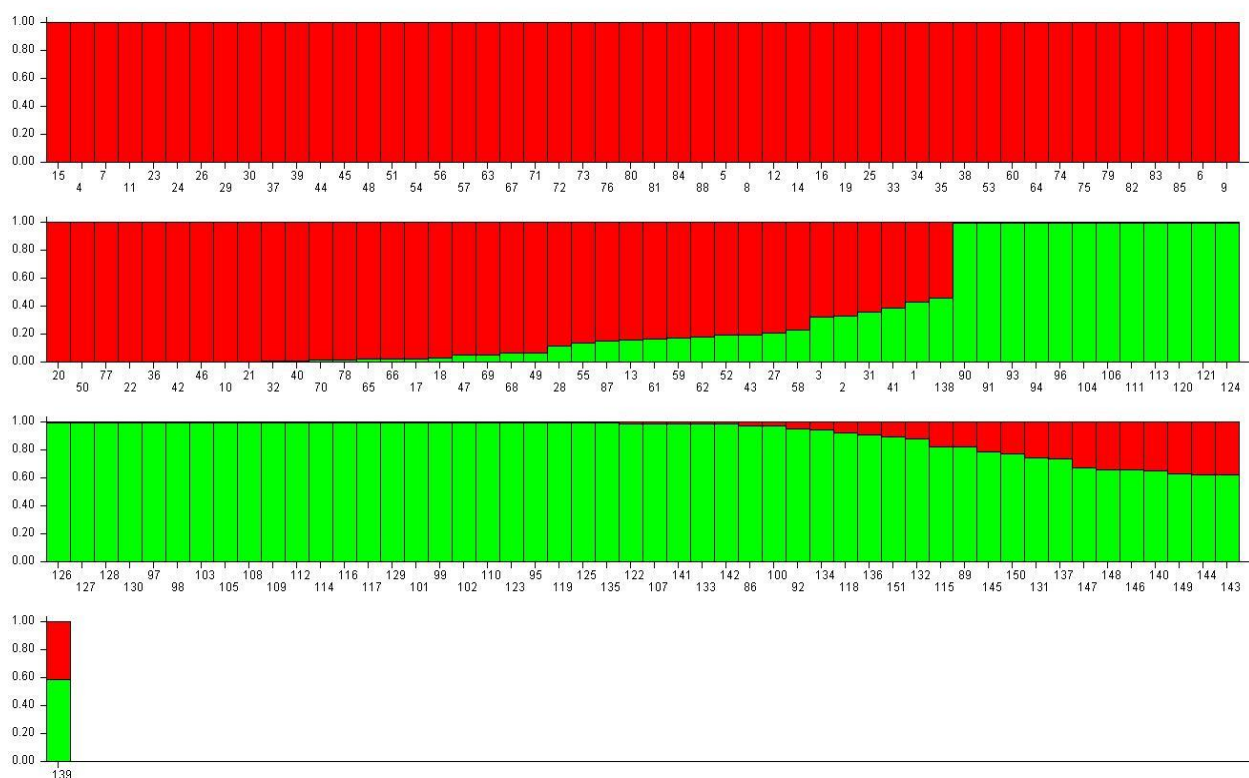


Figure 18 - Population structure of durum wheat germplasm KASIB using the iPBS-retrotransposon marker system based on the STRUCTURE program. (Population A is marked in red, population B is marked in green)

5.2.2 Construction of genetic populations using the NJ tree

The NJ tree divided the entire collection of 151 images, just like STRUCTURE, into 2 groups - A, B. Population A contained 86 genotypes while population B contained 65 genotypes. Additionally, populations A and B were divided into subgroups or subpopulations A 1, A 2, and B 1, B 2. Group A 1 - consists of 40 samples, and group A 2 consisted of 46 samples, group B 1 were assigned 58 genotypes, group B 2 contained 7 genotypes (Figure 19). The analysis performed using the NJ tree was closer to the phenological data, but was still excluded from further statistical analyzes with agronomic indicators. In group A 1, the following genotypes were identified: Kargala 1408, Kargala 1514/06, Kargala 1538, Kargala 1539, Kargala 1540, Kargala 1671, Kargala 69, Altayskiy Yantar, Hordeiforme 553, Hordeiforme 561, Hordeiforme _573, Hordeiforme 587, Hordeiforme 616, Hordeiforme 864, Altyn Dala, Altyn Shygys, Bolashak, Hordeiforme 113/01, Kostanayskaya 10, Line G 1549, Line G 1612, Lan, Line 18404, Line 18472-3-2, Corona, Durum 2, Line 54- 02-2 L, Line e145-z, Line e147-z, Line 653 d -44, Line 688 d -4, Hordeiforme_00-96-8, Hordeiforme 94-24-12, Hordeiforme 94-94-13, Hordeiforme 95-139-4, Hordeiforme 97-49-1, Hordeiforme 98-42-1, Omksiy Izumrud, Omskaya Stepnaya, Omskiy Cirkon.

In group A there are 2 samples: 383-MC, 452-MC, Kargala 18, Kargala_24, Kargala_303, Kargala_447, Altayskaya_Niva, Hordeiforme_415, Hordeiforme_417, Hordeiforme_426, Altyn_Dala (LC-2), Hordeiforme_127-89, Hordeiforme_207-92, Hordeiforme_242-93, Hordeiforme_362 -91, Hordeiforme_430-88, Hordeiforme_59-

92, Karabalykskaya_chernokolosaya, Kostanayskaya_1, Kostanayskaya_12, Kostanayskaya_30, Line_160.93, Line_362.91, Ertol, Line_18485-2, Line_17590, Line_17950, Line_18022-1, Line_18053, Line_654-1-2-3 -4, Line_6801-34-6, Nauryz_8, Seymur, Toma, Durum_49, Damsinskaya_Yantarnaya, Ametist, Angel, Hordeiforme_91-102-6, Hordeiforme_91-144-4, Hordeiforme_91-22-2, Hordeiforme_94-71, Omskaya_Yantarnaya, Omskiy_korund, Omskiy_Rubin, Zhemchuzhina_Sibiri.

In group B 1 the following samples were isolated: Kargala_1514, Kargala_228, Kargala_238, Kargala_66, Soyana, Hordeiforme_627, Hordeiforme_628, Hordeiforme_719, Hordeiforme_748, Hordeiforme_829, Hordeiforme_881, Sharifa, Hordeiforme_18567-6, Hordeiforme_18585-2, Line_18987, Line_19003, Line_19029, Damsinskaya_Yubileynaya, Hordeiforme_178-05-2, Hordeiforme_69-08-2, Lavina, Shortandinskaya_256, Bezenchikskaya_139, Hordeiforme_1591-21, Leucurum_1307 D -51, Leucurum_1307 d -54, Leucurum_1469 d -21, Leucurum_1506-36, Leucurum_1594 d -3, Annishka, Elizavetinskaya, Luch_25, Valentina, Hordeiforme_01-115-5, Hordeiforme_04-76-5, Hordeiforme_05-42-12, Omskiy_Korall, Zhemchuzhina_Sibiri (LC-3), Yantarnaya_60, Hordeiforme_895, Hordeiforme_910, Hordeiforme_924, Kostanayskaya_15, Line_19029, Nauryz_6 (LC -1), Serke, Seymur_17, 19055/ Hordeiforme, Line_18093-7-2, Line_18924, Line_250-06-14, Line_69-08-2, Line_1693 d -71, Line_1970 d -5, Line_2021 d -1, Line_D -2165, Hordeiforme_08-25-2, Hordeiforme_08-67-1.

And group B 2 included samples P-1409, Hordeiforme_2264, Asangali, Orenburgskaya_2, Hordeiforme_1790, Leucurum_1429-10, Leucurum_1469-21.

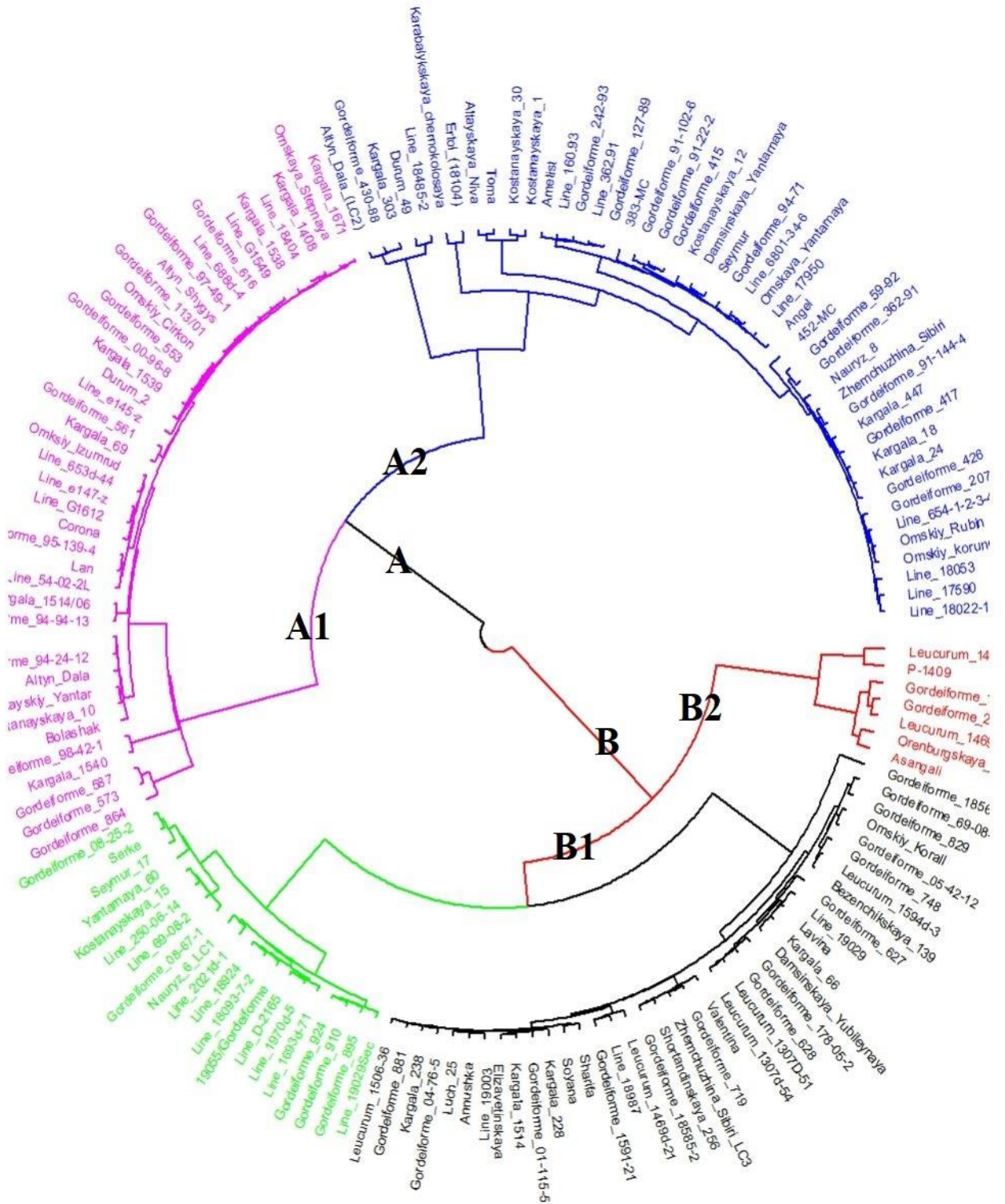


Figure 19 - Clustering of durum wheat germplasm KASIB based on neighbor-joining analysis using the iPBS-retrotransposon marker system.

5.2.3 Constructing genetic populations using GenAlex

Using principal component analysis in the GenAlex program, the following results were obtained by dividing all samples into separate groups depending on their geographic location (Figure 20).

Principal component analysis showed that the entire collection was divided into 2 populations and 4 subpopulations, regardless of place of origin. Subpopulation 1 (pop 1) included 42 genotypes, the second subpopulation included 53 genotypes, the third subpopulation included 45 genotypes, and the fourth subpopulation included 11 genotypes (Table 10).

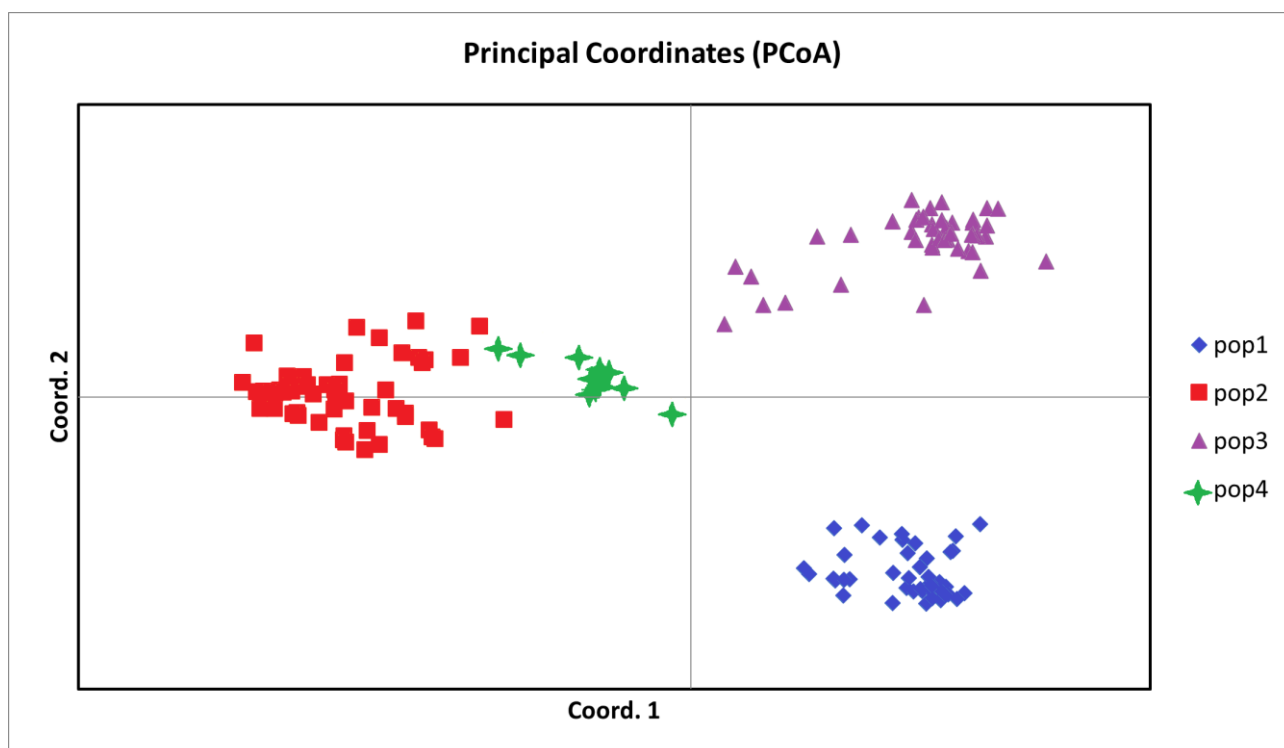


Figure 20 - Principal component analysis (PCA) for durum wheat germplasm KASIB using iPBS retrotransposons.

So, for the first time, the program identified 7 genotypes from the Aktobe AES: Kargala_1408, Kargala_1514/06, Kargala_1538, Kargala_1539, Kargala_1540, Kargala_1671, Kargala_69. 6 genotypes Altayskiy_Yantar, Hordeiforme_553, Hordeiforme_561, Hordeiforme_573, Hordeiforme_587, Hordeiforme_616 were assigned from the Altai Research Institute of Agriculture, 7 genotypes from the Karabalyk AES Altyn_Dala, Altyn_Shygys, Bolashak, Hordeiforme_113/01, Kostanayskaya_10, Line_G1549, Line_G1612, KazRIAPG – 5 samples: Lan, Line18404, Line_18472-3-2, Ertol, Line_18485-2, SPC GF n.a. A.I. Baraeva – 6: Corona, Durum_2, Line_54-02-2L, Line_e145-z, Line_e147-z, Durum_49. From Omsk ASC was greatest quantity samples - 9: Hordeiforme_00-96-8, Hordeiforme_94-24-12, Hordeiforme_94-94-13, Hordeiforme_95-139-4, Hordeiforme_97-49-1, Hordeiforme_98-42-1, Omksiy_Izumrud, Omskaya_Stepnaya, Omksiy_Cirkon. The

smallest number in the first subpopulation were samples from the Samara and Saratov selection: Line_653 d -44, Line_688 d -4.

Secondly, the largest number of samples was isolated from the Samara and Saratov selection - 13 samples: Leucurum_1429-10, Leucurum_1469-21, Bezenchikskaya_139, Hordeiforme_1591-21, Leucurum_1307 D -51, Leucurum_1307 d -54, Leucurum_1469 d -21, Leucurum_1506-36, Leucurum_1594 d -3, Annushka, Elizavetinskaya, Luch_25, Valentina. From Aktobe AES, Altai RIA and SPC GF n.a. A.I. Baraev and Omsk ASC, 7 samples were identified: P-1409, Kargala_1514, Kargala_228, Kargala_238, Kargala_66, Soyana, Yantarnaya_60; Hordeiforme_627, Hordeiforme_628, Hordeiforme_719, Hordeiforme_748, Hordeiforme_829, Hordeiforme_881, Hordeiforme_864; Damsinskaya_Yubileynaya, Hordeiforme_178-05-2, Hordeiforme_69-08-2, Lavina, Shortandinskaya_256, Line_250-06-14, Line_69-08-2; Hordeiforme_01-115-5, Hordeiforme_04-76-5, Hordeiforme_05-42-12, Omskiy_Korall, Zhemchuzhina_Sibiri (LC -3), Hordeiforme_08-25-2, Hordeiforme_08-67-1 respectively. 9 genotypes from KazRIAPG: Hordeiforme_18567-6, Hordeiforme_18585-2, Line_18987, Line_19003, Line_19029, Line_19029, Nauryz_6 (LC-1), Serke, Seymour_17. And the smallest number of samples from the Karabalyk AES is 3 Hordeiforme_2264, Sharifa, Kostanayskaya_15.

Table 10 - Number of varieties from different originators represented in genetic populations according to PCA

Originators	Total samples	Pop1	Pop2	Pop3	Pop4
Aktobe AES	20	7	7	6	-
Altai SRIA	20	6	7	4	3
Karabalykskaya AES	26	7	3	15	1
KazRIAPG	26	5	9	9	3
SPC GF n.a. A.I. Baraev	14	6	7	1	-
Samara/Saratov	19	2	13	-	4
Omsk ASC	26	9	7	10	-
Total	151	42	53	45	11

In the third genetic subpopulation, the largest number of samples was isolated from the Karabalyk AES of 15 genotypes: Asangali, Orenburgskaya_2, Altyn_Dala (LC -2), Hordeiforme_127-89, Hordeiforme_207-92, Hordeiforme_242-93, Hordeiforme_362-91, Hordeiforme_430-88, Hordeiforme_59-92, Karabalykskaya_chernokolosaya, Kostanayskaya_1, Kostanayskaya_12, Kostanayskaya_30, Line_160.93, Line_362.91. There were 10 samples from the Omsk ASC: Ametist, Angel, Hordeiforme_91-102-6, Hordeiforme_91-144-4, Hordeiforme_91-22-2, Hordeiforme_94-71, Omskaya_Yantarnaya, Omskiy_korund, Omskiy_Rubin, Zhemchuzhina_Sibiri. KazRIAPG - 9 samples: Line_17590, Line_17950, Line_18022-1, Line_18053, Line_654-1-2-3-4, Line_6801-34-6, Nauryz_8, Seymour, Toma. Also, in this population there are 6 samples from the Aktobe AES - 383-MC,

452-MC, Kargala_18, Kargala_24, Kargala_303, Kargala_447. From the Altai RIA - 4 samples Altayskaya_Niva, Hordeiforme_415, Hordeiforme_417, Hordeiforme_426. From the SPC GF n.a. A.I. Barayev is just one example of Damsinskaya_Yantarnaya.

The fourth subpopulation included the smallest number of samples, 11, among them the largest number were from the Samara and Saratov selection of 4 genotypes: Line_1693d-71, Line_1970 d -5, Line_2021 d -1, Line_D -2165. Next, 3 samples each from KazRIAPG and Altai RIA: 19055/Hordeiforme, Line_18093-7-2, Line_18924 and Hordeiforme_895, Hordeiforme_910, Hordeiforme_924, respectively. And one sample from the Karabalyk AES Hordeiforme_1790.

Analysis of molecular variance (AMOVA) showed higher genetic diversity in the populations accounting for 59% compared to other populations (Table 11, Figure 21). AMOVA estimates genetic variation at three levels: within populations, between populations within groups, and between groups. It uses genetic distance matrices between populations, which are constructed from genetic marker data, and estimates the contribution of each of these matrices to overall genetic variation.

High variation within genotypes may be due to selection, adaptation, gene flow, genetic drift, ecotype variation, and pollination method. In addition, human activities and environmental fluctuations over time may also be responsible for higher variations [146, 147]

Table 11 - Results for AMOVA among wheat germplasm studied using the iPBS-retrotransposon marker system.

Source	df	SS	MS	Est,Var,	%
Between populations	3	2467.708	822.569	22,257	41%
Within populations	147	4765.921	32,421	32,421	59%
Total	150	7233.629		54,678	100%

Note df: Degrees of freedom, SS: Sum of squares, MS: Standard deviations, EV: Estimated variation

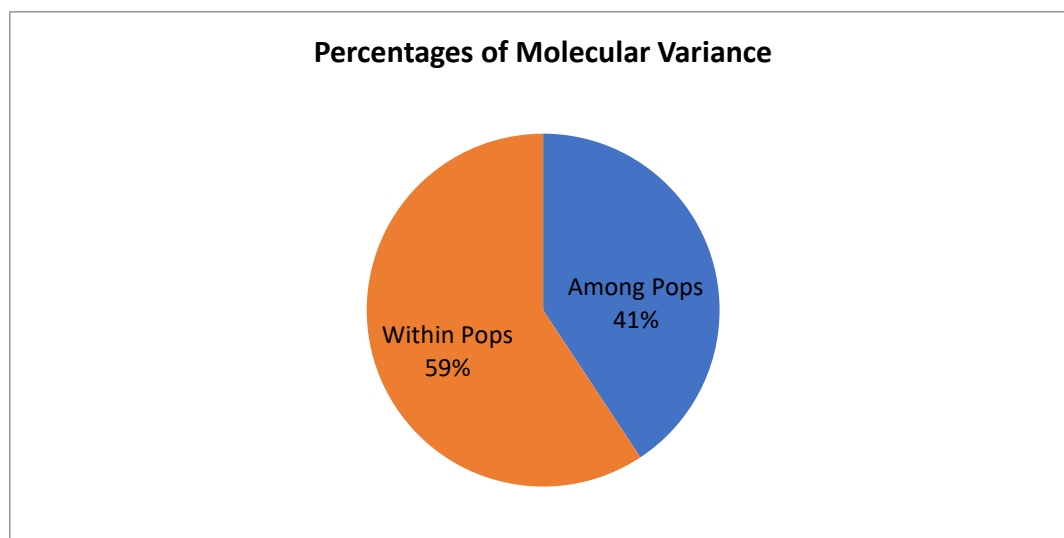


Figure 21 - Percentage within and between populations

5.3 Analysis of agronomic indicators based on the obtained genetic populations using iPBS retrotransposons

The greatest importance in genetic studies is phenotypic data. Phenological observations were analyzed based on the constructed genetic populations.

Analysis of phenological data based on genetic populations and subpopulations using the STRUCTURE and GenAlex programs. showed the following. The yield of varieties in the first subpopulation in the Almaty region varied from 127 g/m² to 399 g/m², while the average yield of varieties in this group was 256 g/m² (Table 12). Plant heights ranged from 97 to 115 cm with an average plant height of 104 cm, and the growing season of this group of varieties lasted from 98 to 112 days with an average of 104 days. The weight of a thousand grains averaged 40.0 g, the minimum was 27.9 g and the maximum was 49.4 g. In the second subpopulation, the duration of the growing season averaged 103 days and varied from 95 to 108 days. The height of the plants on average reached 101 cm and varied from 77 to 117 cm. The yield of these samples averaged 231 g/m² and varied from 114 to 436 g/m², with a weight of 1000 grains from 30.9 g to 39.7g. In the third subpopulation, the average yield was 241 g/m², the smallest was 100 g/m², and the maximum was 411 g/m², with an average weight of a thousand grains of 38.9 g, with a maximum weight of 1000 grains - 49.0 g and a minimum - 29.2 g. Plant height averaged 105 cm and varied from 92 cm to 128 cm. The duration of the growing season for this group of varieties averaged 103 days and ranged from 98 to 109 days. The fourth smallest subpopulation generated an average yield of 247 g/m², with a minimum of 146 g/m², and a maximum of 341 g/m², while the weight of 1000 grains averaged 40.8 g, a maximum of 46.7 g and a minimum of 36.6 g. This yield was formed over the duration of the growing season, which averaged 101 days, a minimum of 95 days and a maximum of 107 days. And the height of plants of this group of varieties reached an average of 105 cm, the tallest samples were up to 120 cm in height and the shortest ones were 93 cm.

Table 12 - Agronomic indicators based on genetic subpopulations

Value	Amount	Pop	Almaty region					Akmola region					ALL
			DM	PH	Yield, t/ha	TKW	St error	DM	PH	Yield, t/ha	TKW	St error	Yield, t/ha
Mean	42	Pop1	104	104	2.56	40.0	8.12	88	74	1.68	44.1	4.99	2.12
	53	Pop2	103	101	2.31	39.7	7.54	88	70	1.67	44.8	4.17	1.99
	45	Pop3	103	105	2.41	38.9	8.98	88	72	1.74	42.6	3.56	2.08
	11	Pop4	101	105	2.47	40.8	19.1	86	71	1.73	45.6	17.6	2.10
Max	42	Pop1	112	115	3.99	49.4	-	94	89	2.86	50.6	-	2.77
	53	Pop2	108	117	4.36	49.0	-	93	85	2.40	51.6	-	3.22
	45	Pop3	109	128	4.11	49.5	-	93	85	2.41	50.0	-	2.79
	11	Pop4	107	120	3.41	46.7	-	92	84	2.68	52.2	-	2.89
Min	42	Pop1	98	97	1.27	27.9	-	82	60	1.13	35.2	-	1.37
	53	Pop2	95	77	1.14	30.9	-	82	52	1.10	37.9	-	1.27
	45	Pop3	98	92	1.00	29.2	-	83	62	1.05	34.9	-	1.42
	11	Pop4	95	93	1.46	36.6	-	79	61	0.87	38.2	-	1.49

In the Akmola region, the duration of the growing season of the first subpopulation took on average 88 days and varied from 82 to 94 days. The height of the plants on average reached 74 cm and varied from 60 to 89 cm. The yield of these samples averaged 168 g/m² and varied from 113 to 286 g/m², with a weight of 1000 grains from 35.2 g to 50.6 g and on average was 44.1 g. Secondly, the average yield of the second subpopulation was 167 g/m², the lowest was 113 g/m², and the maximum was 240 g/m², with an average weight of thousand grains of 44.8 g with a maximum weight of 1000 grains - 51.6 g and a minimum - 37.9 g. Plant height averaged 70 cm and varied from 52 cm - 85 cm. The duration of the growing season for this group of varieties averaged 88 days and ranged from 82 to 88 days. The third subpopulation generated an average yield of 174 g/m² with a minimum of 105 g/m² and a maximum of 241 g/m², while the weight of 1000 grains averaged 42.6 g, maximum was 50.0 g and minimum were 34.9 g. This yield was formed over the duration of the growing season, which averaged 88 days, a minimum of 83 days and a maximum of 93 days. And the height of plants of these varieties reached an average of 72 cm, the tallest samples were up to 85 cm in height and the shortest ones were 62 cm. The yield of varieties in the fourth subpopulation varied from 87 g/m² to 268 g/m², while the average yield of varieties this group was 173 g/m². Plant heights ranged from 61 to 84 cm with an average plant height of 71 cm, and the duration of the growing season for this group of varieties lasted from 79 to 92 days with an average of 86 days. The weight of a thousand grains averaged 45.6 g, the minimum was 38.2 g and the maximum was 52.2 g.

Table 13 contains data from the analysis of iPBS retrotransposon marker data and the average yield of clusters built on the basis of iPBS. Clusters built using marker 2074 showed an average yield in the Almaty region of 253 g/m² in the first cluster, in the second cluster 233 g/m², in the third cluster 245 g/m², and in the fourth cluster 249 g/m². The first cluster of marker 2226 generated a yield of 262 g/m², the second cluster of 240 g/m², the third cluster of 232 g/m² and the 4th cluster of 258 g/m². Clusters based on the iPBS 2228 marker formed the yield: the first was 241 g/m², the second was 231 g/m², and the third was 294 g/m². The iPBS 2239 marker was divided into four clusters and formed a yield of 240 g/m², 246 g/m², 240 g/m², 247 g/m², respectively. The iPBS 2245 marker is divided into 5 clusters; in the first cluster there are 48 samples with an average yield of 232 g/m², in the second cluster there are 43 samples with a yield of 237 g/m², in the third cluster there are 11 samples with a yield of 257 g/m², in the fourth In the cluster, the yield was 241 g/m² and there were only 3 samples; in the fifth cluster, 46 samples were identified with a yield of 254 g/m². The yield in the first cluster with 40 samples of the iPBS 2252 marker was 239 g/m², the second cluster showed a yield of 253 g/m², the third - 228 g/m², the fourth - 273 g/m² and the fifth cluster showed a yield of 278 g/m². The iPBS 2256 marker was divided into 5 clusters. The first cluster showed a yield of 246 g/m² with 62 samples, the yield of the second cluster with 43 samples was 235 g/m². 40 samples were identified in the third cluster and the average yield of these samples was 243 g/m². In the fourth cluster, 5 samples were identified; their average yield was 248 g/m², and in the fifth cluster, only one number was identified with a yield of 230 g/m². The iPBS 2270 marker is

divided into 4 clusters. The first cluster includes 11 samples with a yield of 242 g/m², the second cluster includes 55 samples with a yield of 234 g/m². The third cluster includes 82 samples and their average yield is 247 g/m². The fourth cluster includes one genotype whose yield is 253 g/m². The iPBS 2271 marker is also divided into 4 clusters. In the first cluster, 45 samples with an average yield of 241 g/m² were identified.

Table 13 - Average yield of a group of varieties built on the basis of genetic populations within each iPBS marker

iPBS	Cluster	No samples	Average cluster yield by points and years, g/m ² :								
			Almaty region,				Akmola region,				Total
			2021	2022	2021-2022	St error	2021	2022	2021-2022	St error	
2074	1	38	261	245	253	8.03	204	133	168	5.32	211
	2	61	228	237	233	7.29	203	134	169	4.69	201
	3	50	235	255	245	7.68	204	141	172	3.53	209
	4	2	198	301	249	14.9	194	146	170	14.3	210
2226	1	34	260	264	262	9.20	204	139	171	5.82	217
	2	53	233	248	240	7.96	210	138	174	3.63	207
	3	61	229	235	232	7.28	198	133	165	4.52	199
	4	3	284	231	258	10.3	182	147	164	4.84	211
2228	1	142	237	245	241	4.77	203	137	170	2.68	205
	2	4	260	202	231	34.4	196	132	164	6.23	197
	3	5	262	294	278	20.1	210	135	173	17.8	226
2239	1	20	234	247	240	12.8	200	139	169	4.33	205
	2	51	247	245	246	7.32	197	133	165	4.56	205
	3	75	234	246	240	7.11	210	137	173	3.98	206
	4	5	239	255	247	14.1	182	151	166	8.36	207
2245	1	48	231	232	232	8.40	203	134	168	5.06	200
	2	43	226	248	237	9.86	201	142	172	3.93	204
	3	eleven	248	265	257	10.8	224	128	176	11.9	216
	4	3	245	237	241	22.5	185	151	168	22.2	204
	5	46	255	253	254	7.59	202	135	168	4.75	211
2252	1	40	228	251	239	10, 1	201	144	173	3.94	206
	2	39	258	249	253	8.60	200	135	168	4.97	211
	3	57	223	232	228	6.70	198	133	165	4.78	197
	4	13	271	275	273	16, 6	234	131	182	8.42	228
	5	2	279	277	278	17.8	266	149	207	8.65	243
2256	1	62	250	243	246	6.89	207	135	171	3.91	209
	2	43	233	237	235	8.13	211	140	176	5.49	205
	3	40	229	258	243	10.5	189	133	161	4.40	202
	4	5	236	261	248	24.1	219	145	182	12.1	215
	5	1	184	276	230	0	119	174	147	0	188

2270	1	eleven	217	267	242	13, 8	237	128	183	6.76	212
	2	55	235	233	234	7.95	200	134	167	3.86	200
	3	84	243	252	247	6.23	201	140	170	3.78	209
	4	1	285	221	253	0	207	97	152	0	203
2271	1	45	228	253	241	8.97	204	143	173	3.61	207
	2	59	259	248	254	6.88	207	134	170	4.78	212
	3	45	226	236	231	8.45	199	134	166	4.74	199
	4	2	160	208	184	35.9	171	127	149	23.5	167
2389	1	15	271	256	264	18.6	194	130	162	9.70	213
	2	38	234	257	245	9.80	207	143	175	4.03	210
	3	6	288	235	262	25.8	190	132	161	12.9	211
	4	7	222	236	229	24.0	252	152	202	16.7	215
	5	79	233	242	237	5.74	198	134	166	3.55	202
	6	6	229	221	225	22.7	232	125	179	10.7	202
Total	1	42	260	252	256	8.12	202	134	168	4.99	212
	2	53	223	239	231	7.54	201	132	167	4.17	199
	3	45	230	252	241	8.98	206	142	174	3.56	208
	4	eleven	266	229	247	19.1	206	141	173	17.6	210

The second cluster includes 59 genotypes with a yield of 254 g/m². The third cluster contains 45 samples with a yield of 231 g/m², and the fourth cluster contains 2 samples with a yield of 184 g/m². The iPBS 2389 marker was divided into 6 clusters. The first cluster included 15 samples with an average yield of 264 g/m², the second cluster showed a yield of 245 g/m² among 38 samples. The third cluster includes 6 samples with an average yield of 262 g/m². The fourth cluster also includes a small number of samples 7 and their average yield of 229 g/m². The fifth cluster included 79 samples with a yield of 237 g/m², and the sixth cluster with 6 samples shows a yield of 225 g/m².

The average yield of the Akmola region according to the formed clusters based on iPBS markers was as follows. The iPBS 2074 marker was divided into four clusters, the first cluster included 38 samples with a yield of 168 g/m², the second cluster included 61 samples and the average yield was 169 g/m², the third cluster included 50 genotypes with a yield 172 g/m², and 2 genotypes classified in the fourth cluster show an average yield of 170 g/m². The iPBS 2226 marker was divided into 4 clusters. The first cluster showed a yield of 171 g/m², with 34 samples, the second cluster yield with 53 samples was 174 g/m². 61 samples were identified in the third cluster and the average yield of these samples was 165 g/m². In the fourth cluster, 3 samples were identified; their average yield is 164 g/m². The iPBS 2228 marker is divided into 3 clusters. The first cluster includes 142 samples with a yield of 170 g/m², the second cluster includes 4 samples with a yield of 164 g/m². The third cluster includes 5 samples and their average yield is 173 g/m². The iPBS 2239 marker is divided into 4 clusters. In the first cluster, 20 samples were identified with an average yield of 169 g/m². The second cluster included 51 genotypes with an average yield of 165 g/m², the third cluster showed an average yield of 173 g/m², with 75 samples, and the fourth included 5 samples with a yield of 166 g/m². The yield in the first cluster with 48 samples of the

iPBS 2245 marker was 168 g/m², the second cluster showed a yield of 172 g/m², the third - 176 g/m², the fourth - 168 g/m², and the fifth cluster showed a yield of 168 g/m². The iPBS 2252 marker was divided into 5 clusters. The first cluster showed a yield of 173 g/m², the yield of the second cluster was 168 g/m². The selected samples in the third cluster showed an average yield of 165 g/m². In the fourth cluster, the genotypes showed an average yield of 182 g/m², and in the fifth cluster the yield was 207 g/m². The iPBS 2256 marker is divided into 4 clusters. The first cluster with a yield of 171 g/m², the second cluster with a yield of 176 g/m². The third cluster with an average yield of 161 g/m². The fourth cluster showed a yield of 182 g/m², and the fifth cluster showed a yield of 147 g/m². The iPBS 2270 marker is divided into 4 clusters. In the first cluster, the average yield reached 183 g/m². The second cluster showed a yield of 167 g/m², the third cluster showed a yield of 170 g/m². In the fourth cluster, the yield was 152 g/m². The iPBS 2271 marker, also divided into 4 clusters, showed the following yields: 173 g/m², 170 g/m², 166 g/m², 149 g/m², respectively, from the first to fourth clusters. The iPBS 2389 marker divided into 6 clusters in the Akmola region showed the following average yield for each cluster. The first cluster is 162 g/m², the second cluster is 175 g/m², the third cluster is 161 g/m², the fourth cluster is 202 g/m², the fifth cluster is 166 g/m², and the sixth cluster is 179 g/m².

5.4 Discussion of the results of the iPBS-retrotransposon marker system

The study used PCA (principal component analysis), AMOVA (analysis of molecular variance) and genetic distance methods. PCA allows genotypes to be divided into distinct groups based on their genetic structure. AMOVA analysis identifies differences in genetic structure between plant groups. Genetic distances between genotypes are calculated based on differences in genetic structure.

In the study, 10 polymorphic markers showed the best results. These markers showed that the genetic diversity of durum wheat germplasm KASIB is quite high, and the iPBS-retrotransposon marker system is effective for its assessment.

Polymorphisms (PICs) related to iPBS retrotransposons indicate the presence of genetic variant or variation in the distribution and insertion of these elements in the genome of durum wheat populations. The durum wheat genome contains various polymorphic iPBS retrotransposons, which contribute to the genetic diversity and evolution of this set of genotypes. The average polymorphism obtained in this study is very high. The results reflect the high efficiency of iPBS retrotransposon markers, which can be used to study new variations. The PIC (Polymorphic Information Content) coefficient value reflects the ability of a marker to detect genetic variation. The mean PIC value obtained in this study was 0.251, indicating a moderate discriminatory ability of this marker. The iPBS 2226 marker with the highest PIC value (0.308) was identified as the most effective tool for distinguishing the KASIB durum wheat set.

The average effective number of alleles (1.42) indicates that some genetic variation exists in the durum wheat populations studied. This value indicates the presence of an average of 1.42 different alleles for each locus or genetic marker examined.

The higher the average effective number of alleles, the greater the genetic diversity in the population. This information is very useful in studies of genetic structure, evolution and selection within a given durum wheat population. A high average effective number of alleles indicates the presence of genetic diversity in the durum wheat population. For breeding to create new varieties, a greater variety of genetic variants provides more opportunities to select desired traits, such as yield, disease resistance and adaptation to different conditions. Knowledge of genetic diversity in a population helps in assessing the extent of loss of genetic resources and planning conservation programs. In our studies, the average effective number of alleles is average, indicating average genetic diversity; to conserve genetic resources and ensure their availability for future use, it is necessary to diversify this durum wheat collection.

The average Shannon information index (0.39) indicates the level of genetic diversity in the durum wheat population under study.

The Shannon index is used to measure the diversity of genetic data. A higher Shannon index value indicates greater diversity of genetic components in a population.

In this case, the Shannon index value is 0.39, which indicates a moderate level of genetic diversity in the durum wheat population under study. This means that there are some genetic variants in this population, but they are not overly diverse. However, this set of genotypes is more diverse than in other studies cited in the literature review, which may also be due to the high efficiency of the iPBS-retrotransposon marker system.

Using analysis of molecular variance (AMOVA), the variation in KASIB germplasm was found to be significantly higher.

The analysis of molecular dispersion showed that the largest share of genetic variability is observed in genotypes. This means that variation associated with genetic characteristics or the state of intrapopulation diversity is more significant in the germplasm of this particular durum wheat population.

These results may have important practical implications, since genotypes may play a key role in the inheritance of various traits and properties in plants. Understanding genetic variation in KASIB nursery durum wheat genotypes can be useful in breeding new wheat varieties with desired genetic characteristics and in understanding evolutionary processes within a given population. Higher variation within genotypes can be explained by various factors, including selection, adaptation, gene flow, genetic drift, ecotype variation, and pollination method. In addition, human activities and changes in the environment may also contribute to higher levels of variation over time.

To study connections in the genetic germplasm of durum wheat, clustering algorithms - Structure and NJ tree - were used. These algorithms were chosen to analyze and classify genetic data to identify structural relationships and relatedness between samples.

And the STRUCTURE analysis allowed us to divide the germplasm under study into two main populations, designated population A and population B, based on a membership coefficient equal to or greater than 75%. Of the 151 genotypes studied, 82

genotypes were clustered in population A, and 54 genotypes were clustered in population B. Population A combined germplasm from all originators except Saratov. On the other hand, population B included genotypes from all eight regions. It is interesting to note that samples from the Saratov region were clustered in population B, and not in population A. A possible reason for this clustering of samples from the Saratov region in population B may be their genetic similarity to samples from the Samara region. This indicates a common ancestry or genetic connection between these areas.

One of the main reasons for combining germplasm from different breeding programs in the structure algorithm is their similar genetic composition. The lines and varieties that were evaluated were derived from the eight breeding programs mentioned. That is, although these programs may differ in other aspects, such as breeding goals and growing conditions, the genetic material used in them is similar. Therefore, their varieties/lines have a similar genetic composition.

Separate groups of genotypes were identified, and the maximum genetic distance was found between the two genotypes Seymour_17 and Hordeiforme_430-88, that is, the greatest number of genetic or mutational changes occurred between these genotypes. Hordeiforme_430-88 was transferred to population A and Seymour_17, respectively, to population B. In turn, the genotypes Hordeiforme_98-42-1 and Altyn_Shygys were the most closely related. These results have practical implications as they can be used in future breeding programs for durum wheat. Knowing the genetic structure and diversity of genotypes will help breeders more accurately select parents for crossing and creating new varieties of wheat with desired characteristics. It will also help improve the genetic diversity of the population.

One reason for combining genotypes from different locations in the structural algorithm is their similar genetic composition. Line and cultivar data were obtained from the eight breeding programs mentioned. This means that they share genetic characteristics.

It is obvious that the presence of a common pedigree has led to the grouping of different varieties and advanced lines together in the structural algorithm. Their genetic affinity and similarity is due to common ancestors or parents that were used in these breeding programs. [148]

In addition to populations A and B, 15 genotypes were found that could not be assigned to either population with a membership coefficient equal to or less than 75%. These genotypes were classified as a mixed population or population B. It is interesting to note that these 15 genotypes represent all locations except the Omsk region.

The largest number of genotypes from population B belongs to the Kostanay and Almaty regions. This means that the genetic composition of these genotypes is different from the genetic composition of populations A and B, and they cannot be clearly assigned to one of the two main populations.

This mixture of genotypes in population C may result from differences in genetic diversity or ancestry between these locations and other regions. This indicates the presence of unique genetic characteristics or the influence of specific factors inherent in the Kostanay and Almaty regions, which distinguish them from other locations.

Neighbor-joining (NJ) analysis was also performed to examine the relationship between 151 durum wheat lines and cultivars. Neighbor-joining analysis (NJ Tree) also separated the genotypes studied into two distinct populations, designated population A and population B.

Clustering using the NJ method showed that most of the studied germplasm was consistent with the structural clustering results, with a few exceptions. This confirms the genetic similarity between the different genotypes of the germplasm studied based on their common parents. [148] Population A was further divided into subpopulations A1 and A2. Similarly, population B was divided into B1 and B2. The structural algorithm identified 15 genotypes that did not belong to a specific population based on their membership coefficient. In the NJ analysis, most of these samples formed their own subclusters (indicated in green) in population B. All samples from the Saratov region were grouped into subpopulation B1 (indicated in black) of the main population B, and the same was found when clustering using structural algorithm.

Having analyzed all the iPBS retrotransposon data and agronomic indicators, we can make a preliminary conclusion that in each of the originators there are at least two populations and four subpopulations of spring durum wheat. Which, in turn, is of great importance for the further development of breeding programs, since the basis for the development of breeding is genetic material for crossing and selection in order to improve the adaptive potential, yield and quality indicators of varieties, and the more diverse the genetic population, the greater the opportunity for creating high-yielding varieties and most importantly, preventing a deadlock in selection with a small number of genetic populations, since the smaller the genetic population, the faster the possibilities for creating lines necessary for adaptability will be exhausted. Nevertheless, replenishment of the KASIB collection and each breeding program separately should continue.

Further analysis of the constructed genetic subpopulations showed that these subpopulations are predominantly divided according to their adaptive potential to certain regions, which in turn confirms various studies presented in the literature review. It is most likely that the genotypes are most adapted to the region where their originators are based, but they also show excellent results in similar agro-climatic conditions, as observed in the data analysis performed. For example, subpopulations 2, 3, and 4 perfectly form crop yields in the Almaty region. To a greater extent, these are subpopulations 2 and 3, which are based on genotypes in the second genetic population, genotypes of the Samara and Saratov selection, and in the third, genotypes of the Karabalyk AES and Omsk ASC. Regarding the Akmola region, genotypes belonging to subpopulations 1, 3, and 4 perform best here. High yields in this region are shown by the genotypes of the Karabalyk AES and the Omsk ASC. The first genetic population most likely belongs to another agro-climatic region similar to the Akmola region, where these genotypes can manifest themselves to a greater extent than in the Almaty region. The fourth genetic subpopulation is based on genotypes from most originators almost equally, that is, these lines/varieties are most likely widely adaptive and can grow in different regions without losing their genetic potential in yield formation. Also in Figure 20, it is observed that the fourth subpopulation is located

almost at the center of the graph, which means these samples are based on genes of all three genetic subpopulations and formed the fourth subpopulation.

The economic value of the identified markers is of great importance in plant breeding when selecting parental pairs, conducting selection in a certain region and determining genetic populations.

The relationship of all genotypes can be more accurately determined using GWAS and further study of CASP markers.

High adaptive potential to various regions is observed in the genotypes of the Aktobe AES, Karabalyk AES, Omsk ARC, Samara RIA, Saratov RIA and Altai RIA. The variety lines of other originators belong to the same genetic population, but the set of varieties also contains genotypes from another genetic population.

CONCLUSION

I. Based on classical field studies conducted during pre-breeding work in the KASIB-DW nursery, a number of conclusions were made.

1. adaptive genotypes were identified in two regions of Kazakhstan (Almaty and Akmola regions)

2. High-yielding and adaptive samples of spring durum wheat were identified in the Almaty region and adaptive samples in the Akmola region. Based on these data, a recommendation was written for the transfer of varieties for state variety testing for each originator.

3. For breeding lines, it is necessary to carry out selections taking into account genotype and environmental interaction.

4. To achieve maximum yield, it is recommended to use varieties with both long and short growing seasons, using different sowing dates for each length of the growing season of the varieties. This is especially important for farms as it helps mitigate possible adverse climate conditions.

5. Based on field testing based on economically valuable traits, genotypes were identified for further breeding work.

II. Based on highly effective phenotyping, it was established:

6. reducing the cost of digital measurements and obtaining additional parameters in plant breeding. This highly effective phenotyping method is recommended for implementation in plant breeding.

7. obtaining additional parameters of green mass, green area, plant wilting index, to identify high-yielding and highly adaptive lines in the early stages of plant development.

8. Environmentally stable and highly adaptive genotypes from the KASIB-DW collection were identified based on highly efficient phenotyping

9. A probable correlation between digital indicators and the photosynthetic activity of plants, ears and awns has been established, which requires additional research.

III. Based on iPBS markers of retrotransposons, the following was revealed:

10. the main genetic populations of spring durum wheat and a genetic population created artificially from the three presented genetic subpopulations.

11. Based on iPBS retrotransposon markers, 10 markers out of 83 were identified; these markers can be used to trace the evolution and regulation of the durum wheat genome

12. A relationship has been established between iPBS retrotransposon markers and the adaptive potential of the studied genotypes - however, this theory requires additional research

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APPENDIX A

Temperature regime during the growing season during the research years 2020-2022
in two regions

Almaty region

Months	Almaty region				Akmola region			
	LT	2020	2021	2022	LT	2020	2021	2022
March	6.0	6.4	4.9	5.6	-4.4	-3.1	-7.2	-7.2
April	12.8	14.0	12.5	16.7	7.2	10.8	6.1	9.8
May	17.9	18.8	19.5	19.0	15.1	18.9	18.7	16.5
June	22.6	22.0	23.0	24.3	19.7	19.2	18.5	20.4
July	25.0	24.3	27.2	26.4	20.7	22.1	21.7	21.9
August	23.6	24.0	24.6	22.6	19.2	19.9	20.9	18.3
September	18.5	16.8	20.5	21.1	13.0	12.1	10.7	15.5

The amount of precipitation during the growing season during the research years 2020-
2022 in two regions

Region	Years	March	April	May	June	July	August	September	Veg. period
Almaty	2020	26	69	37	15	16	20	10	193
	2021	56	27	34	10	11	11	1	150
	2022	83	22	71	18	7	4	1	207
	LT	42	58	49	28	17	15	13	223
Akmola	2020	4	22	7	48	26	19	14	140
	2021	26	2	5	11	22	4	26	97
	2022	16	4	5	9	17	13	8	71
	LT	13	12	16	20	28	14	10	112

APPENDIX B

List of varieties used in the thesis

Variety	Originator	A country
Kargala_18	Aktobe AES	Kazakhstan
383-MC	Aktobe AES	Kazakhstan
452-MC	Aktobe AES	Kazakhstan
Kargala_24	Aktobe AES	Kazakhstan
Kargala_447	Aktobe AES	Kazakhstan
Kargala_303	Aktobe AES	Kazakhstan
Kargala_1514/06	Aktobe AES	Kazakhstan
Kargala_69	Aktobe AES	Kazakhstan
Kargala_1538	Aktobe AES	Kazakhstan
Kargala_1540	Aktobe AES	Kazakhstan
Kargala_1539	Aktobe AES	Kazakhstan
Kargala_1671	Aktobe AES	Kazakhstan
Kargala_1408	Aktobe AES	Kazakhstan
Kargala_66	Aktobe AES	Kazakhstan
Kargala_1514	Aktobe AES	Kazakhstan
Kargala_228	Aktobe AES	Kazakhstan
Kargala_238	Aktobe AES	Kazakhstan
P-1409	Aktobe AES	Kazakhstan
Soyana	Aktobe AES	Kazakhstan
Yantarnaya_60	Aktobe AES	Kazakhstan
Kostanayskaya_30	Karabalykskaya AES	Kazakhstan
Kostanayskaya_1	Karabalykskaya AES	Kazakhstan
Orenburgskaya_2	Karabalykskaya AES	Kazakhstan
Line_160.93	Karabalykskaya AES	Kazakhstan
Line_362.91	Karabalykskaya AES	Kazakhstan
HordeIforme_430-88	Karabalykskaya AES	Kazakhstan
HordeIforme_59-92	Karabalykskaya AES	Kazakhstan
HordeIforme_207-92	Karabalykskaya AES	Kazakhstan
HordeIforme_362-91	Karabalykskaya AES	Kazakhstan
HordeIforme_242-93	Karabalykskaya AES	Kazakhstan
HordeIforme_127-89	Karabalykskaya AES	Kazakhstan
Kostanayskaya_12	Karabalykskaya AES	Kazakhstan
Asangali	Karabalykskaya AES	Kazakhstan
Karabalykskaya_chernokolosaya	Karabalykskaya AES	Kazakhstan
Altyn_Dala (LC-2)	Karabalykskaya AES	Kazakhstan
Altyn_Shygys	Karabalykskaya AES	Kazakhstan
Altyn_Dala	Karabalykskaya AES	Kazakhstan
Kostanayskaya_10	Karabalykskaya AES	Kazakhstan
Bolashak	Karabalykskaya AES	Kazakhstan

HordeIforme_113/01	Karabalykskaya AES	Kazakhstan
Line_G1549	Karabalykskaya AES	Kazakhstan
Line_G1612	Karabalykskaya AES	Kazakhstan
Sharifa	Karabalykskaya AES	Kazakhstan
HordeIforme_2264	Karabalykskaya AES	Kazakhstan
Kostanayskaya_15	Karabalykskaya AES	Kazakhstan
HordeIforme_1790	Karabalykskaya AES	Kazakhstan
Line_6801-34-6	KazRIAPG	Kazakhstan
Line_654-1-2-3-4	KazRIAPG	Kazakhstan
Line_17950	KazRIAPG	Kazakhstan
Line_17590	KazRIAPG	Kazakhstan
Line_18053	KazRIAPG	Kazakhstan
Line_18022-1	KazRIAPG	Kazakhstan
Nauryz_8	KazRIAPG	Kazakhstan
Toma	KazRIAPG	Kazakhstan
Seymur	KazRIAPG	Kazakhstan
Lan	KazRIAPG	Kazakhstan
Ertol_(18104)	KazRIAPG	Kazakhstan
Line_18485-2	KazRIAPG	Kazakhstan
Line_18404	KazRIAPG	Kazakhstan
Line_18987	KazRIAPG	Kazakhstan
Line_18472-3-2	KazRIAPG	Kazakhstan
HordeIforme_18567-6	KazRIAPG	Kazakhstan
HordeIforme_18585-2	KazRIAPG	Kazakhstan
Line_19003	KazRIAPG	Kazakhstan
Line_19029	KazRIAPG	Kazakhstan
Seymur_17	KazRIAPG	Kazakhstan
Serke	KazRIAPG	Kazakhstan
Line_18093-7-2	KazRIAPG	Kazakhstan
19055/Hordelforme	KazRIAPG	Kazakhstan
Line_18924	KazRIAPG	Kazakhstan
Line_19029	KazRIAPG	Kazakhstan
Nauryz_6 (LC-1)	KazRIAPG	Kazakhstan
Damsinskaya_Yantarnaya	SPC GF n.a. A.I. Baraev	Kazakhstan
Corona	SPC GF n.a. A.I. Baraev	Kazakhstan
Durum_2	SPC GF n.a. A.I. Baraev	Kazakhstan
Durum_49	SPC GF n.a. A.I. Baraev	Kazakhstan
Line_e145-z	SPC GF n.a. A.I. Baraev	Kazakhstan
Line_54-02-2L	SPC GF n.a. A.I. Baraev	Kazakhstan
Line_e147-z	SPC GF n.a. A.I. Baraev	Kazakhstan
Lavina	SPC GF n.a. A.I. Baraev	Kazakhstan
Damsinskaya_Yubileynaya	SPC GF n.a. A.I. Baraev	Kazakhstan
Shortandinskaya_256	SPC GF n.a. A.I. Baraev	Kazakhstan
HordeIforme_69-08-2	SPC GF n.a. A.I. Baraev	Kazakhstan

HordeIforme_178-05-2	SPC GF n.a. A.I. Baraev	Kazakhstan
Line_69-08-2	SPC GF n.a. A.I. Baraev	Kazakhstan
Line_250-06-14	SPC GF n.a. A.I. Baraev	Kazakhstan
Altayskaya_Niva	Altai RIA (FASCA)	Russia
HordeIforme_415	Altai RIA (FASCA)	Russia
HordeIforme_417	Altai RIA (FASCA)	Russia
HordeIforme_426	Altai RIA (FASCA)	Russia
HordeIforme_553	Altai RIA (FASCA)	Russia
Altayskiy_Yantar	Altai RIA (FASCA)	Russia
HordeIforme_561	Altai RIA (FASCA)	Russia
HordeIforme_573	Altai RIA (FASCA)	Russia
HordeIforme_616	Altai RIA (FASCA)	Russia
HordeIforme_587	Altai RIA (FASCA)	Russia
HordeIforme_627	Altai RIA (FASCA)	Russia
HordeIforme_628	Altai RIA (FASCA)	Russia
HordeIforme_719	Altai RIA (FASCA)	Russia
HordeIforme_748	Altai RIA (FASCA)	Russia
HordeIforme_829	Altai RIA (FASCA)	Russia
HordeIforme_864	Altai RIA (FASCA)	Russia
HordeIforme_881	Altai RIA (FASCA)	Russia
HordeIforme_895	Altai RIA (FASCA)	Russia
HordeIforme_910	Altai RIA (FASCA)	Russia
HordeIforme_924	Altai RIA (FASCA)	Russia
Line_688d-4	Samara RIA	Russia
Line_653d-44	Samara RIA	Russia
Leucurum_1307D-51	Samara RIA	Russia
Leucurum_1307d-54	Samara RIA	Russia
Leucurum_1469d-21	Samara RIA	Russia
Leucurum_1594d-3	Samara RIA	Russia
Bezenchikskaya_139	Samara RIA	Russia
Leucurum_1429-10	Samara RIA	Russia
Leucurum_1506-36	Samara RIA	Russia
HordeIforme_1591-21	Samara RIA	Russia
Leucurum_1469-21	Samara RIA	Russia
Line_1693d-71	Samara RIA	Russia
Line_1970d-5	Samara RIA	Russia
Line_2021d-1	Samara RIA	Russia
Elizavetinskaya	Saratov RI of the South-East Region	Russia
Valentina	Saratov RI of the South-East Region	Russia
Annushka	Saratov RI of the South-East Region	Russia
Luch_25	Saratov RI of the South-East Region	Russia
Line_D-2165	Saratov RI of the South-East Region	Russia
Angel	Omsk ASC	Russia
Amethyst	Omsk ASC	Russia

Omskaya_Yantarnaya	Omsk ASC	Russia
Omskiy_Rubin	Omsk ASC	Russia
Omskiy_korund	Omsk ASC	Russia
HordeIforme_94-71	Omsk ASC	Russia
HordeIforme_91-102-6	Omsk ASC	Russia
HordeIforme_91-22-2	Omsk ASC	Russia
Zhemchuzhina_Sibiri	Omsk ASC	Russia
HordeIforme_91-144-4	Omsk ASC	Russia
HordeIforme_94-94-13	Omsk ASC	Russia
HordeIforme_94-24-12	Omsk ASC	Russia
HordeIforme_95-139-4	Omsk ASC	Russia
Omskaya_Stepnaya	Omsk ASC	Russia
HordeIforme_97-49-1	Omsk ASC	Russia
HordeIforme_98-42-1	Omsk ASC	Russia
Omksiy_Izumrud	Omsk ASC	Russia
Omskiy_Circon	Omsk ASC	Russia
HordeIforme_00-96-8	Omsk ASC	Russia
Omskiy_Korall	Omsk ASC	Russia
HordeIforme_01-115-5	Omsk ASC	Russia
Zhemchuzhina_Sibiri (LC-3)	Omsk ASC	Russia
HordeIforme_04-76-5	Omsk ASC	Russia
HordeIforme_05-42-12	Omsk ASC	Russia
HordeIforme_08-25-2	Omsk ASC	Russia
HordeIforme_08-67-1	Omsk ASC	Russia

APPENDIX A

Акт
передачи материала

В ТОО «Казахский Научно Исследовательский Институт Земледелия и Растениеводства» отдел генофонда образцов яровой твердой пшеницы питомника КАСИБ – ТП 2000-2020гг. для хранения в холодильнике в течении 2021-2023 гг.

Список прилагается.

Передал:
Приняла:



Таджибаев Д. Г.
Есимбекова М.А.

20.01.21.

APPENDIX B

Акт передачи материала

В ТОО «Научно-производственный центр Зернового хозяйства имени А.И. Бараева» образцов яровой твердой пшеницы питомника КАСИБ – ТП 2000-2020гг. для посева в 2021 году. Итого - 17,5 кг.

И образцов яровой твердой пшеницы питомника КАСИБ – ТП 2000-2020гг по 5 грамм, итого 955 грамм для дальнейшей передачи во «Всероссийский НИИ фитопатологии», г.Москва.

Списки прилагаются.

Передал:
Принял:

 Таджибаев Д. Г.
 Бабкенов А. Т.

APPENDIX C

RECOMMENDATION FOR TRANSFER OF VARIETIES FOR STATE VARIETY TESTING

Based on the data obtained from field research, a recommendation was made for submitting varieties for state variety testing.

For zoning in the Almaty region, the lines of spring durum wheat of LLP “KazRIAPG” can be transferred to SVT 19055/Hordeiforme, Line_17950, Line_19003. The yield of the line 19055/Hordeiforme averaged 239 g/m² (2.39 t/ha), the weight of 1000 grains was 38.0 g, the plant height was 110 cm, and the duration of the growing season was 95 days. The yield of the Line_17950 line is 211 g/m² (2.11 t/ha), weight of 1000 grains is 40.9 g, plant height is 93 cm, the duration of the growing season is 98 days. The yield of the Line_19003 line is 209 g/m² (2.09 t/ha), the weight of 1000 grains is 36.5 g, the plant height is 101 cm, the duration of the growing season is 100 days.

Lines of LLP “SPC GF n.a. A.I. Baraev” Line_250-06-14 with a yield of 230 g/m² (2.30 t/ha), weight of 1000 grains - 38.6 g, duration of the growing season 107 days, plant height 96 cm.

Lines of the Aktobe AES Kargala_1540, Kargala_1514/06, 452-MC. The yield of the Kargala_1540 line is 216 g/m² (2.16 t/ha), the weight of 1000 grains is 46.9 g, the plant height is 104 cm, the duration of the growing season is 98 days. The yield of the Kargala_1514/06 line is 207 g/m² (2.07 t/ha), the duration of the growing season is 100 days, the plant height is 111 cm, the weight of 1000 grains is 40.7 g. The yield of the 452-MC line is 206 g/m² (2.06 t/ha), weight of 1000 grains 45.7 g, plant height – 101 cm, duration of the growing season 105 days.

The Karabalyk AES Line_G1612 with a yield of 212 g/m², a weight of 1000 grains of 34.9 g, a plant height of 101 cm, and a growing season of 105 days.

Recommendation for transfer to state variety testing in Akmola region :

Lines of the Karabalyk AES: Hordeiforme_242-93, Hordeiforme_1790, Hordeiforme_113/01. The yield of the Hordeiforme_242-93 line is 241 g/m² (2.41 t/ha), the weight of 1000 grains are 46.1 g, the duration of the growing season is 90 days, the plant height is 77 cm. The yield of the Hordeiforme_1790 line is 225 g/m² (2.25 t/ha), weight of 1000 grains 43.0 g, plant height – 80 cm, duration of the growing season 91 days. The yield of the line Hordeiforme_113/01 is 206 g/m² (2.06 t/ha), the weight of 1000 grains is 44.9 g, the plant height is 88 cm, the duration of the growing season is 92 days.

Lines of the Aktobe AES: Kargala_238, Yantarnaya_60, Kargala_1540, Kargala_1538. The yield of the Kargala_238 line is 239 g/m² (2.39 t/ha), the weight of 1000 grains is 45.7 g, plant height is 77 cm, the duration of the growing season is 92 days. The yield of the Yantarnaya_60 line is 217 g/m² (2.17 t/ha), the weight of 1000 grains is 48.5 g, the plant height is 81 cm, the duration of the growing season is 86 days. The yield of the Kargala_1540 line is 216 g/m² (2.16 t/ha), the weight of 1000 grains is 48.1 g, the plant height is 73 cm, the duration of the growing season is 89 days. The yield of the Kargala_1538 line is 213 g/m² (2.13 t/ha), the weight of 1000

grains is 46.3 g, the plant height is 72 cm, the duration of the growing season is 82 days.

Variety of LLP “KazRIAPG” Seymour - with a yield of 235 g/m² (2.35 t/ha), weight of 1000 grains of 37.9 g, plant height of 71 cm, duration of the growing season 93 days.

Lines of the LLP “SPC GF n.a. A.I. Barayev” Line_250-06-14 with a yield of 208 g/m² (2.08 t/ha), weight of 1000 grains of 44.7 g, plant height of 71 cm, duration of the growing season of 93 days. The yield of the Line_69-08-2 line is 204 g/m² (2.04 t/ha), the weight of 1000 grains is 45.6 g, plant height is 73 cm, the duration of the growing season is 88 days.

APPENDIX D

RECOMMENDATION FOR IMPLEMENTING HIGH-EFFICIENT PHENOTYPING TECHNOLOGY IN PLANT BREEDING

Based on the data obtained from field research and relying on the research of other scientists, a recommendation has been made.

With the development of new technologies, opportunities are emerging for phenotyping plants without invasive intervention, which plays an important role in plant breeding when there is a lack of seeds in the early stages of selection and other reasons. The method of highly effective phenotyping makes it possible to determine the adaptive potential, photosynthesis of plants, and monitor the progress of diseases of various cultivated plants. The big advantage of this method is its low cost, and in some cases it does not involve any financial costs at all. Identifying key stages of plant development that influence yield makes it easier to model varieties and predict early plant yields and quality in the field. Thus, this method increases the efficiency of plant selection.

Required materials: Digital camera with a tripod or drone with the ability to install a digital camera, personal computer, MS software package Excel, photo viewer, Fiji with CIMMYT plugin installed Maize Scanner.

Necessary measures when conducting highly efficient phenotyping experiments.

Since the program is not designed to recognize weeds in photographs, 99–100% cleaning of the studied plots from weeds is necessary throughout the entire period of experiments with a digital camera.

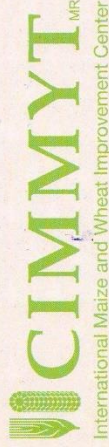
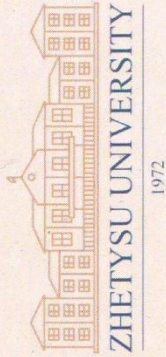
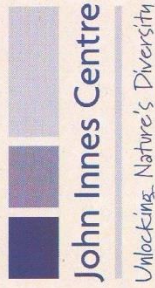
Preventing foreign objects, mostly green ones, from getting into photos. Also, to reduce the error in the experiment, the time for taking photographs is from 11:00 to 14:00.

The camera should be at a height of 1 meter from the crown of the plants.

Conducting highly effective phenotyping or the date of phenotyping depends on weather conditions (in bright sunny weather or cloudy weather, but with sufficient lighting); the frequency of images depends on the experience and the desire to obtain more accurate data; the higher the frequency of images, the more accurate the data obtained.

Photo processing is possible as the experiment progresses.

APPENDIX E



CERTIFICATE

it is hereby certified, that

Daniyar Tajibayev

successfully completed the "2023 Workshop on Wheat Genetics and Genomics in Central Asia"

January 30th - February 02nd 2023, Taldykorgan



Prof. Kuat Baimyrzaev

Prof Kuat Baimyrzaev
Chairman of the Board of Rector
Zhetysu University

Prof. Cristobal Uauy

Prof Cristobal Uauy
Group Leader
John Innes Centre



APPENDIX G



To:
Mr. Daniyar Tajibayev

May 30, 2022

Subject: Training on Structural Bioinformatics in plants

Dear Mr Tajibayev,

On the behalf of Sivas University of Science and Technology, faculty of agricultural sciences and technologies, I am pleased to confirm that Mr. Daniyar Tajibayev who is a PhD student at the department of Agronomy, Kazakh National Agrarian Research University, Almaty, Kazakhstan has completed his training on structural bioinformatics techniques in plants in the period of 1st April-31th May 2022 with Associate Professor. Dr. Faheem Shehzad Baloch at Molecular genetics laboratory of Sivas University of Science and Technology, faculty of agricultural sciences and technologies, Sivas, Turkey.

The course provided insight into practical background of genome wide association studies (GWAS) in plants-based association mapping using diversity panel of wheat germplasm. The training includes theoretical introductions, calculation exercises and practical with various computer software such R, TASSEL etc.

I believe that his stay at Sivas was highly productive for his training on the bioinformatics tools for GWAS analysis in wheat

Your's Sincerely



Prof. Dr. Tolga Karaköy
Dean & Vice-Rektor
Faculty of Agricultural Sciences and Technologies
Sivas University of Science and Technology

Yenişehir Mahallesi Kardeşler Caddesi
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bilgi@sivas.edu.tr



THE INTERNATIONAL MAIZE AND WHEAT IMPROVEMENT CENTER

presents this

Certificate

to

Daniyar Tajibayev

In formal recognition for successfully completing the

Basic Wheat Improvement Course - 2022

January 24th to May 31st of 2022

El Batán, Texcoco, Mexico, May 2022

Bram Govaerts

Dr. Bram Govaerts
CIMMYT
Director General

Bhoja Raj Basnet

Dr. Bhoja Raj Basnet
GWP
Training Coordinator

Alison Bentley

Dr. Alison Bentley
Director
Global Wheat Program



APPENDIX I



Tuesday, June 15, 2021

Mr. Daniyar Tajibayev
Kazakh National Agrarian Research University
+7 708 55 7 489
daniyar.taj@gmail.com

We are glad to inform you that Mr. Daniyar from Kazakh National Agrarian Research University, has successfully completed his student research from March 21, 2021, to May 31, 2021.

During this time Mr. Daniyar worked on the project titled: " Evaluation of durum wheat of KASIB (Kazakhstan – Siberia) network and identification of affecting agronomic traits "under the direct supervision of Abdelfattah A.S. Dababat and Gul Erginbas-Orakci (CIMMYT Supervisors). Some of the activities that Mr. Daniyar did in this research were the following:

- Writing of planned proposals, planning under supervision of supervisors.
- Theoretical and practical work on soil borne diseases.
- Trial set up for soil borne diseases (nematode and Fusarium) in growth room conditions.
- Trial assessment of cereal cyst nematodes in wheat.
- Trials assessment for crown rot-Fusarium culmorum.
- Sampling techniques in field conditions.
- Isolation and extraction process of soil borne diseases.
- Assessment of greenhouse trials.

We wish him all the best in his future endeavors.

Best Regards.

Mr. Jean-Flavien Le Besque
CIMMYT Legal Representative
Deputy Director of Human Resources
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