gained its revolutionary value only after 1900, when the Pisum paper, translated in different languages, marked a fruitful contribution to the developement of genetics in the first half of the 20th century.

At the new level of knowledge Mendel's experimental approach instigated the elaboration of the concept of chromosomal heredity and later led to the elaboration of the principles of genetics of populations and finally to the synthetic understanding of the process of evolution, including such phenomena as genetic erosion or genetic sedimentation.

In the perspectives of germplasm research and future genetic manipulations, the achievements of G. Mendel are fundamental not only in the history of biological science in Moravia, but in the science of the world as a whole, comparable, in Central Europe, only with the discoveries of Copernicus, Kepler and Bolyai regarding the science of space

Rezumat

OREL V., 1984, Gregor Mendel şi începuturile cercetărilor genetice în botanica agricolă. Not. bot. hort. agrobot., Cluj, XIV. Principiile, ce stau şi la baza cercetărilor referitoare la resursele genetice pe plan mondial au fost formulate prima dată de G. MENDEL (1822-1884) ca rezultat al unor experienţe riguroase de hibridare la Pisum sativum. Cercetările efectuate de colectivul din Mendelianum (Muzeul Moraviei) au demonstrat că geneza acestor descoperiri nu reprezintă o enigmă în istoria ştiinţei, cum se presupunea de obicei pînă în prezent ci este adînc ancorată în tradiţiile ameliorării plantelor. S-a dovedit că planul experimental cu Pisum a fost conceput în vederea rezolvării unor probleme fundamentale cu caracter practic. Se arată că interacţiunea metodelor experimental-inductive ale lui MENDEL ca amelioratur cu cele ipotetico-deductive ale lui MENDEL ca matematician-fizician au avut o importanţă majoră în descoperire.

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INSTITUTUM AGRONOMICUM "DR. PETRU GROZA" CLUJ-NAPOCA (ROMANIA)
NOTULAE BOTANICAE HORTI AGROBOTANICI, 1984, XIV

THE PISUM MODEL

A.T. SZABÓ

Abstract:

SZABÓ T.A., 1984, The Pisum Model. Not. bot. hort. agrobot Cluj., XIV, 53-58. Connected with the centennial anniversary of the death of Gregor Mendel, an important achievment of Pisum genetics is briefly discussed: the Pea Model proposed by S. BLIXT and J.T. WILLIAMS (1982) for use in computerised documentation of plant genetic resources.

Key words: genetic resources, computer, Pisum, history of biology

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The first basic laws of inheritance were stated by GREGOR MENDEL based on experimental results obtained with Pisum sativum (5). There has frequently been emphasized, that the genius of MENDEL is demonstrated, after all, by the choise of the pea plant as the main experimental organism. This statement is important for the present day research and reflects the impact of early Pisum genetics in the history of biology. Today, especially after the lectures of the last Mendel-Symposium (6) we realize more clearly the greatness of this scientist, who first connected correctly the characters of an organism to material factors hidden in gamets. Ever since its rediscovery, this knowledge has been an important part of our culture (1, 4, 8).

The new principles expressed in a new book of basic importance (2) are mainly based on results in Pisum genetics too. These principles may be regarded as the beginning of a new period in the history of plant biology. Implicitly, the best way of MENDEL's commemoration is not by raising the past, but by calling forth the future.

The International Board for Plant Genetic Resources (IBPGR), sponsoring the edition, was created to co-ordinate the collection, study, conservation and utilization of the genetic variability still preserved in economically important plant populations. The work itself is based on the principles discovered by MENDEL, i.e. every character of an organism is determined by distinct hereditary factors. The Pea Model is focused on these factors -- now called genes -- in order to promote a higher level of integration of the knowledge accumulated in plant biology. Recently, the perspectives of some highly sophisticated genetic techniques have stressed the importance of the gene-resource studies. At the same time, the economy, the industry, the agriculture, the urbanisation and the different "prewar situations" are acting against the genetic diversity of the biosphere. The short term efficiency is often oposed to our long term interests (7, 8, 9, 1o, 11, 12).

The tapering of some small populations or the disappearance of rare spontaneous species seems to be, for the time being, nothing else but scientific values. In reality, even the economic worth of these lost specific gene constellations cannot be overestimated. In the case of crop plants, the value of the genes is more evident. The steady disappearance of the variability hidden in the land races of crops have both practical and theoretical consequences (1o, 11, 12). The world-network of genetic resource collections have the call for the gathering of the economically important local populations, for the preservation and utilisation of the available information and the integration of results obtained by different specialists.

And there it is where past and future trends converge; Pisum has again become the model plant for a new way of thinking. This new approach will allow the simultaneous handling and the integration of the information available in different specialities for a species or a gene pool (2).

According to our knowledge, the Pea Model is the first computerized approach, which applies consequently the biological principles in information handling and retrieval. Between 196o and 198o, many computerized gene resource studies were performed throughout the world and a great number of different descriptor lists were compiled (3). These were all characterised by a degree of artificialization and applied mostly the data handling principles and practices worked out for non-living, technical systems. The situation was somewhat similar

to that created in the time of Linnaeus: the computer treatment was based on the registration and manipulation of conventionally selected characters. There were important results too, but without a sound basic principle such an approach could not entirely reflect the essence of the phenomena, and the quantity of potentially available information was hardly manageable with the desired scientific efficiency even by computers. The conceptual field of most computerized gene bank systems is somewhat similar to that of botanists and plant breeders before MENDEL -- they consider characters and character combinations instead of factors and factor interactions.

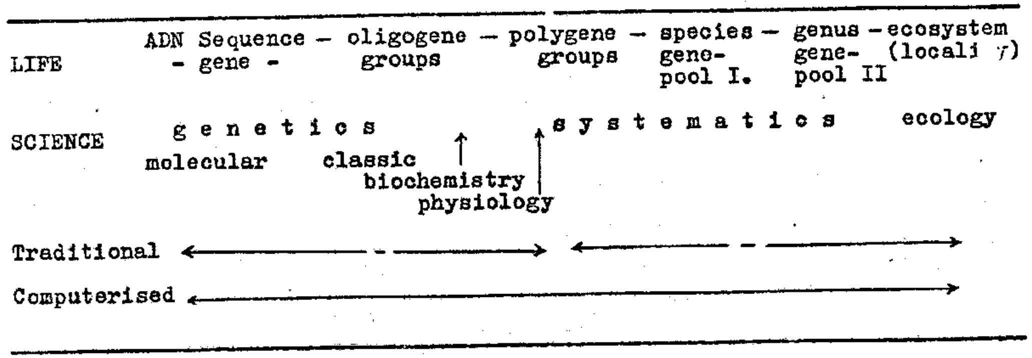

Fig.1. Information flow in biological systems and in science

The Pea Model (2) allows for the simultaneous handling of different data sets accumulated on more or less distinct scientific fields. It tries to follow the principles of the information retrieval process coded in DNA sequences and to registrate the interaction between the genetic and environmental information (Fig.1). A true three-dimensional approach was built up (Fig.2) which considers simultaneously at least three different categories of data:

1. DNA sequences; alleles, genes, linkage-groups, chromosomes;
2. gene products; enzymes, proteins and other metabolites;
3. phenotypic characters

The first category traditionally belongs to genetics, the second to the physiology and biochemistry, the third one to the systematic botany and morphology. Further information, e.g. the passport data of the collections are of ecological importance, others, e.g. the experimental results of the field experiments, are agronomical ones, etc. This approach creates a real framework for the complex use of any information obtained at different levels of science.

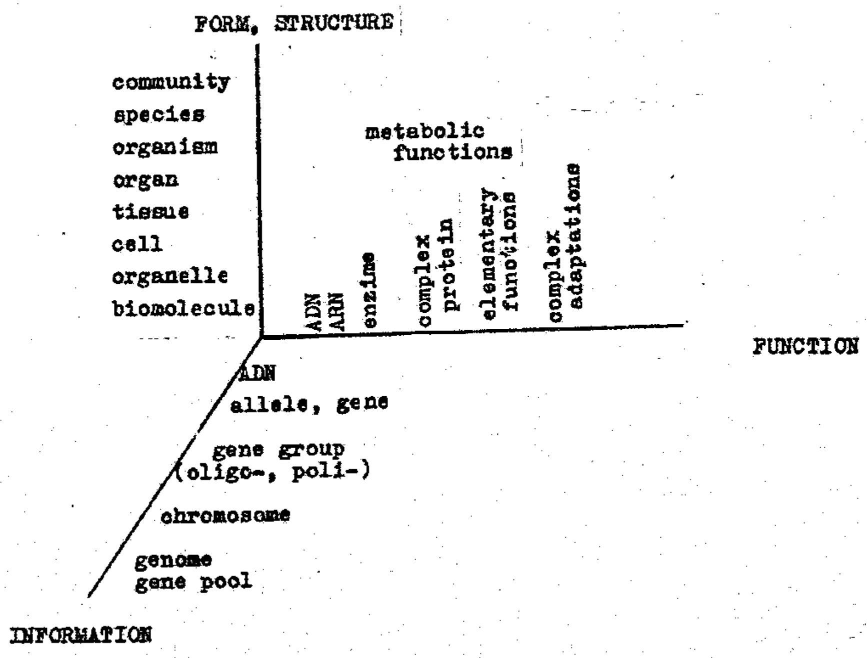

Fig.2. Three-dimensional approach of the informations in PISUM MODEL

The Model reduces the great diversity of the possible descriptors on a much restricted number of factors grouped on the following levels:

1. regulator genes (RG);
2. structure genes (SG);
3. monogenes (G);
4. oligogenes (O);
5. polygenes, polygene-low, polygene-high (PL);
6. infraspecific taxon descriptors (I);
7. species descriptors (SP);
8. descriptors for higher taxa;
9. ecological descriptors (passport data).

In order to exemplify the utility of the Pea Model the authors make use of the classical character of pea seed colour. In the cultivated species this character is determined at monogenic level by 8 allels, at oligogenic level by 7, and at poligenic level by 12 genes. In the case of the wild pea the corresponding values are 26, 8 and 6 respectively. If expressed by phenotypically observable characters in the first case 1 million and in the second case 4 million descriptors and descriptor states would be necessary to express all the possible combinations. This would not only be superfluous, but also useless. Introducing genes instead of characters means not only a more logical and biologically more effective way of thinking, but also spearheads possibilities for further development.

In the expectations of the history of sciences the importance of the Pea Model is somewhat similar to that of the development of Linnean systematics after the medieval botany or to that of the emergence of the Mendelian genetics. The principles formulated and the system created urgently calls for a worldwide network of similar computerized biological information handling systems. The huge amount of the already accumulated botanical, physiological, biochemical, genetical and other data, piece by piece, lonely and isolated may be more or less irrevelant, but can gain new and full importance, if integrated with the aim of the Pisum Model.

BLIXT and WILLIAMS (1982) are of the opinion, that such a worldwide computerized network, with high integrative power should evolve naturally, from self-organized computerized units which recognize the advantage of the new principles. The sole condition of the organic growth and evolution -- besides political ones -- is a common way of thinking, a compatibility between elementary research units.

The progress achieved in Pisum genetics during the last century (1,5) was perhaps not so spectacular as that of the technology which today, raises us above clouds. It however is worth to remember: it was hardly possible for MENDEL to forsee the level of our science and technology. Who is now able to forsee, even with approximation, the level of biology in 2o84 ? Mutatis mutandis -- we only can hope, that "once the time will surely come" for contemporary discoveries and our descendants will have full use of all available knowledge.

Rezumat

SZABÓ T. A., 1984, Modelul Pisum (în engleză), Not. bot. hort. agrobot., Cluj., XIV, 53-58 În lucrare este discutat Modelul Pisum propus de S. BLIXT şi J.T.WILLIAMS (1982) pentru documentarea resurselor genetice. Modelul se bazează pe utilizarea analogiilor în prelucrarea informaţiilor în sistemele biologice şi cele electronice de calcul. Concepţia nouă elaborată deschide perspective noi în valorificarea integrată a datelor acumulate în diferitele domenii ale cercetărilor biologice. Datorită acestor perspective modelul este şi un omagiu adus amintirii lui G. MENDEL în preajma anului aniversal.

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NOTULAE BOTANICAE HORTI AGROBOTANICI, 1984, XIV.

AUTOMATIC REGRESSION ANALYSIS FOR USE IN A COMPLEX SYSTEM OF EVALUATION OF PLANT GENETIC RESOURCES

CS. ÁRKOSSY, A. T. SZABÓ

Abstract

ÁRKOSSY CS., SZABÓ T.A., 1985, Automatic regression analysis for use in a complex system of evaluation of plant genetic resources Not. bot. hort. agrobot., Cluj., XV.59-62 .
In accordance with the general requirements regarding computerisation in gene banks and germplasm research a computer program has been compiled for the analysis of univariate response in crop germplasm evaluation. The program is compiled in COBOL and run on a FELIX C-256 computer. The different modules of the program allows for: (1.) data control and error listing; (2.) computation of the regression function; (3.) listing of the differences between the values measured and computed; (4.) sorting of the individual samples; (5.) construction of scattergrams in two dimensions for measured values with the simultaneous representation of the regression line; (6.) listing of examined samples in a sequence required in evaluation.

Key words: automatic regression analysis, crop germplasm, gene bank

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Seed samples stored in gene banks are preserved especially for plant breeders, so the samples need to be well documented. In an attempt to raise standards (HANSON et al. 1984) the duties of genebank curators were identified and gradual application of the more efficient documentation principles were suggested (BLIXT and WILLIAMS 1982). Paralelly, in many countries, a computerised documentation system emerged in agriculture research and gene bank documentation as well (CRISTEA 1981, FRANKO et al. 1982, KNUPFER 1983, KOVACS 1984, VARGA et al. 1979 etc.). In order to