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BIOINFORMATION TECHNOLOGIES IN PLANT BREEDING

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ABSTRACT

Plants are comprised of a complex network of interrelated characteristics, where a change in one characteristic may cause a change in another, or in a combination of characteristics. Crop breeding techniques for selection of specific characteristics is largely constrained by insufficient theoretical levels in many branches of modern genetics, the basis of which should be corresponding mathematical models. Development of mathematical models for quantitative characteristics in "genotype-environment" systems, using molecular- and bio-technology in plant breeding can help to significantly reduce the time and cost required to create new varieties of agricultural plants, and can significantly improve breeding efficiency by constructing reliable predictive estimates and identifying selected genotypes.

Key words: plant breeding, biotechnology, genomics, bioinformatics, modeling, variety.

INTRODUCTION

The main challenge of the current century is to ensure the security of food supply in a changing climate and to roughly double the demand for food by 2050, compared with the current one, most of which must be met by crops, rice, corn and barley. In the future, agricultural production will be particularly threatened by the increasing frequency and severity of extreme events, such as heat and drought, which pose particular challenges to plant breeders and scientists. The program developed for the simulation of interactions between genotype, environment and management, are widely used to assess the impact of environmental change on yield potential, phenology, water use, etc. In recent decades, modeling of agricultural production has become an important tool for the development of plant breeding, in particular, the development of model plants for different crops and conditions. Combining traditional crop modelling with new breeding methods and genetic modelling will help accelerate the creation of new plant varieties for different conditions.

The vital activity of mankind depends crucially on the growth of crop yields, the processing of crops for the production of various products and the distribution of the obtained products to different consumers. The biological basis on which the success of this complex industrial hierarchy of activities is based is plant breeding. New plant varieties should provide acceptable quality end products, but they should minimize the likelihood of crop failure and thus ensure food security, as well as being resistant to diseases and pests.

The success of such efforts depends on the quality of breeding research, which has become very difficult in recent years. Selection from the point of view of modern understanding of plant genetics and the increasing complexity of experiments and instruments has significantly increased the rate of output varieties. The implementation of new plant breeding programs creates a need for improved quantitative evaluation through the use of mathematical modeling, as well as the use of bioinformatics, biotechnology and genetic editing [1].

The use of modern achievements of biology and related sciences (mathematics, computer science, chemistry, nanotechnology and others) is an urgent need for modern plant breeding.

THE REQUIREMENTS OF BREEDERS TO THE MODELING OF THE NEW VARIETY

According to the international Organization for food and agriculture at the UN (FAO), the need for agricultural products in the next 20 years will grow and to meet it, the growth of world agricultural production should be on average 1.7-2.6% per year [2]. Therefore, the search and breeding of new varieties of plants that combine yield, quality and nutritional value is considered a priority.

When creating a variety, the breeder seeks to improve the efficiency of the breeding process, to ensure its acceleration, to reduce labor and material costs – in short, to optimize it. Optimization of the breeding process is carried out to improve the existing methodological approaches or the development of new techniques of breeding, the construction of rational models of class on the specified parameters, to improve the scheme of breeding process and the applied breeding technologies, as well as the use in the breeding process elements of mathematical processing of the data [3].

There are certain requirements that should be followed when creating new varieties of plants:

- the variety must guarantee a given level of yield;
- the variety must be plastic, to be adapted for cultivation in a fairly wide range of environmental conditions;
- the variety should be technological, allowing mechanized cultivation and harvesting;
- the variety must have a sufficiently high quality;
- the variety must be immune.

It is desirable that these requirements are implemented in their entirety, but to create a variety that would meet all these requirements, it is almost impossible. The variety is a complex system of cumulative genotypes that appeared in the late stages of splitting as a result of free re-pollination, spontaneous mutagenesis and many other reasons. At the same time, each plant is a complex set of interrelated features, where the change of one leads to a change in the other or a set of features, sometimes undesirable for the breeder [4, 5].

In the course of breeding it is very difficult to combine in one genotype high potential of productivity with wide ecological plasticity. That is why it is essential to develop variety models for each agroclimatic zone [1, 3, 6]. At the same time, the most complete implementation of the hereditary capabilities of the variety is manifested only if it combines the maximum adaptation to the conditions of a particular zone and other economically valuable features. Since the plant phenotype is the result of genotype realization in certain environmental conditions, the model is based on the phenotypic features of plants.

The creation of a better variety than existing ones is still possible, as the genetic limit has not yet been reached in any of the crops. The success of any crop breeding for specific agroecological conditions depends largely on the objectivity of the development of the parameters of the variety model, which allows the breeder to more effectively and economically create varieties as close to ideal as possible. The variety model is a scientific prediction showing what combination of traits plants should have to provide a given level of productivity, sustainability and other required production qualities [5, 7].

MODELING OF BREEDING PROCESSES

The development of crop breeding is largely constrained by the lack of theoretical level of many branches of modern genetics, the basis of which should be appropriate mathematical models. The presence of such models can significantly simplify and accelerate the solution of genotype identification problems, as well as predict the combination of quantitative characteristics of newly created varieties. Mathematical models quantitative characteristics of the system "genotype – environment" provide an opportunity to significantly improve the efficiency of breeding work due to the appearance of the possibility of building reliable predictive estimates of these signs and identification of genotypes according to the results of the breeding tests [8].

Environmental factors often make a decisive contribution to the formation of breeding characteristics in generations, since the manifestation of any sign of productivity is the result of the interaction of "genotype - environment". The controllability of environmental factors will significantly improve the quality of genotype identification by phenotypes and thereby significantly accelerate the production of new varieties [9].

The main objective of plant breeding programs is to develop new genotypes that are genetically superior to the currently existing ones for a specific target environment or target population environment. To achieve this goal, breeders use a number of breeding methods [10, 11]. Quantitative genetic theory as a whole provides most of the framework for the development and analysis of selection methods used in breeding programs, based on various assumptions in order to make mathematically or statistically acceptable theories [11-13]. Some of these assumptions can be easily verified or satisfied by pilot projects. Others are rare, such as assumptions about the lack of communication and lack of interaction of the genotype with the environment. Others, such as the presence or absence of epistasis and pleiotropy, difficult to verify. Field experiments are conducted to compare the effectiveness of different breeding methods. However, due to the time and effort required to conduct field experiments, the concept of modeling and forecasting has always been of interest to breeders. Computer simulations allow breeders to reduce the impact of these assumptions, thereby creating more reliable genetic models for use in plant breeding. Modeling as a tool is used in many plant breeding studies that use relatively simple genetic models. A tool capable of simulating the effectiveness of a breeding strategy for a number of genetic models from simple to complex, embedded in a large practical breeding program, including marker selection, was not available until recently [14].

Mathematical models quantitative characteristics of the system "genotype – environment" provide an opportunity to significantly improve the efficiency of breeding work due to the appearance of the possibility of building reliable predictive estimates of these signs and identification of genotypes according to the results of the selection tests.

The interaction of genotypes with the environment is an important phenomenon in plant breeding. Realistic modeling of genotypic differences in several media requires complex mixed models to ensure heterogeneity of genetic variances and correlations between media. The use and interpretation of all models is illustrated by a sample data set from the CIMMYT maize breeding program, which differs in the degree of moisture and nitrogen nutrition [15].

It is known from quantitative genetics [12] that the phenotypic variability of any quantitative trait observed by the naked eye in a splitting population is described as Vph = Vg + Ve, where Vph is a phenotypic, Vg is a genotypic and Ve is an environmental variance caused by variations in environmental conditions for individual plants from the population.

The reliability of simulation can be further enhanced by continuous improvement of simulation prototyping, for better extrapolation of the effects of extreme situations and the use of multi-model ensembles [16].

Of all the problems solved with the help of such models, the most important are:

- evaluation of the source material and selection of parent pairs to ensure the desired result of crossing;
- assessment of contributions of genetic and physiological systems of parent pairs;

- predicting transgressions of the breeding traits in the offspring;
- crossing and obtaining F2 population;
- isolation (identification) of genotypes by their phenotypes;
- identification of the resulting progeny by DNA markers / genome sequencing.

These tasks are inextricably linked and as a whole represent aspects of the generalized problem-strict management of successive stages of the genetic-selection process [9].

The initial stage is the selection of parent pairs to provide a given result of crossing and to optimize such selection the problem of predicting the results of crossing the parent pair is used, and the real results of crossing are analyzed at the stage of identification of genotypes by phenotypes and genotypes, they are also used to correct models of predicting the results of crossing. At each of the above stages, mathematical models of the system of interaction "genotype—environment" are used.

USE OF BIOINFORMATICS, GENOMICS AND BIOTECHNOLOGY IN PLANT BREEDING

Classical breeding depends largely on the phenotypic selection and the experience of the breeder, so the efficiency of breeding is low and the forecasts are inaccurate. Along with the rapid development of molecular biology and biotechnology, there is a large amount of biological data for genetic studies of the most important plant traits, which, in turn, allows for genotypic selection in the breeding process. However, gene information is still not effectively used in plant breeding, due to the lack of appropriate tools and technologies. The simulation approach can use extensive and varied genetic information, predict cross-performance and compare different breeding methods. Thus, it is possible to identify the most effective crossing technologies and effective breeding strategies. Modeling the breeding process allows to determine the complex genetic model consisting of multiple alleles and genes, effects of pleiotropy and epistasis, the interaction with the environment and represents a useful tool for breeders to effectively use a wide range of genetic data and other available information [17].

With the advent of accessible and affordable genomic information of important agricultural crops, it is necessary to radically change the emphasis on research to resolve the shortage of high-quality phenotypic information. Currently, traditional phenotyping is gradually replacing genotyping (PCR analysis and full-genome sequencing) as the main bottleneck due to limited funding for genetic analysis studies. Unlike genotyping, which is currently highly mechanized and automated and essentially uniform across all organisms, phenotyping is still a cottage industry, species-specific, labor-intensive and inevitably sensitive to the environment. Furthermore, although the variability of the sequence is theoretically finite and thus all sequence variants can be apparently detected for a given crop species, it is not entirely certain that each phenotype will ever be fully characterized [18].

Finer and more precise phenotyping strategies are needed to enhance the ability to map high-resolution genetic relationships and to study genome-to-genome relationships and to train predictive models of genomic selection in plant breeding. In this framework, the objective of modern phenotyping is to increase precision and throughput of phenotypic estimation at all levels of the breeding process while reducing costs and minimizing labor through automation, remote sensing, improved data integration and experimental design. Like efforts to optimize genotyping in the 1980s and 1990s, the development of effective phenotypic initiatives today requires multifaceted collaboration among biologists, computer scientists, statisticians and engineers. To characterize the full set of genetic factors that contribute to quantitative phenotypic changes in cells, organs and tissues and stages of development, reliable phenotyping systems are required.

The new generation phenotyping generates significantly more data than previously and requires new data management systems, data access and storage, increased use of ontologies to facilitate data integration, and new statistical tools for enhancing experimental design and extracting biologically meaningful signal from environmental and experimental noise. To ensure relevance, the implementation of effective and informative experiments full also requires familiarity with the various resources germoplasma, structures of the populations and the target populations of environment. Today, phenotyping is rapidly becoming a major bottleneck, limiting the possibilities of genetic analysis and genomic prediction. The challenge for the next generation of quantitative geneticists and breeders is not only to understand the genetic basis of complex trait variations, but also to use this knowledge to effectively synthesize new varieties of twenty-first century crops [19].

The decisive task of molecular genetic research today is the use of theoretical generalizations for the development of DNA technologies for practical use and the introduction of such bioinformatics technologies in the breeding of agricultural plants. The use of molecular markers opens up prospects for the study of the genetic nature of quantitative traits by marking the loci that determine their development, and on this basis for the practical improvement of the efficiency of breeding methods [20-23]. This direction is associated with the development of the modern approach of MAS (marker assisted selection), selection based on markers and does not work on the results of standard mapping, but on the information about the dynamics of the nature of the relationship of markers with the level of development of the quantitative characteristic in natural populations. Despite the relevance and applied importance of this approach, it is still only beginning to be used in plant breeding in Kazakhstan. The use of DNA markers in breeding work will significantly increase the efficiency of the breeding process.

With the growing needs of the population in quality agricultural products, the growing of the diversity of varieties, the identification of species and varieties of DNA markers becomes an increasingly important task. Molecular markers and developed on the basis of their molecular passports varieties of Kazakhstan breeding will acquire a single value in seed production to control the varietal purity during the multiplication of varieties.

Improved DNA sequencing and computational technologies allow us to track plant genetic variability at a level unthinkable a few years ago. This radically improves plant breeding and makes the process much cheaper and faster. This allows scientists to work with very complex properties and makes it possible to use the valuable genetic diversity of wild relatives of crops. The arrival of affordable, high-throughput DNA sequencing, combined with improved bioinformatics and statistical analysis, provides significant advances in molecular plant breeding [24, 25]. Multi-disciplinary programs for the breeding of major crops allow genomic variations of DNA sequences to be investigated and associated with the inheritance of very complex traits controlled by many genes [26, 27].

Biotech crops have already helped make great strides in improving the productivity and sustainability of plants. Therefore, new principles of biotechnology should be put in the basis of agricultural production. Increasing the efficiency of agricultural crops by classical breeding methods has almost developed its full potential and to accelerate this process and improve its efficiency it is necessary to use modern bioengineering and molecular genetic methods.

Today, the leaders in the use of double haploids in the breeding process are the EU, Canada, Australia, the USA and China. Every year an impressive number of new variants of doubled haploids recorded in the world [28]. As an example of the usefulness doubled haploid technology - successful breeding of lines with different genes of resistance against mosaic virus of barley [29]. And from an economic point of view, this technique will significantly reduce the routine manual operations, subject to the development of suitable protocols for the main plant species [30-36].

Development of technology for mass production of homozygous double haploids resistant to abiotic and biotic environmental factors is a very relevant research topic. Biotechnological methods of obtaining homozygous doubled haploids will significantly reduce the time and cost of breeding programs.

MATHEMATICAL MODELING IN PLANT BREEDING

The central element in the conceptual scheme of mathematical modeling in plant breeding is the information-analytical system, which carries out the correction of the planned parameters set by the user-breeder. Its development requires a complex of databases, knowledge bases, necessary organizational, technical, expert, information, mathematical and software [8].

Statistical analysis has many applications to ensure the validity and reproducibility of plant breeding and genetics studies. Crop gene pool collections are often too large for regular use. The main collection of breeders with fewer samples can increase utility while maintaining most of the genetic diversity of the entire gene pool [37].

The widespread use of information technology in breeding is constrained mainly by the lack of a set of mathematical models that most fully reflect the complexity of the real object and would give a higher accuracy of the scientific forecast. In this case, it is necessary to limit the degree of complexity of the task, as the introduction of a large number of parameters in the model complicates it, which causes an increase in uncertainty associated with errors in the definition of individual parameters of the model. At the same time, excessive simplification leads to a loss of the model's ability to adequately reflect the breeders characteristics and properties of the variety. Finding a compromise between complexity and simplicity when selecting the parameters taken into account in the model requires, first of all, professional knowledge in the field of breeding and crop production of the studied crops. In terms of a complete integrated approach to optimizing the construction of variety models, they are designed for a specific breeding station, group of breeders or a specific breeding task. In addition, there is no consensus on the algorithm of computer simulation of the breeding process. Computer programs are mainly designed to clarify the inheritance of quantitative traits using various genetic and mathematical methods [38].

When developing technologies for optimizing the construction of models of varieties, it is necessary to have information that comprehensively reflects the interaction of the biological system (variety) with different soil and climatic conditions. Therefore, before proceeding to the correction of expert models for the construction of varieties, we need data on the basis of which it would be possible to develop a complex system of the variety model, which allows the introduction of certain input data to solve specific breeding problems [38].

Modeling in biology is still a very serious research activity related to hypotheses and tests, as there is not enough information about the context of the problem to give a clear guide on how to "uniquely" determine the likely solution to various possibilities [39].

It is necessary that mathematical modeling should be included in breeding programs. Various modeling tools exist, but the community of scientists using these tools is still small and needs to improve their use. In the field of plant genetics, some of the issues that need to be addressed are highly speculative and their resolution depends on identifying and conducting the most appropriate experiments.

INFORMATION SYSTEM AS THE BASIS OF MODELING

Information retrieval (analytical) system (IPS) is intended to support breeding processes in the analysis of the source material and lines obtained in the breeding process, as well as their interaction with the environment. IPS increases the efficiency and effectiveness of breeders through the use of advanced information technologies, operational formation on the basis of their complex analytical information necessary for the development and adoption of research and management decisions. The structured data will allow to carry out high-quality scientific analysis and forecasting using statistical data processing applications (SQL, R, Python, etc.).

The creation of an interactive information and research database will provide a systematic knowledge of plant genomics, gene interactions, the manifestation of the genes in the form of phenotypic features and the impact on these processes of environmental factors. Today, the world is in the process of intensive creation of electronic databases, libraries and reference and information systems for use in breeding research. It is necessary to collect, store, systematize and visualize these data obtained in the course of time-consuming research breeding work.

An essential feature of the information system is its interactivity, that is, researchers are given the opportunity not only to take the data presented in the database and process them, but also to place the results of their research in the system. The creation of an interactive information and research database will provide some access to the collected and systematized scientific information not only to the staff of breeding centers, but also in general - a wide range of potential users of the global Internet: teachers, politicians, farmers, economists, etc.

Functional information and communication modules can be used in any research, educational or public organization. The access of the users of the research database will be through the Internet. First, the interactivity of the database implies the possibility of creating new knowledge by processing the available data. Secondly, a format for the presentation of new knowledge is being developed, thus the database is being developed in the direction of the knowledge base.

The IPS should contain a relationship describing the different characteristics of the plant, its genotype, phenotype and some environmental factors. The database allows one to establish the relationship between genetic and phenotypic characteristics of plants and environmental parameters.

The system is intended for information support of breeding processes in the analysis of source material and new varieties, as well as their interaction with the environment to improve the efficiency and effectiveness of breeders through the use of advanced information technologies, operational formation on the basis of complex analytical information necessary for the development and adoption of research and management decisions. The use of IPS will allow to solve the following tasks:

- creation of a common information space for the availability of source material on the basis of a centralized data warehouse, which provides the accumulation of relevant and storage of historical data;
- integration of existing local databases within the centralized information data warehouse and creation of a common information database;
- comprehensive analysis of the current plans of breeders, timely detection of imbalances in the structure and dynamics of scientific data;
- management of the scientific process in terms of internal audit of performance with access to the targets of scientific programs;
- visualization and publication of data and results of calculations / reports in tabular, graphical, XML and JSON formats, including the Internet;
- administration and integrity of information resources;
- providing employees with universal access to information - from any personal computer or mobile device connected to the Internet;
- improving the efficiency of the scientific process and the stability of the system due to:
- improving the efficiency and effectiveness of the coordination of scientific programs;
- improving the efficiency and quality of decisions on the implementation of individual activities;
- providing analysis of the impact of decisions on research and management processes;
- ensuring the openness of the state of scientific research;

- possibility of interaction with similar international systems for data search and analysis.

The aggregation and analysis of large volumes of long-term data (Big Data) will allow to model both the variety as a whole and its individual indicators in their interaction with environmental factors, which will allow to identify the most significant features/characteristics in relation to specific soil-climatic zones. In addition, it is possible to find suitable parent pairs, which are most likely to appear in the simulated lines.

IPS allows to systematize and process the material which is saved up as a result of breeding work with application of the computer program of creation of the grades possessing the required combination of economically important signs.

Information retrieval (analytical) system allows to speed up the work of a biologist breeder, automating the process of identifying the relationship between the phenotype, genotype and the environment. With this system, the breeder can analyze hundreds and thousands of lines in a matter of minutes, which increases the speed of data processing and, accordingly, productivity.

CONCLUSION

The vagaries of climate change make it difficult for producers and scientists to adapt new varieties. Climatic conditions never remain unchanged, which makes it difficult to breed varieties for a specific ecological and geographical zone. The tools used to classify varieties to specific soil and climate zones are called simulation modeling. With software that uses weather data and specific characteristics of cultures as a source of data, these models can simulate yield in different locations and in different years, as well as to capture spatial variation in soil, weather, practice agriculture, and other factors affecting the crop [40].

As we learn more about the extremely diverse conditions and climate variability faced by farmers, scientists can find the most suitable varieties/plants faster and more easily using simulation modeling. For example, scientists can test how plants with different genetic characteristics can manifest themselves in different growing conditions and more easily select varieties that will feel good in different places. Modeling of varieties is very useful for understanding what a plant needs to achieve higher yields in a given environment [40,41].

The analysis of the results will provide valuable scientific information to identify and justify promising areas for further breeding. The total set of the revealed morphobiological signs of plant is offered as scientifically proved model of a variety. The proposed optimal parameters of the variety model will help to improve the efficiency of breeding of economically valuable genotypes and targeted selection for adaptability to the conditions of the region for the creation of new high-yield varieties of agricultural plants.

The use of information technologies for the creation of science-based models of varieties will not only reduce the time and cost of breeding research, but also improve the efficiency of the breeding process due to the quality of interpretation of the results of experiments, reliability and reliability of the findings.

The use of modern technologies (mathematical modeling, bioinformatics, Big Data analysis, drone, satellite and aerial photography, electronic field maps, GPS tracking and geolocation programs and others) will significantly simplify, accelerate and improve the efficiency of breeding processes, reduce the cost of creating a new variety, and also to get rid of routine operations due to the quality of interpretation of the results of experiments, reliability, simplicity and reliability of research results.

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