K o n a r e v V.G.
Morphogenesis and molecular-biological analysis of plants:
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This book is devoted to autor's, his pupils and collaborators long-time investigations on plant morphogenesis: structural and functional organization of genetical, metabolic and morphogenetic plant systems in connection with problems of applied botany, genetics and plant breeding on the basis of principles and methods of molecular biological analysis. The principle of the molecular markers and the ways of their use in studies of plant biological problems, in revealing potential of plant gene fund for breeding and in solving practical tasks of plant breeding, seed production and seed testing are considered.

Tabl. 16. Fig. 55. Ref.: 437.

SUMMARY

The most responsible part of a breeder's work is the revelation of genetic variation and the selection of desired genotypes. Special difficulties arise in this respect due to phenotypic variation of complex biological properties and agronomic characters, as well as due to the presence in varieties, populations and species of so-called latent genetic variability which is inaccessible by means of classical genetics. This problem, however, is being solved by combining the methods of molecular biology with classical genetics. As the main analytical tools, the proteins and nucleic acids are employed which constitute the molecular basis for all genetic and morphogenetic processes in the organism.

Morphogenesis is the becoming of living forms in the process of their individual and historical development. It is based on the organically linked methabolic path ways, processes of structure formation and various mechanisms and factors of information and regulation which provide interaction, continuity and determination in systems of an organism at all stages and levels of its development. The highest principle of the living matter organization is expressed in self-regulation, self-reproduction and active interaction with the enviromment with which living forms make a unity.

The material basis of morphogenesis is represented by the four major classes of biomolecules: proteins, nucleic acids, carbohydrtaes and lipids, of which the two former are playing the leading role. All fundamental properties of the organism and its vital functions are related to proteins and nucleic acids. Protein properties determine molecular organization of cell structures, metabolism, protective functions and reactions of the organism to external factors. Proteins serve as the basis of metabolism and the process of arising and development of forms. These processes make the essense of morphogenesis. Nucleic acids are the molecular basis of the organism genetic functions. They are connected with the storage of hereditary information and the determining role of protein biosynthesis, the central biological process, by the means of which realization of genetic information under specific conditions of the environment takes place in morphogenesis.

Protein and nucleic acid molecules are the most complex informative biological systems. They are inexhaustible as both sources for the cognition of life processes, and as means for the development of new technologies. Within the strategy of plant production, two major ways in using these biological molecules have been identified:

- genetic systems marking and evaluation of plants' genetic constitution for solving topical needs of genetics and breeding;

- genetic systems reconstruction through manipulating nucleic acids by means of various protein factors, including enzymes. It was called gene engineering and is meant for the genetic improvement of varieties and creating new plant forms with predetermined characters.

The above said refers to all the organic world. At the same time, in terms of metabolism and formation, especially in the phase of the secondary, or the specialized metabolism, the photosynthesizing plants differ sharply from animals, as in the former practically all the nitrogen-containing compounds are involved in active metabolic processes and metaplasmic formations are represented almost exceptionally by nitrogen-free compounds, i.e. cellulose, pectin, lignin, suberin, etc., while in animals these are nitrogen-containing compounds and proteins like keratin, collagen, elastin, etc. In addition, the character and products of specialized metabolism distinctly show in all cases the biological specificity of the organism, e.g. specific, generic, etc., the bases of which are laid in genetic systems and are realized in the processes of metabolism and morphogenesis.

The specialized metabolism is of great scientific and practical interest because it is predominantly with that the processes of storage nutrients build-up and the yield useful part formation in most cultivated plants are associated. This metabolism occurs in the ontogenesis of cells and the organism in general as a derivative of the essential (fundamental, embrional) metabolism based on the central molecular-biological

process. It may be expressed with the following formula: DNA-RNA-PROTEINS-MORPHOGENESIS that indicates the major flow of genetic, functional and structural information on the basis of which becoming of an organism is developing.

In the cell of a higher plant, the fundamental molecular-biological process handled by the genetic and protein-synthesizing systems, is represented by the three types, namely the nuclear-cytoplasmic, mitochondrial and plastidic.

The nuclear-cytoplasmic type is the main one which is characterized by a complex (nucleosomic and chromosomal) organization of the genetic apparatus with the involvement of histones and a large number of nonhistonic proteins, a total set of genes that via the mRNA ensures the encoding of practically all proteins in the organism, a complex genome which includes an abundance of the noncoding (service) nucleotide sequences and the nucleolus organizer that provides ribosomal RNA and proribosomal units for the 80S-type ribosomes. The cell nucleus genome provides the protein synthesizing system of cytoplasm with the necessary set of tRNA and encodes synthesis of the corresponding aminoacylsynthetases.

The translating part of the protein synthesizing system of the nuclear-cytoplasmic type is located mostly in cytoplasm and through its internal membranes is included into the complex morphogenetic process of the cell. The main function of cytoplasm is in the realization in metabolic and morphogenetic processes - via its protein synthesizing system - of genetic information coming from the nucleus. The essential part of these processes, connected mainly with the functions of respiration and photosynthesis, is provided by auxiliary genetic and protein synthesizing systems located in mitochondrias and plastids.

The mitochondrial and plastide types of genetic and protein synthesizing systems organization are more simple and have the “bacterial”-type design: their genome is represented by the circular DNA with a limited number of structural genes. All of the above mentioned elements in the protein synthesizing system are reduced, and it works on the basis of the 70S-type ribosomes. In this case, genesis and functioning of the organoids in question proceed with the involvement and under the governance of the nuclear-cytoplasmic encoding and morphogenesis. In the evolutionary respect, these systems of mitochondrias and plastids may be regarded as relicts which survived from procariots since the times of emergence and morphogenetic, i.e. structural, as well as functional shaping of the corresponding organoids for the aerobic respiration and autotrophic nutrition.

The origin of the plant world was connected with the appearance of the photosynthetic autotrophic way of nutrition and with the formation on its basis of the plastome – a unity of multiple cell plastids, an autonomous formation, but integrated into the cell’s genetic and morphogenetic systems. This integration is clearly visible in respect of metabolism. As is seen from the diagram (Fig. 55) and figures 7, 9 and 10, the light and dark photosynthetic reactions organically join the main metabolic ways of the cell, thus confirming the ancient origin of photosynthesis. It is also proved by the diverse contribution of photosynthesis and its fundamental importance for the morphogenetic processes in plants, and one of their manifestations is *photomorphogenesis*. Especially distinctively it reveals itself in the phase of differentiation and specialized metabolism of a plant cell and determines the characteristic direction in morphogenesis.

In this relation, of special interest is the formation of cell walls and extracellular bodies in plants. These are complex derivatives of the protoplast’s morphogenetic functions, i.e. of those of cytoplasm and the nucleus. Their anlage takes plase on the basis of the main metabolism with direct involvement of morphogenetic systems of cytoplasm, under control of the nucleus, and formation proceeds mainly at the expense of products of the specialized (secondary) metabolism. Here the *autotrophogenic* principle of metabolism and photomorphogenesis is most conspicuous.

One of important factors of photomorphogenesis is phytochrome, the genesis and functions of which are connected with chlorophyll. The direction of metabolism and morphogenetic processes characteristic of plants is determined also by other phytohormones and a set of many diverse factors related to different spheres of metabolism. Some of them may be judged by those ingredients or products of metabolism which

are provided by plants to heterotrophic organisms in the form of vitamins or other "essential" factors (some aminoacids, nonsaturated fatty acids, etc.) because the latter, i.e. heterotrophs, due to this or that reason do not possess mechanisms of their biosynthesis. In this respect, the organism of a photosynthesizing plant represents by itself the most perfect biological organization on the Earth which is capable of providing in full all factors of metabolism for itself and supplying the missing ones to all other life forms on the planet.

When discussing molecular organization and properties of biostructures, some details are considered which relate to the initial stages of formation at both molecular and supramolecular organizational level. It has been noted that the formation of some quite significant elements of these structures proceeded as far back as in the period of pre-biological evolution as a consequence of selection and integration into the generating biological systems where these elements occupied the basic position and got incorporated into mechanisms of morphogenesis. Here belong the processes of biological molecules conformation on which their spatial organization depends, as well as the systems of the conjugated ion-hydrogen bonds which are responsible for supplying energy to all molecular and supramolecular biosystems.

All the supramolecular structurally functional organizations are built and exist in the organism due to the conformation ability of their ingredients and in the presence in them of continuous systems of conjugated ion-hydrogen bonds which are used as energy transfer channels.

These both factors underlie the most important morphogenetic processes among which structural transitions of the cell nucleus chromosomes and cytoplasm membrane systems should be noted. They comprise a considerable part of mechanisms regulating genetic activity of the genome and morphogenetic functions of cytoplasm.

Enzymes and hormones may be the factors regulating structural transitions. For example, the DNA superspiralization in the nucleus is known to be maintained by topoisomerases. The substances that affect these enzymes change the DNA degree of spiralization and packing, and strongly influence the chromosomes genetic activity and the cell functional status.

Among very important factors of the functional changes regulation in the genome is the DNA methylation by methyltransferases. It makes nucleic acids resistant to nucleases and plays an important role in providing the organism's immunity, that is, its protection from the intrusion of a foreign DNA and genomic mobile elements, and serves as the main reason of the foreign gene "silence" in transgenosis. The DNA methylation in plants is regulated by phytohormones; its inhibiting may be a significant component of the mechanism of cell differentiation by cytokinins. The nucleic acids methylation is generally held to be associated with their major functions, them being replication, transcription, translation and recombinations.

The DNA methylation influences the chromatin structure and is related to the genome functional status: "silence" of transgenes during transcription, associated with the DNA methylation in the promoter, is followed by their packing into the condensed chromatin.

Since structural transitions of the cell nucleus chromosomes and the cytoplasm membranes reflect functional state of both the cell and the entire organism, methods of their evaluation may be used in the genetic and biological analyses of plants when solving various theoretical and practical problems of plant production. For example, biochemical and cytochemical methods of evaluating functional status of a genome proved to be very efficient in studies of plants' response to unfavourable factors of the environment, to physiologically active substances, as well as in revealing the nature of heterosis and determining its predictability.

In Chapter 4 which is devoted to the role of biotechnology in studies of intracellular and cellular bases of morphogenesis, it is shown that in the last decades a breakthrough has been made in plant biology in respect of molecular mechanisms of genetic processes. It allowed attaining the modern level in biotechnology, including gene, chromosome and cell engineering. It was accompanied by transition from molecular to supramolecular biology, from intracellular to supracellular processes, i.e. those occurring in tissues, organs and organisms. For the cognition of plant morphogenesis and the solution of many biotechnological

tasks, cells, supracellular organizations and their interaction within the organism acquire special importance as objects of research. Of special importance to this end are the notions of unity of a multicellular organism, its structural, functional and, first of all, cellular integration. The most important factors of such integration are as follows:

- intercellular communications that provide interaction of each cell with the neighbouring ones via plasmodesms with the involvement of the protoplast's peripheral membrane (plasmalemma), cytosol and a net of fibrillary elements of the cytoskeleton;

- extracellular systems that include cell walls, and other elements of the extracellular matrix which are functionally linked with genetic and morphogenetic systems of the nucleus and cytoplasm and ensure the all-round functional and information integration of cells in the organism;

- hormonal systems that provide coordination of life processes in the organism through metabolic, morphogenetic and genetic processes;

- molecular-genetic unity of all parts of the organism that reveals itself in biological specificity mainly at the expense of protein, the obligatory ingredient of all its biostructures. This unity is a factor of organisms' integration within a biological species. For some characters and properties, this unity is historically retained up to the tribal or even family level.

Integrity of an organism is also expressed in such biological categories as specificity, biological recognition and ability to integration on the basis of its molecular biostructures complementarity.

Among many factors and mechanisms that ensure integrity of the entire organism, there should be specially noted the structural and functional interrelation of genetic, metabolic and morphogenetic processes. Structurally it reveals itself in the tandem location of genes as their "true" linkage, and functionally it is manifested in the course of metabolism and morphogenesis involving genetic, hormonal and other regulating systems that ensure precise coordination of all genes' work. Such a mechanism was well labelled as the *functional linkage of genes regulated in a coordinated way* (see Ch. 5, Sect. 5.2).

The functional linkage of genes located in different parts of the genome but regulated in a coordinated manner is basic to the organization of many molecular-genetic systems of metabolism and morphogenesis. Especially often it realizes itself in the encoding of general metabolic ways and subunits of heteromeric multimolecular structures of the protein. Even the interorganoid functional linkage of genes regulated in a coordinated manner is possible and may take place, for instance, during joint encoding by genomes of the nucleus and organoids of cytoplasm of a series of multimolecular protein structures in mitochondrias and plastids. As a classic example of this may serve the biogenesis of ribulose diphosphate carboxylase, a multiple enzyme of the chloroplast (see Ch. 2, Fig. 8).

The structural and functional interrelation of genetic, metabolic and morphogenetic systems in the organism is regarded as a main prerequisite for the development of plant bioanalysis methods which employ molecular marking and are based on the use of two categories of biological molecules, that is proteins and DNA. The former, as it has been noted, are essential to metabolism, biogenesis and functioning of all cellular structures including the genetic apparatus, while the latter provide molecular basis of all genetic systems. This places them among the most important factors of molecular-biological identification of genetic systems, and of morphogenetic ones as in the case with proteins. Besides, proteins and DNA possess the main attributes of a genetic marker, that is genotipicity, codominance in heredity and lack of pleiotropic effect.

The main advantages of a DNA marker are in its accumulation in individual structures like chromosomes, mitochondrias and plastids, and in the possibility to use this feature for analyzing any organ at any stage of plant development. The peculiarities and a high degree of genetic specificity make it an ideal marker, the potential of which are still far from being revealed. However, the associated methodological difficulties and expensiveness of DNA technologies for the time being are restraining their wide-scale application in plant production.

Proteins, as a structural and functional keystone of an organism, encompass all spheres of life. All forms of biological specificity and biological recognition are linked with them. They are involved in all mechanisms of biological reproduction. There is not a single biological structure or life function where proteins would be absent or play a role less significant than one of the first. In this respect, i.e. in their importance for metabolic and morphogenetic processes and in the scope of their participation in biosystems, proteins considerably exceed all other categories of biological molecules.

This statement is based on the following conception.

Protein biosynthesis goes through many stages; it includes transcription, splicing, translation and various post-translation modifications occurring practically in all stages of molecule formation – up to the membrane transit and its inclusion into biostructures (see Chapters 1 and 3). All these stages are genetically determined, but in the process of development a protein molecule nevertheless sort of "absorbs" additional ("superencoded") structural and functional information, already more bound with the conditions of the organism's development. That is why a "mature" molecule of protein, as a rule, appears to be morphogenetically richer, especially at the expense of its higher structures, than it might be provided by the sole genetic locus of the genomic DNA which encodes it.

A certain share of superencoded information may be actualized in DNA-related genetic shifts and become the basis of evolutionary variation in an organism. However, its major part is actualized in metabolic and morphogenetic processes and revealed in the organism's phenotypic variability, which supplies protein with the properties of a highly efficient morphogenetic marker.

Now, some words about markers.

In common use, a marker is a marking tool or label, in biochemistry it is a factor of identification, while in genetics it is a gene of known localization which may help to reveal other genes. Usually, not the marker gene itself is dealt with, but its phenotypic expression, which represents a well-discernible, discrete (i.e. qualitative) character. Such character is regarded as an identification factor for its corresponding gene, i.e. as a marker of the gene itself as well as other genes functionally linked with it.

In view of this, only such DNA loci should be recognized as proper genetic markers, which encode proteins. In higher organisms, they constitute only 3-5% of their genomic DNA. The remaining part of the genome is similarly specific and informative, therefore it is successfully used in genetic and phylogenetic analyses, genotype identification, etc., but in the genome it performs "auxiliary" (regulatory, stabilizing, etc.) functions, providing conservation and realization of genetic information in metabolic and morphogenetic processes. In a direct way, this information is received by proteins. Being primary and, therefore, genotypic products of the encoding loci in the genome, they must be attributed to a category of reliable genetic markers with distinct expression of the genes marked by them.

In molecular genetic analysis of plants, we use two marker characters of protein: the molecule's electrophoretic mobility determined by its charge, size and structure, and immunochemical specificity manifested in immunological reactions. The first one is convenient for genetic analysis and intraspecific differentiation, i.e. for identification of varieties and inbred lines, analysis of populations, etc.; whereas the second is quite efficient in genome analysis, i.e. in identification of genomes, evaluation of genomic composition of allopolyploids and genome transformation, study of genomic relations between species in connection with the problems of origin of cultivated plants, etc. With this, electrophoresis of polymorphic proteins makes it possible to mark allelic variants of a gene and reveal its allelic structure within species and populations, whereas electrophoresis of monomorphic proteins allows identification of gene loci and determination of the genome's specific affiliation.

Antibodies, obtained by immunizing animals (rabbits) for species-specific protein antigens of plants, serve as immunochemical markers.

Thus, protein markers make it possible to perform biological analysis of plants on all main levels of genetic variability, i.e. the allelic, gene and genomic ones.

The above-mentioned functional linkage of genes regulated in a coordinated way lying in the basis of the conjugation between genetic, metabolic and morphogenetic processes within an organism may be expressed through a combination of electrophoretic components of a multivariate and polymorphic marker protein. This principle is taken as the basic one in marking a genotype according to the electrophoretic pattern of storage proteins, enzymes and other marker proteins, and, through the genotype, in the assessment of numerous genetically and morphogenetically complex characters and properties possessing varietal and species specificity.

For solving many problems of applied botany, genetics and especially plant breeding and seed production, the most convenient, in both technical and methodological aspects, are seed storage proteins. They are multivariate, genetically polymorphic, and species-specific, they are present in seed or grain in great amounts, are localized in a morphogenetically uniform tissue, and may easily be subjected to isolation and consequent immunochemical and electrophoretic analyses. Other seed proteins, whose functional state is in the same phase, may be used as auxiliary markers in the cases when storage protein resolution is found insufficient. They may be represented by enzymes, their inhibitors, and glutenin subunits.

Considering the everywhere effective phenomenon of the above-stated "functional linkage" of genes and genetic systems, it is possible to assume that seed proteins, in the aggregate, may provide for quite complete marking of the loci responsible for genetic and phylogenetic plant variability.

Factually, it was on seed proteins that the main principles of molecular genetic marking of plants were developed to solve burning problems of plant production. They were the first to be included in the methodology of plant breeding and seed production, and they served as a catalyst or, in some cases, even as a key element for the development of new molecular marking technologies based on DNA utilization.

Great advantages are expected from combining DNA technologies with the principles and methods of protein markers.

The second half of the book is devoted to the application of the described principles of protein markers in solving burning problems of applied botany, genetics and plant breeding. The researches undertaken in these directions have shown that these principles appear quite efficient for biological analysis of plants, especially for solving such problems as identification of a species or genome, genomic analysis of allopolyploids, the origin of cultivated plants, degree of their relationships with wild relatives, and heterosis as a way of realizing genetic and morphogenetic potential of plants in evolution and plant breeding. Protein markers have for the first time been used for making a molecular genetic method of seed evaluation for hybridity in the first generation with the purpose of its application in heterosis breeding.

Detailed study has been conducted on the biochemical and molecular genetic essence and genesis of such genetically and morphogenetically complex character as baking and pasta-making qualities of flour made of bread and durum wheat or other relative cereals. It has been shown that this and other complex traits are typically characterized by varietal, specific and even generic specificity and by wide limits of phenotypic variability, which is stipulated by their polygene coding and by involvement of all inheritance levels, i.e. the allelic, gene and genomic ones.

It is notable that heterosis is the major phenomenon specifically in the expression of complex and quantitative characters, because it is realized, first of all, in their development.

Polygeny and influence of the environments determine a smooth fashion of complex character variation; with this, the variability of quantitative characters is adequately described by a Gauss distribution curve. This fact has preconditioned the situation when mathematical approach, namely the method of classical statistics, has become dominant in their genetic analysis. Quantitative genetics was shaped as a discipline in the first decades of the 20th century, when no methods had yet been available to reveal the nature of complex characters. As soon as molecular biology and genetics started their advancement, the need for statistical methods in complex character analysis began to pass gradually off, or they acquired a different designation – merging with the methods of molecular biology, they descended deep to the entrails of the

characters, into the calculations of inter-gene and inter-molecular relations, undoubtedly with the status of an auxiliary means of biological analysis. By the way, the analysis of many complex polygenic characters, such as insusceptibility to diseases or resistance to unfavourable factors, is not associated directly with mathematical methods.

The category of the most important and most complex characters or, to be more precise, biological properties includes *adaptation* – capability of a plant to get accustomed to ever changing environments. This is a very wide notion, as it is interlinked with many life functions, in fact, with all of them. Accordingly, any success in disclosing the genetic and morphogenetic essence of all aspects of adaptation in each separate case would depend on the degree of cognition of these functions.

One of the basic and universal mechanisms, directly or indirectly connected with resistance to unfavourable environmental factors and adaptability to changing conditions of plant life, are structural transitions in cytoplasm membranes and chromosomes of cell nuclei. The former are connected with the morphogenetic regulation of an organism, while the latter with the genetic one.

It is marked out in Chapter 11 that the development of plant breeding for complex traits in many ways depends on the state of gene fund, because they are formed on a wide genetic and morphogenetic base of populations and species with participation of genetic systems of all complexity levels – from allelic to genomic, i.e. specific, generic and even tribal ones.

Chapter 12 presents a review of the structure of crop gene fund. It is represented by three main gene pools: varietal, specific and supraspecific. Basic gene fund of each crop is confined to the limits of a biological species, whose representatives demonstrate practically full compatibility. The volume of varietal gene fund and its limiting reproductive boundaries are defined by plant breeders and maintained (monitored and guarded) by seed producers. Gene fund of natural populations is formed and exists according to the laws of plant population development in natural conditions, provided that they are spatially isolated from other populations of the same species.

Attribution of the status of a varietal pool to varietal and natural populations has become possible when "single seed analysis" of varieties and populations by electrophoresis of proteins from individual seeds in standard samplings was introduced in seed production.

Supraspecific gene fund constitutes additional and potential sources of genetic variability. Considering the possibilities offered by modern biology, with a certain degree of conventionality, realistic limits of availability of this gene fund to breeding practice may be set at the boundaries of a tribe.

In supraspecific gene fund, we have expressly emphasized *"gene fund of polyploid complexes"* – a group of the species, relations between which are realized through allopolyploidy. Importance of analyzing genomic relations between species with the purpose of identifying polyploid complexes lies in the fact that it is one of the ways of plant species' evolution and one of the modes of the development of their forms; and their identification supplies a plant scientist with a strategy of employing supraspecific gene fund in breeding practice and with initial breeding materials tested by the nature for genomic compatibility.

It should be expressly stressed here that the use of proteins as markers in biological analysis of plants has already ensured progress in the development of many trends in applied botany, genetics and breeding. As stated earlier, protein markers help to solve problems of the species and the genome as a genetic system of the species category, identify the ways of origin of crop species and genomes, and assess the degree of their relationship with wild relatives. They provide an opportunity to reveal genetic and morphogenetic nature of allopolyploidy and heterosis, as well as the essence of genetically and morphogenetically complex biological properties and commercial traits of plants.

Consequently, molecular biological analysis of plants, including genomic analysis according to species-specific protein antigens, genotypic analysis according to the single seed protein banding pattern, and genetic analysis according to separate components of polymorphic marker protein lay out wide prospects for solving theoretical problems of botany and genetics, and carrying out practical activities in plant breed-

ing and plant production.

Genomic DNA, especially DNA of encoding loci, which determinates through proteins all metabolic and morphogenetic processes, is an ideal source of genetic and even morphogenetic markers. Its capabilities in this respect are far from being disclosed. Intensive work in gene mapping of the genome and revealing functional significance of its non-encoding parts and loci is currently underway. In future, research is expected to be targeted at studying interaction between genes and identifying functional gene associations and genetic systems including the genome non-encoding areas, with which determination of many complex characters and properties of an organism may be connected.

A number of laboratories all over the world have started the development of DNA conservation methods and a system of corresponding technical and organizational measures for setting up DNA banks to ensure conservation of the most valuable genetic materials of cultivated plants and their wild relatives, and above all, extinguishing plant species and forms.

In the selection of markers for genetic and morphogenetic analyses, little attention has yet been paid to the remaining two categories of biological molecules – lipids and heteropolysaccharides. They are quite diverse in the cell, and in combination with protein carriers they can form highly specific and bioactive systems that have been used by now only sporadically, for instance, as efficient antigens in genetic and, especially, in phylogenetic analyses.

Molecular biological approaches acquire special significance in solving the problems of crop gene fund. It has already been shown on numerous examples of protein marker utilization that these markers help to identify and document in a convenient form not only genetic systems (genes, their allelic structure, gene complexes, chromosomes and genomes), but also taxonomic and biological units (lines, biotypes, varieties, populations and species).

In the past decades, molecular marker methods have increasingly been entering practically all spheres of applied botany, genetics and plant breeding. Most active and successful introduction into breeding practice and seed production is demonstrated by principles and methods of protein markers. In several countries they have replaced such cumbersome, expensive and less efficient seed control technique as ground control. Protein marker methods are used in combination with other breeding techniques and in all phases of the breeding process – from the search for initial breeding sources to variety testing, seed production and seed control of the released cultivars. In a number of cases, they have already being naturally merged with the methods of genetics and plant breeding and provide for the development of new methodology in these fields of science.

Principles and methods of marking genetic systems with proteins have been formed on a broad theoretical and experimental background. They have incorporated achievements in many biological disciplines, such as, first of all, biochemistry, genetics and evolution of different classes of proteins, on one hand, and genetics, phylogenesis and various aspects of apprehending plant morphogenesis, on the other. Decisive argumentation is provided to them by molecular biology. Further development of protein marker principles and methods will depend upon general progress in biology, especially in molecular and physicochemical ones, which determine theoretical and technical levels of the work with proteins and research on the genetic and morphogenetic plant systems marked by them.

In the outlook, further development of the works in the sphere of molecular biological analysis of plants would lead to complete gene marking of crop genomes, mapping of their loci, and fundamental study of the systems encoding commercial characters and biological properties. It will create a practical basis for transgenous and other forms of modern breeding, as well as for implementation of desirable and realisable reconstruction of the genome and corresponding morphogenetic systems by the methods of molecular biological technologies.

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