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M.S. SWAMINATHAN

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November 1988

Dear Dr. Moens,

I thank you for your letter enclosing 2 copies of the paper of Dr. Shumny. I am returning this paper with a few changes. I also enclosed two copies of the paper of Prof. Li Zhensheng.

With warm regards,

Yours sincerely,

Sent

(M.S. SWAMINATHAN)

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Editor
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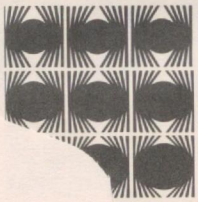

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Spelling should follow that of *Webster's Third New International Dictionary* or the *Oxford English Dictionary*. Authors are responsible for consistency in spelling. Abbreviations, nomenclature, and symbols for units of measurement should conform to international recommendations. Metric units should be used or metric equivalents should be given and the use of SI units (Système international d'unités) is encouraged. This system is explained in the *Metric Practice Guide* (1979) published by the Canadian Standards Association (178 Rexdale Blvd., Rexdale, Ont., Canada M9W 1R3) and *Quantities, Units, and Symbols* (1971) published by the Symbols Committee of the Royal Society (6 Carlton House Terrace, London, England SW1Y 5AG). As a general guide for biological terms, the *CBE Style Manual: A Guide for Authors, Editors, and Publishers in the Biological Sciences* (5th edition, revised and expanded, 1983) published by the Council of Biology Editors, Inc. (Bethesda, MD, 20814) is recommended. Biochemical nomenclature and abbreviations should follow the recommendations of the International Union of Biochemistry, such as those on enzyme nomenclature (*Enzyme Nomenclature (1984): Recommendations of the Nomenclature Committee of the International Union of Biochemistry on the Nomenclature and Classification of Enzyme-catalysed Reactions* (Academic Press, Orlando, 1984)). A complete listing of the more recent IUPAC – IUB bulletins can be found in the *European Journal of Biochemistry*, 151: A5–A11 (1985). Abbreviations and contractions of the names of substances, procedures, etc., must be defined the first time they occur. Symbols and unusual and Greek characters should be identified clearly; superscripts and subscripts should be legible and carefully placed, and they should be explained by marginal notes when necessary.

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Editor: Peter B. Moens

6 September 1988

Dr. M. S. Swaminathan
I.U.C.N.
B-4/142 Safdarjung Enclave
New Delhi 110 029
INDIA

Dear Dr. Swaminathan,

Re: Manuscripts for the National Programs and Policies in Genetics symposium (24.7) - 16th International Congress of Genetics

---

Enclosed are two copies of "Development of genetic research in the U.S.S.R." (24.7.~~5~~) by V. K. Shumny. We would like to ask you to write the other ~~four~~ three contributors to your symposium, D. Nasser (24.7.2), S. H. M. Naqvi (24.7.3), ~~E. Paterniani (24.7.4)~~ and Zh. Li (24.7.~~5~~) to ask them for their manuscripts, if they have not already sent them to you. Naturally we look forward to your own paper," Overview and Major Issues" (24.7.1). We are grateful that you have agreed to check (or have your reviewers check) the manuscripts for errors in fact or for serious discrepancies with existing concepts.

Although instructions and a sample article were sent to all invited contributors, we would ask you to check that the papers are submitted in triplicate, and contain an abstract as well as 4-6 key words, and original figures. Please send us all available copies after editing.

We expect that the proceedings of a good number of symposia will be completed and in our hands by 1 October 1988. These will then be forwarded to the National Research Council of Canada for copy editing and typesetting. Proceedings that reach us after that date will be accumulated and published as a second issue of Genome Volume 31. 15 October 1988 is the deadline for receiving manuscripts from the contributors.

Thank you very much for your help in handling these manuscripts. If you require additional information, feel free to call me or my assistant Maria Jacobs collect at (416) 736-5358.

Sincerely,

Peter B. Moens
mj

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GENOME

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I just noticed that Dr. Paterniani has withdrawn.
Sorry.
Maria Jacobs

Department of Biology
York University
4700 Keele Street
Downsview, Ontario Canada
M3J 1P3
(416) 736-5358

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In the reference list:

Kerby, K., and Kuspira, J. 1987. The phylogeny of the polyploid wheats *Triticum aestivum* (bread wheat) and *Triticum turgidum* (macaroni wheat). Genome, 29: 722–737.

In references to papers in periodicals and books, titles and inclusive page numbers are required. Articles "submitted" and "in preparation" may be mentioned as footnotes but should not appear in the references. Papers "in press" may be listed among the references. Authors must give assurances to the Editors that the paper has been accepted for publication. Volume and page numbers can be completed at the galley proof stage. The names of serials are abbreviated in the form given in *CASSI (Chemical Abstracts Service Source Index,* Chemical Abstracts, P. O. Box 3012, Columbus, OH, U.S.A. 43210) or in *Serial Sources for the BIOSIS Data Base* (BioSciences Information Service, Philadelphia, PA, U.S.A. 19103). For serials not given in these guides, the abbreviated name is constructed from the *NCPTWA Word-Abbreviation List*, 1971 edition, American National Standards Institute, Standards Committee Z39, and its supplements. In doubtful cases, authors should write out the name of the serial in full. References to conference proceedings should also be written out in full and should include the complete title, editors' names, location and date of conference, and name and location of publisher.

Footnotes—Footnotes should be designated by superscript arabic numbers in serial order throughout the manuscript except in tables. Each footnote should be placed at the bottom of the manuscript page where reference to it is made.

Equations—These must be set up clearly in type, triple-spaced. They should be identified by numbers in square brackets placed flush with the left margin. In numbering, no distinction is made between mathematical and chemical equations. Routine **structural formulas** can be typeset and need not be submitted as figures for direct reproduction, but they must be clearly depicted.

Tables—Each table should have an arabic number and a brief title and be referred to in the text. Column headings and descriptive matter in tables should be brief. Vertical rules should not be used. A copy of the journal should be consulted to see how tables are set up and where the lines in them are placed. Footnotes in tables should be designated by symbols (*, †, ‡, §, ||, ¶, #) or superscript small italic letters. Descriptive material not designated by a footnote may be placed under a table as a NOTE. Each part of the table (title, headings, stub, body, and footnotes) must be typed double-spaced.

Supplementary material—The National Research Council of Canada maintains a depository in which supplementary material such as extensive tables, detailed calculations, and coloured illustrations may be placed. Authors wishing to use it should submit their complete work and mark the part to be considered for deposition. The editors may require that portions of some papers be placed in the depository. When material is deposited, this is indicated by a footnote to an appropriate part of the paper. Copies of material in the depository may be purchased from Depository of Unpublished Data, CISTI, National Research Council of Canada, Ottawa, Canada K1A 0S2.

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Revised manuscripts—When submitting a revised manuscript, authors should follow all of the instructions outlined above.

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General—Each figure, or group of them, should be planned to fit into the area of either one or two columns of text. The maximum finished size of a one-column illustration is 8.8 × 24.0 cm and that of a two-column illustration is 18.3 × 24.0 cm. The figures (including halftones) are numbered consecutively in arabic numerals, and each one must be referred to in the text but should be self-explanatory. All terms, abbreviations, and symbols must correspond with those in the text. Only essential labelling should be used, with detailed information given in the caption. Each illustration should be identified by the figure number and the author's names, preferably written below the illustration at the left. Do not fold illustrations for mailing.

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First Class Première classe

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Dept. of Biology
York University
North York ON
Canada M3J 1P3

13 July 1988

Dr. Ken J. Kasha
Program Chairman
XVI International Congress of Genetics
Crop Science Department
University of Guelph
Guelph
Ontario
Canada N1G 2W1

I enclose copies of letters I have written to Prof. Orodowaldo Pavan and Dr. Graham Strachan.

I plan to reach Toronto by flight UA 460 at 1616 hrs. on Friday 19 August 1988. I enclose an invoice relating to my ticket New Delhi-Toronto-New Delhi. I shall be very grateful if this amount would be reimbursed to me in Toronto by a cheque.

With all the trouble you and your colleagues have taken we should have an outstanding Congress.

With warm regards

Yours sincerely

M.S. SWAMINATHAN

13 July 1988

Prof. Crodowaldo Pavan
President
Brazilian National Research Council
P.O. Box 11-1142
70740 Brasilia, DF
Brazil

Dear Prof. Pavan

I am very happy to learn from Prof. Ernesto Paterniani that you will be willing to speak in his place at the Symposium on 'National Policies in Genetics' on August 27th at Toronto. I am requesting Dr. Ken J. Kasha, Chairman to send you further information. Your contribution on 'National Policies in Genetics' in Latin American countries will make an important part of this closing Symposium. Please convey my regards to Prof. Ernesto Paterniani.

With regards

Yours sincerely

M.S. SWAMINATHAN

Copy : Dr. Ken J. Kasha

Genome Génome

5 August 1988

REMINDER

Dear Dr. Swaminathan,

This is to remind you that the proceedings of the XVIth International Congress of Genetics will be published in Genome, and that you have been requested to bring your manuscript to the meeting.

In most cases, the chairman or co-chairman of the symposium will collect the manuscripts. If there is any uncertainty you can check in at the editorial room at the Convention Centre, room 203A.

You can reach me, or the editorial assistant Maria Jacobs, at (516) 736-5358.

Yours sincerely,

Peter B. Moens
hmj

Peter B. Moens
Editor, Genome

Department of Biology
York University
4700 Keele Street
Downsview, Ontario Canada
M3J 1P3
(416) 736-5358

Genome Génome

24.7
Theatre
27/8 9:00

MEMO TO: Symposium Chairmen M.S. Swaminathan

FROM: Maria Jacobs, Assistant to Editor Peter Moens, GENOME

DATE: 21 August 1988

RE: Manuscripts

If you would be kind enough to come by the Editorial Room (203A) any time after your symposium, I would be glad to register the manuscripts you have collected from the contributors and fill out a checklist for each.

I can then provide you with the necessary instructions and stationery for handling the papers and furnish you with forms for manuscripts that may be sent to you later.

MS for 24.7.6 by Shumway already in Room 203A

Department of Biology
York University
4700 Keele Street
Downsview, Ontario Canada
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(416) 736-5358

SATURDAY, AUGUST 27 (Morning) | SYMPOSIA 09:00-11:30 | LE SAMEDI 27 AOÛT (Matinée)

Molecular biology of natural selection | 23.5 Room 105 salle | **Biologie moléculaire de la sélection naturelle**

Chaired by: D.L. Hartl, USA; T. Mutangadura, Zimbabwe — présidé par

23.5.1 SELECTION AND BACTERIAL OPERONS, **B.G. Hall**, *University of Connecticut, Storrs, CT, U.S.A.*

23.5.2 MOLECULAR BIOLOGY OF ENZYME ADAPTATIONS IN HIGHER EUKARYOTES, **D. Hickey**, B. Benkel, C. Magoulas, *University of Ottawa, ON, Canada*

23.5.3 TRANSPOSABLE ELEMENTS AND FITNESS IN *Drosophila melanogaster*, **T.F.C. Mackay**, *North Carolina State University, Raleigh, NC, U.S.A.*

23.5.4 NATURAL SELECTION AND RIBOSOMAL DNA IN *Drosophila*, **A.R. Templeton**, *Washington University, St. Louis, MO, U.S.A.*

National programs and policies in genetics | 24.7 Theatre | **Politiques et programmes nationaux en génétique**

Chaired by: J. Evans, Canada; M.S. Swaminathan, India — présidé par

24.7.1 OVERVIEW AND MAJOR ISSUES, **M.S. Swaminathan**, *I.U.C.N., New Delhi, India*

24.7.2 **D. Nasser**, *National Science Foundation, Washington, DC, U.S.A.*

~~24.7.3 S.H.M. Naqvi, *Nuclear Institute for Agriculture and Biology, Faizalabad, Pakistan*~~

~~24.7.4 E. Paterniani, *Escola Superior Agricultura, São Paulo, Brazil*~~

Prof. Pavan

24.7.5 DEVELOPMENT OF GENETIC RESEARCHES IN SYSTEM OF ACADEMIA SINICA AS EFFECT OF APPLICATION OF STATE POLICIES IN GENETICS, **Zh. Li**, *Academia Sinica, Beijing, China*

24.7.6 DEVELOPMENT OF GENETIC RESEARCH IN THE U.S.S.R., **V.K. Shumny**, *U.S.S.R. Academy of Sciences, Novosibirsk, U.S.S.R.*

Prof. Crodowaldo Pavan, President of the Brazilian National Research Council.

Impact of Economic Policy on the Development of Genetics in China

Li zhensheng*

The Chinese Academy of Sciences

52 San Li He Road

Beijing, China

Tel.8011305

*Secretary General, Genetics Society of China

Vice President of the Chinese Academy of Sciences

Impact of Economic Policy on the Development sof Genetics in China

Li Zhensheng
(The Chinese Academy of Sciences)

Great progress in genetics has been achieved in China in the last 40 years. However, this branch of science had witnessed twists and turns during its development. In the early 50s, affected by an international ideological trend and national political factors, there existed once a tendency of advocating one theory and negating another, and discussions on some divergent academic problems were improperly interfered. This hindered the development of genetics in China. In 1956, the central government put forward the policy of "letting a hundred flowers blossom and a hundred schools of thought contend" which aims at promoting the progress of arts and sciences. Later in the same year, a genetic conference was held in Qingdao cosponsored by the Chinese Academy of Sciences (CAS) and Ministry of Higher Education, this conference created a better environment for the development of genetics. In the following ten years, the number of personnel for genetic research and teaching, laboratory equipments and funds were rapidly increased. For example, there were established two genetic institutes in China, one in Beijing, the Institute of Genetics, and the other, the Genetic Institute of Fudan University in Shanghai. They started or continued carrying on research in the area of microbial genetics, plant genetics, animal genetics and human genetics. Meanwhile in Fudan and other universities, a great number of students (including MS and Ph. D students) in genetics were trained. Thus a good foundation was laid for the progress of genetics. Unfortunately, the work of genetics, same as in other fields, was disturbed again during the ten years of "cultural revolution". In 1978, the central government set forth the general principles for the development of national economy. Since then genetics has stepped on to a new road for its development.

China's reform has succeeded first in the countryside, which has brought into full play the initiative of the farmers for production and greatly

promoted the development of agriculture. Taking food production as an example, as farmers' investment increased, soil fertility, irrigation system and other conditions have been improved. Thus more and better crop varieties are demanded. Under this new situation, the Chinese geneticists and plant breeders have developed a great number of new and improved crop varieties, which have played a significant role in raising the country's food production. For example, Yuan Longping's laboratory of Hunan Academy of Agricufltural Sciences developed rice male sterile line and hybrid rice by crossing rice with barnyard grass. Dozens of superior cross combinations have been made in the whole country. The cultivated area of hybrid rice has reached more than 10 million hectares, and more than 10 million tons of rice are being increased every year. Li Zhensheng's laboratory of Northwest Institute of Botany has developed a number of superior wheat varieties by transferring the genes resistant to disease and dry-hot-wind from Agropyron elongatum into common wheat. The cultivation area of the variety, "Xiao Yan 6", alone has amounted to over 3 million hectares, which has resulted in a yield increase of 1.5 million tons. In recent years, the studies on haploid breeding through anther culture are being extensively carried out in many research institutions in China, such as laboratories of Hu Han and Chen Ying (Institute of Genetics, CAS), Li Meifang (Chinese Academy of Agricultural Sciences) and Hu Daofen (Beijing Agricultural Academy). A number of new crop varieties, such as "Jing Hua 1" of wheat and "Zhong Hua 8 and 9" of rice, have been developed by this method and used in commercial production. Besides, about 160 varieties of different crops have been obtained using radiation breeding method. Octoploid triticale developed by Bao Wenkui's laboratory of the Chinese Academy of Agricultural Sciences was planted on a large scale in the mountain area of Guizhou Province. In recent years, Li Dianrong, a plant breeder in Huaxian Agricultural Experimental Station, obtained sterile line, maintainer line and restoring line of rapeseed; the hybrids were widely grown in the Central Shaanxi Plain. At the same time, a great number of improved crop varieties, about 3000, have been developed by conventional breeding and used in production. Much work has been done also in economic plants. For example, Chen

Zhenghua's laboratory of the Institute of Genetics, CAS has obtained an improved strain of rubber tree by anther culture method, its dry rubber content was 29.4% higher than that of the original cultivar. Using the same breeding technique, the scientists in the Chinese Academy of Agricultural Sciences have developed several improved tobacco varieties which have been widely used in production. These results have shown that the genetic theories and new breeding techniques have contributed much to agricultural production, and they are receiving increasing attention and support from the government and farmers.

In recent years, a number of new genetic laboratories have been set up in some research institutes and universities, and the already established research units have been reinforced with personnel and equipments. Guided by the government's open policy, many of the laboratories have set up close ties and established cooperative relationship with foreign partners. Meanwhile, the Genetics Society of China, initiated by C.C.Tan, has organized nationwide professional activities and academic exchanges, all of these has greatly promoted genetic research and led to a great number of new research results.

Some of the results obtained recently are creative in various fields of genetics. The regeneration of protoplasts of rice, soybean and corn has achieved success respectively in the Institute of Genetics,Institute of Plant Physiology and Institute of Botany, CAS. A Hubei photo-period sensitive genic male sterile rice line (HPGMR) has been discovered in Hubei Province and Wuhan University, which has brought the utilization of rice heterosis to a new era. A kind of virus-like particles, which contain dsRNA was first discovered in this HPGMR line in Wang Bin's laboratory of Institute of Genetics, CAS. Two plasmid-like mtDNAs associated with cytoplasmic male sterility of rice were found also in this laboratory. The blue grained monosomic system of wheat, a new breeding material easy for gene localization and chromosome engineering, has been developed in Northwest Institute of Botany (Li Zhensheng, Mu Shumei et al.), and it has been partly used in practical breeding. The studies on gene engineering in plants have achieved

impressive successes in China. For example, Mang Keqiang's laboratory of the Institute of Microbiology, CAS has cloned a full-length cDNA of TMV and transferred the TMV coat protein gene into tobacco plant by Ti-mediated transformation with tobacco leaf discs; Tian Bo's laboratory of the same institute has introduced the cDNA of satellite RNA from CMV infected plant into tobacco and obtained transgenic plants with resistance to the virus infection; an atrazine resistant gene from Solanum nigrum has been cloned and transferred into tobacco plant in Zhu Lihuang's laboratory of the Institute of Genetics, CAS. and the transgenic plant was shown to be herbicide resistant; the work on expression of human interferon gene in tobacco plant has achieved success in Li Xianghui's laboratory of the Institute of Genetics, CAS and a salt-tolerant gene has been isolated from microbes in Chen Shouyi's laboratory of the Institute of Biophysics, CAS. Work on hepatitis B vaccine has been done in the laboratories of Li Zaiping and Ren Guifang, and the research on piglet diarrhea vaccine has been carried out in the laboratories of Hong Mengmin, Fan Yuliu and Huang Cuifen. Both work has led to industrial production.

In medical genetics, the Chinese scientists have discovered 180 kinds of chromosome aberrations that had not been reported in the world and since 1979 the genetic patterns of over 20 types of eye diseases have been found out based on a survey of 700000 people. Scientists in the Institute of Basic Medicine, Chinese Academy of Medical Sciences have discovered the - thalassanemia gene in the Chinese population for the first time. In Recent years, antenatal diagnosis has been developed rapidly in China and the examination of chorionic villi in early pregnancy is being commonly carried out. In gene diagnosis, several new techniques are being used, such as DNA restriction fragment mapping, restriction fragment linkage analysis, and oligonucleotide probes. Certain genetic diseases, such as hemophilia and phenylketonuria, can be diagnozed before birth in some hospitals. Using the techniques of somatic cell genetics, a cloning plate of man and rat hybrid cell has been established in Fudan University. Much work has been done on investigation of gene frequency among isolated groups of Chinese populations. The studies on gene localization have also achieved substantial improvements.

In the area of basic research, Tong Kezhong's laboratories of the Institute of Genetics, CAS has found that ribosomal proteins have different translational specificities to mRNAs.

Looking forward to the future, the development of agricultural production and population control will still be two long-standing problems in China, which need to be solved with great efforts. Considering these facts, the Chinese geneticists and breeders should, and must work hard to promote the constant increase of national economy. As for basic research of genetics, it will be conducted in the national and key laboratories in CAS and unviersities supported by the government, and some other research units supported by science foundations. These laboratories will also carry out the open policy and further strengthen international cooperation and exchange in order to achieve faster and greater progresses.

21 July 1988

My dear Dr. Paterniani,

I thank you very much for your kind letter. I am sorry you will not be able to come to Toronto. I am, however, grateful to you for arranging for the participation of Prof. Pavan in the symposium.

I hope you had a useful visit to India. Please let me know when you come to New Delhi next.

With warm regards,

Yours sincerely,

M.S. SWAMINATHAN

Dr. Ernesto Paterniani
Universidade De Sao Paulo
Escola Superior De Agricultura
"Luiz De Queiroz",
Institututó De Genetica,
Calza Postal 83
13,400-Piracicaba,
S.Paulo - BRASIL.

The International Rice Research Institute

Memorandum

To: Radioroom
From: Vicky
Subject:

Date: 12 July 88

(13)

GHILDYAL
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FOR MSS PLS:LTR RECVD TODAY FROM ERNESTO PATERNIANI WHO IS UNABLE TO ATTEND TORONTO GENETICS CONGRESS INSPITE OF FUNDING. SUGGESTING INSTEAD PROF. CRODOWALDO PAVAN, PRESIDENT OF BRAZILIAN NATIONAL RESEARCH COUNCIL WHO CAN SPEAK ON NATIONAL POLICIES IN GENETICS IN LATIN AMERICAN COUNTRIES WITHOUT PREVIOUS TIME FOR PREPARATION. HIS ADDRESS: P.O. BOX 11-1142, 70740 BRASILIA, DF, BRAZIL TLX 061-1089. POSTING HIS LTR TO YOU. REGARDS

VICKY

UNIVERSIDADE DE SÃO PAULO
ESCOLA SUPERIOR DE AGRICULTURA "LUIZ DE QUEIROZ"
INSTITUTO DE GENÉTICA

Caixa Postal 83
13.400 - PIRACICABA
S. PAULO - BRASIL

mhr

Dr. M.S. SWAMINATHAN

Dear Dr. Swaminathan:

I regret to inform you that I will not be able to participate at the Internationl Congress of Genetics in Toronto. Just recently, I received a communication from Dr. D.B. Walden, with the registration form, informing about the need for me to provide finance for travel and acommodation. I received this letter just one day before my departure to India for a TAC meeting. So, I rushed a letter asking to widraw my name from the program. On my return from India I received a telex informing that 2000 CDN Dollars would be available. Unfortunately by now I have no possibility to attend the Congress.

I should have sent to you copies of the mentioned communications, but, I do not have your present address. Also I was in a hurry. I am sorry for the inconvenience although involuntary I am causing to you. But I would like to express my deepest appreciation to you, which was the reason I decided to accept the task.

Now if you allow me, I would like to make a suggestion. I see that one of the Honorary Vice-Presidents is Prof. Crodowaldo Pavan. He is a distinguished Brazilian Geneticist at present/ President of the Brzilian National Research Council. I am sure he would be able to make a good presentation of the topic: "National Policies in Genetics in Latin American Countries", without the need of any previous time for preparation.

His address is the following Prof. Crodoaldo Pavan.

P.O. Box 11-1142
70740 Brasília, DF. Brazil
Telex: (061) 1089

With best wishes, I remain

Sincerely yours,

Ernesto Paterniani

27 February 1988

Academician V. Ye. Sokolov

Dear Academician Sokolov,

I am very grateful to you for your letter of January 27th. I am glad that Corresponding Member of the USSR Academy of Sciences, V.K. Shumniy, will be able to speak on "The National Policies in Genetics in The Soviet Union". I am conveying this information to Dr. K.J. Kasha, Chairman of the Programme Committee. I am most grateful to you for all trouble you have taken in this matter.

With warm personal regards,

Yours sincerely,

M.S. SWAMINATHAN

cc : Dr. K.J. Kasha

АКАДЕМИЯ НАУК СССР
ОТДЕЛЕНИЕ ОБЩЕЙ БИОЛОГИИ

117901, ГСП, Москва, В-71
Ленинский просп., 14
Тел. 232-50-07

Prof. M.S.Swaminatham,
Director General
International Rice Research Instit.

P.O. Box 933
Manila, Philippines

I9 January №1988

На №

JAN 27 1988

Dear Dr. Swaminathan,

Your invitation to participate in the 16-th International Congress of Genetics (Canada, August 1988) is mach appreciated.

On behalf of academician V.A. Strunnikov and myself may I inform you that the report "The National Policies in Genetics in The Soviet Union" will be delivered by corresponding member of the USSR Ac. Sci. V.K. Shumniy.

With best wishes.

Yours sincerely,

V. Sokolov

Academician V.Ye. Sokolov

pavan

IRRI LIAISON OFFICE
NEW DELHI
12 JUL 1988
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GHILDYAL

FOR MSS. LTR RECD TODAY FROM ERNESTO PATERNIANI WHO IS UNABLE TO ATTEND TORONTO GENETICS CONGRESS INSPITE OF FUNDING. SUGGESTING INSTEAD PROF. CRODOWALDO PAVAN, PRESIDENT OF BRAZILIAN NATIONAL RESEARCH COUNCIL WHO CAN SPEAK ON NATIONAL POLICIES IN GENETICS IN LATIN AMERICAN COUNTRIES WITHOUT PREVIOUS TIME FOR PREPARATION. HIS ADDRESS: P.O. BOX 11-1142, 70740 BRASILIA, DF, BRAZIL, TLX 061-1089. POSTING HIS LTR TO YOU. REGARDS.

VICKY

REPLY TO U.S. TELEX NO. 4900009251(4900009251 IRR UI)

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REPLY VIA WORLDCOM
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WIN TRIP TO SEOUL OLYMPICS 88 TLX USA 472222+ CODE 2020

19 October 1988

My dear Prof. Li Zhensheng,

I am extremely grateful to you for your letter of Sept. 19, 1988. enclosing two copies of your paper on "Impact of Economic Policy on the Development of Genetics in China". I am forwarding it to the Editor of the Journal.

It was a real pleasure meeting you at Toronto and Mexico. I thank you for all yoour kindness and active collaboration in promoting the cause of Genetics in developing countries.

With warm personal regards,

Yours sincerely,

(M.S. SWAMINATHAN)

Prof. Li Zhensheng, Vice-President, Chinese Academy of Sciences,
52 Sanlihe Road,
100864 Beijing,
CHINA.

(4)

中国科学院

CHINESE ACADEMY OF SCIENCES

Dr. M. S. Swaminathan
President
International Union for the Conservation of Nature
B4/142 Safdarjang Enclave
New Delhi 110029
India
N.A.
679069

September 29 1988

Dear Professor Swaminathan.

Thank you very much for your inviting me to attend the 16th International Congress of Genetics and arranging me to deliver the lecture on the symposium. Two copies of my manuscripts are enclosed, would you be kind enough to check and approve them for me_

I hope to keep the close contact with you in the future.

With best regards.

Yours Sincerely

Li Zhensheng

Li Zhensheng

52 SANLIHE ROAD
100864 BEIJING, CHINA
CABLE ADDRESS: SINICADEMY

TELEPHONE: 868361
TELEX: 22474 ASCHI CN
TELEFAX: 8011095

Reply to : B-4/142 Safdarjung Enclave
New Delhi 110029

27 February 1988

Dr. Ken J. Kasha
Professor and Director
Plant Biotechnology Centre
Guelph-Waterloo Biotech
University of Guelph
Guelph, Ontario
Canada N1G 2W1

My dear Dr. Kasha,

I am writing this to inform you the present position concerning the speakers at the Symposium at National Programmes and Policies in Genetics.

1.

1.	Overview and Major Issues	:	Dr. M.S. Swaminathan
2.	National Programmes and Policies in Genetics in North America	:	Dr. ~~John Evans~~ Grahar Strachan
3.	National Programmes and Policies in Genetics in Pakistan	:	Dr. S.H. Mujtaba Naqvi
4.	National Policies in Genetics in the Soviet Union	:	Professor V.K. Shumniy Corresponding Member of the USSR Academy of Sciences
5.	National Policies in Genetics in Latin America	:	~~Dr. Ernesto Paterniani~~ Prof. Godhalda Pawar.
6.	National Policies in Genetics in China	:	Professor Li Shenzheng

All the speakers have confirmed except Dr. John Evans. I shall be very grateful if you will be kind enough to talk to Dr. Evans on the phone and fix up the details of his presentation.

I enclose the full names and addresses of all the speakers. Kindly send them directly information on the travel and other support which you may be able to give them so that they can start arranging for the travel to Toronto.

With warm regards,

Yours sincerely,

M.S. SWAMINATHAN

- Dr. M.S. Swaminathan
  President
  IUCN
  B-4/142 Safdarjung Enclave
  New Delhi 110029
  India

- ~~Dr. John Evans~~
  ~~Chairman and Executive Officer~~
  Allelix, Inc.
  Toronto, Canada

Dr. Graham Strachan
Vice-President, Allelix

- Dr. S.H. Mujtaba Naqvi
  Director
  Nuclear Institute for Agriculture
  and Biology
  P.O. Box 128, Faisalabad
  Pakistan

- Professor V.K. Shumniy
  Corresponding Member of the
  USSR Academy of Sciences

- Dr. Ernesto Paterniani
  Member, Brazilian Academy of Sciences
  Escola Superior Agricultura
  Piracicaba, Sao Paulo
  Brazil

Prof. Crodoaldo Pavan,
P.O. Box 11-1142
70740 Brasilia
DF - Brazil

- Professor Li Shenzheng
  Vice President
  Academia Sinica
  Director, Genetic Research Institute
  Beijing, China

13 July 1988

Dr. Graham Strachan
Vice President & Commercial Director
ALLELIX
6850 Goreway Drive
Mississauga
Ontario
Canada L4V 1P1

Dear Dr. Strachan

Dr. Gurdev S. Khush has sent me a copy of his letter of July 7 addressed to you. I am glad you will be participating in the closing Symposium at the Genetics Congress. I plan to reach Toronto by UA 460 on 19 August. I shall then look forward to meet you.

With warm regards

Yours sincerely

M.S. SWAMINATHAN

Copy : Dr. Ken J. Kasha

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FAX: 63-2-8178470

July 7, 1988

Dear Dr. Strachan:

This is in response to your letter of June 21, 1988 to Dr. Lampe, our Director General. There seems to be some confusion regarding the invitations to you to present papers on "Genetics and Government Policies in North America".

Dr. M. S. Swaminathan, our former Director General, wrote to Dr. John Evans on December 1987, to present a paper on the said topic at the Symposium on "National Programs and Policies in Genetics" on the forenoon of Saturday, 27 August at Toronto. This is the concluding Symposium of the 16th International Congress of Genetics. Dr. Evans responded to this invitation on February 4, 1988, and informed Dr. Swaminathan that he will not be able to present the paper because of a family wedding on August 27 but suggested that you would deliver a lecture in his place. As far as I know, that symposium will be held on August 27 as planned and the invitation to you stands. However, please write to Dr. Swaminathan, confirming your willingness to give the lecture, if you have not done so already. Dr. Swaminathan's address is as follows:

B-4/142 Safdarjung Enclave
New Delhi 110029
India

The second symposium on "Genetic Manipulation in Crops" is to be held at CIMMYT, Mexico on 29-31 August, 1988 and Dr. Lampe invited you to present a paper on the same topic at this symposium. We are sorry to learn you will be unable to attend this symposium. However, I hope you will be attending the symposium on August 27, 1988.

Best regards.

Sincerely yours,

Gurdev S. Khush
Principal Plant Breeder and Head,
Plant Breeding Dept.

Dr. Graham Strachan
Vice President and Commercial Director
Allelix, Inc.
6850 Goreway Drive
Mississauga, Ontario L4V 1P1
CANADA

cc: Dr. K. J. Lampe, Dr. M.S.Swaminathan, Dr. L. A. Sitch

GSK/lls

graham cc: LAS

Allelix INC

CANADA AWARDS FOR EXCELLENCE 1986

FRANKLIN INSTITUTE

June 21, 1988 LAS

JUL 01 1988

Dr. K.J. Lampe
Organizing Committee
Director General-IRRI
International Rice Research Institute
P.O. Box 933
Manila, Philippines

Dear Dr. Lampe:

I regret that I will be unable to participate in the Second International Symposium on Genetic Manipulation in Crops to be held in Mexico on August 29-31. In accepting the invitation from Dr. Swaminathan to participate (as a substitute for Dr. Evans), I understood the meeting was in Toronto (see attached).

I only now realize the changed location and there is unfortunately a conflict since I am already committed to participate in the Toronto meeting. My apologies. I hope your meeting is successful.

Yours truly,

Graham Strachan /ws.

Graham Strachan
Vice President & Commercial Director

GS/ws

Encl.

6850 Goreway Drive, Mississauga, Ontario, Canada L4V 1P1
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16 April 1988

Dr. Graham Strachan
Vice President & Commercial Director
Allelix, Inc.
6850 Goreway Drive
Mississauga, Ontario L4V 1P1
CANADA

Dear Dr. Strachan,

We are pleased to invite you to attend the Second International Symposium on Genetic Manipulation in Crops to be held in CIMMYT, Mexico on 29-31 August 1988 and to present your paper entitled "Genetics and Government Policies in North America".

Unfortunately our funds are very restricted and we cannot offer you any financial assistance. Nevertheless, we do hope that you will find the necessary funds to enable you to attend. If this is impossible, please contact Dr. L. A. Sitch and she will look into the possibility of providing funds.

You will be receiving additional information and forms very soon.

We are looking forward to seeing you in Mexico.

Yours sincerely,

K. J. LAMPE
Organizing Committee
Director General-IRRI

Encl: Notes to authors.

4 April 1988

Dr. Ken J. Kasha
Program Chairman
XVI International Congress of Genetics
Crop Science Department
University of Guelph
Guelph, Ontario
Canada N1G 2W1

My dear Dr. Kasha,

I am informed by Prof. Shao Qiquan that he will be delivering the lecture in the place of Prof. Li Zhensheng. The address of Prof. Shao Qiquan is - Professor of Genetics, Institute of Genetics, Academia Sinica, Beijing, China. I shall be grateful if you could write to him about the travel and other arrangements. He will be speaking on 'Programs and policies in genetics in China'.

I have not yet heard from Dr. Evans. Please let me know the position. Also, please let me know whether you would like me to purchase my ticket here and seek reimbursement or you will arrange to send the PTA.

With warm regards,

Sincerely yours,

M.S. SWAMINATHAN

4 April 1988

Dr. Shao Qiquan
Professor of Genetics
Institute of Genetics
Academia Sinica
Beijing
China

My dear

I thank you very much for your letter of March 22. I am informing Dr. Ken J. Kasha of the University of Guelph, who is the Chairman of the Program Committee for the XVI International Congress of Genetics that you will be presenting the paper in the place of Prof. Li Zhensheng. You will get an official invitation from Dr. Kasha directly who will also inform you about your travel arrangements. You can also write to him directly at the following address:

Dr. Ken J. Kasha
Program Chairman
XVI International Congress of Genetics
Crop Science Department
University of Guelph
Guelph, Ontario
Canada N1G 2W1

As regards travel support for Dr. Hu Han, I shall explore the possibility of getting him support from the funds available for the Genetic Manipulation Symposium in Mexico.

With warm personal regards,

Sincerely yours,

M.S. SWAMINATHAN

23 May 1988

Dr. Peter B. Moens
Editor, Genome
Department of Biology
York University
4700 Keele Street
Downsview, Ontario Canada
M3J 1P3

Dear Dr. Moens,

I thank you very much for your letter of 25 April concerning the publication of the Proceedings of the 16th International Congress of Genetics. I shall be happy to serve as special editor for the Symposium I am organizing at the Congress.

With warm regards,

Yours sincerely,

M.S. SWAMINATHAN

Genome Génome

FAX:
416-736-5386

TELEX:
065-24736
York U

25 April 1988

Dear Dr. Swaminathan,

Genome will publish the symposium proceedings of the 16th International Congress of Genetics. The proceedings will appear in two or three issues of a separate volume especially dedicated to the Congress.

Contributors to the symposia are requested to bring their manuscripts to the Congress. In most cases the symposium chairman or co-chairman has agreed to act as special editor for Genome and is in charge of his or her symposium proceedings. In your case the special editor is ~~Dr.~~ yourself and you are asked to submit the manuscript directly to this person.

The special editor will have the contributions reviewed to insure against major oversights, inaccuracies, or errors of style or syntax. If such problems are detected, the author can correct them before the final submission to Genome. The order in which the symposia are published will depend on the completion of manuscript editing.

A copy of the normal format for Genome articles, as well as a copy of Instructions to the Authors, are included for your convenience. Some contributions may be more in the nature of a review and need not follow the standard format.

For additional information, feel free to contact the Editor of Genome, Peter Moens, or the Assistant to the Editor, Maria Jacobs, at the address or telephone number below.

Yours sincerely,

Peter Moens.

Peter B. Moens
Editor, Genome

Enclosures

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(416) 736-5358

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THE MANUSCRIPT

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Abstract—An abstract of not more than 200 words, typed on a separate page, is required for each article or note. **No abbreviations should appear in the abstract.** Authors who can submit abstracts in both fluent English and fluent French are encouraged to do so. **Key words** should be typed below the abstract.

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In the reference list:

Kerby, K., and Kuspira, J. 1987. The phylogeny of the polyploid wheats *Triticum aestivum* (bread wheat) and *Triticum turgidum* (macaroni wheat). Genome, 29: 722–737.

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Ascospore abortion in crosses of *Cochliobolus heterostrophus* heterozygous for the virulence locus *Tox1*[1]

CHARLOTTE R. BRONSON
Department of Plant Pathology, Iowa State University, Ames, IA, U.S.A. 50011

Corresponding Editor: A. J. F. Griffiths

Received December 22, 1986

Accepted September 9, 1987

BRONSON, C. R. 1988. Ascospore abortion in crosses of *Cochliobolus heterostrophus* heterozygous for the virulence locus *Tox1*. Genome, **30**: 12–18.

Crosses heterozygous for the virulence locus *Tox1* show a high frequency of nonrandom ascospore abortion, in addition to a high frequency of random abortion seen in homozygous crosses. In crosses among closely related laboratory strains, the frequency of asci with eight mature, viable spores dropped from 35–47% of asci with mature spores in crosses homozygous for *Tox1* to 3–17% in heterozygous crosses. Segregation for alternate alleles of *Tox1* was 2:2 in 98% of asci with four viable spores. Patterns of abortion in crosses involving field isolates were similar to the patterns in crosses among laboratory strains. No recombinants between *Tox1* and the abortion-inducing factor were detected among 112 progeny of laboratory strains. The results suggest that race T (*TOX1*) and race O (*tox1*) strains of *C. heterostrophus* differ by a chromosome rearrangement, possibly a reciprocal translocation, with a breakpoint at or near *Tox1*.

Key words: fertility, T-toxin, *Cochliobolus heterostrophus*, *Helminthosporium maydis*, *Bipolaris maydis*, *Drechslera maydis*, chromosome rearrangement, reciprocal translocation.

BRONSON, C. R. 1988. Ascospore abortion in crosses of *Cochliobolus heterostrophus* heterozygous for the virulence locus *Tox1*. Genome, **30** : 12–18.

Face à la virulence du locus *Tox1*, les croisements hétérozygotes montrent une fréquence élevée d'avortements non-casualisés des ascospores, alors que les croisements homozygotes montrent une fréquence élevée d'avortements casualisés. Chez les croisements entre souches de laboratoire étroitement reliées, la fréquence des asques possédant huit spores matures viables a chuté de 35–47% chez les croisements homozygotes pour le locus *Tox1* à 3–17% chez les croisements hétérozygotes. La ségrégation pour les allèles alternants du locus *Tox1* fut de 2:2 chez 98% des asques ayant quatre spores viables. Les modes d'avortement chez les croisements impliquant des isolats des champs ont été semblables à ceux des croisements entre souches de laboratoire. Aucun recombinant entre le locus *Tox1* et le facteur inducteur d'avortements n'a été décelé chez 112 progénitures des souches de laboratoire. Ces résultats suggèrent que les souches de race T (*TOX1*) et de race O (*tox1*) de *C. heterostrophus* diffèrent par un réarrangement des chromosomes, possiblement une translocation réciproque, avec un bris au niveau du locus *Tox1* ou près de celui-ci.

Mots clés : fertilité, toxine T, *Cochliobolus heterostrophus*, *Helminthosporium maydis*, *Bipolaris maydis*, *Drechslera maydis*, réarrangement des chromosomes, translocation réciproque.

[Traduit par la revue]

Introduction

Cochliobolus heterostrophus (Drechsler) Drechsler is a filamentous ascomycete that causes southern leaf blight of maize (anamorph *Bipolaris maydis* (Nisikado & Miyake) Shoemaker = *Helminthosporium maydis* Nisikado & Miyake = *Drechslera maydis* (Nisikado & Miyake) Subramanian & Jain) (Alcorn 1983). Two subpopulations (races) have been defined by their ability to cause disease on maize with Texas male-sterile (T) cytoplasm. These races differ in their ability to produce a family of linear polyketols collectively known as T-toxin (Daly 1982). Race T, which produces T-toxin, causes long, spindle-shaped lesions on T-cytoplasm maize. Smaller, parallel-sided lesions are produced on maize with other cytoplasms. Race O, which does not produce T-toxin, lacks the high specific virulence for T-cytoplasm and produces small lesions on all maize genotypes (Hooker 1972). Genetic and physiologic studies have shown that T-toxin is responsible for the high specific virulence of race T on T-cytoplasm maize (Yoder 1980). To date, a single locus with two alleles has been demonstrated to control T-toxin production (Leach *et al.* 1982*b*; M. Taga, C. R. Bronson, and O. C. Yoder, unpublished data). The dominant allele *TOX1* specifies T-toxin production; *tox1* specifies the inability to make T-toxin.

The genetic analysis of T-toxin production, as well as of other traits, has been hampered by low sexual fertility. Most crosses involving field isolates and many crosses among laboratory strains yield few or no asci containing all the products of meiosis. Yoder and Gracen (1975) and Yoder (1976) reported that only a few crosses among field isolates produced any complete tetrads and that most produced no asci with more than four mature spores. *Cochliobolus* undergoes a postmeiotic mitosis prior to ascospore delimitation; thus, the expected number of ascospores is eight (Guzman *et al.* 1982). In an effort to overcome these problems, a set of closely related laboratory strains (C-strains) was bred for improved fertility (Leach *et al.* 1982*a*).

Reports of fertility in these C-strains have varied. Leach *et al.* (1982*a*) estimated that crosses among the strains produced 40–50% asci with seven or eight mature spores. Guzman *et al.* (1982) reported approximately 80% asci with eight mature spores (eight-spored asci). Taga *et al.* (1985), using strains from the same set and similar crossing procedures, obtained only 5–6% eight-spored asci. Nearly all of the asci in their crosses (87%) had four or fewer fully developed, viable spores. The deficiency of mature spores was nonrandom. Among asci with four mature spores (four-spored asci), 88–93% segregated 2:2 for toxin production. The

[1]Journal paper No. J-12599 of the Iowa Agriculture and Home Economics Experiment Station, Ames, Iowa. Project No. 2632.

markers *MAT1* and *Alb1* (both unlinked to *Tox1* or to each other) segregated 4:0, 2:2, and 0:4 in approximately 1/6, 2/3, and 1/6, respectively, of the four-spored asci. Nearly all (98–100%) of four-spored asci contained two apparent sets of twins based on the markers *Tox1*, *MAT1*, and *Alb1*. These results suggested that meiosis and mitosis were normal, but that there was preferential abortion of nonsister meiotic products and linkage of *Tox1* either to a centromere or to the locus causing abortion. The cause of this loss was not determined, but it was noted that all the crosses were heterozygous for *Tox1*. In contrast, the report of high fertility in laboratory strains (Guzman *et al.* 1982) involved crosses homozygous for T-toxin production (*TOX1* × *TOX1*). The genotypes used by Leach *et al.* (1982*a*) in fertility estimates were not specified.

A similar correlation exists for crosses among field isolates. Asci with seven or eight mature spores were observed only if the crosses were within a race (i.e., race T × race T). The less fertile crosses were all race T × race O (Yoder and Gracen 1975; Yoder 1976).

This study was undertaken to determine whether heterozygosity at the *Tox1* locus is a cause of low fertility in crosses of *C. heterostrophus* and, if so, whether recombinants could be obtained in which the association between *Tox1* and the factor(s) responsible is broken. The results show a high frequency of nonrandom ascospore abortion in crosses heterozygous for *Tox1* in addition to a high frequency of random abortion in homozygous crosses. The pattern of abortion suggests that *TOX1* and *tox1* strains, and, therefore, the race T and race O subpopulations, differ by a chromosome rearrangement, possibly a reciprocal translocation, with a breakpoint at or near *Tox1*. The significance of this finding to our understanding of the evolution of race T and race O is discussed.

Materials and methods

Strains of *C. heterostrophus* used in this study are listed in Table 1. Nomenclature follows the recommendations of Yoder *et al.* (1986). *Tox1* is a locus with two alleles controlling T-toxin synthesis. *TOX1* is a dominant or semidominant allele (Leach *et al.* 1982*b*) specifying production of T-toxin; *tox1* is the recessive allele for inability to make this metabolite. *ALB1* specifies pigmented mycelia and conidia; strains with *alb1* are albino. *Cyh1R* and *Cyh1S* are alternate alleles specifying resistance and sensitivity to cycloheximide, respectively. *MAT1-1* (previously *Mat*A) and *MAT1-2* (previously *Mat*a) are complementary alleles for mating type. The laboratory strains were developed from the C-strains C3 (*tox1 ALB1 Cyh1S MAT1-2*) (Leach *et al.* 1982*a*), C14 (*TOX1 alb1 Cyh1S MAT1-2*), and 380.2.5 (*TOX1 ALB1 Cyh1R MAT1-1*) and are considered representative of C-strain germplasm. The B30 siblings are progeny from a cross of C3 with a single ascospore isolate with the genotype *TOX1 alb1 Cyh1R MAT1-1* selected from a cross of C14 × 380.2.5. The K22 and K38 siblings (Klittich and Bronson 1986) were the progeny of the 5th and 10th generations, respectively, of backcrossing of *TOX1* from 380.2.5 into C3. The field isolates, C3, C14, and 380.2.5 were kindly provided by Dr. O. C. Yoder, Cornell University. Strains were stored in 15% glycerol (v/v of water) at −75°C.

Crosses for fertility estimates were made as described previously (Leach *et al.* 1982*a*) and incubated at 23°C. Asci were examined at 45–70× magnification after 21 days. Random asci were dissected from pseudothecia, spread on the surface of an agar block (complete medium (Leach *et al.* 1982*a*) with 5% agar), and the number of ascospores with rigid walls and distinct septa (mature ascospores) per ascus was determined. Approximately 99% of mature ascospores germinated. For crosses reported in Tables 2 and 3, ascospores were released by teasing the asci with a fine wire needle. Asci of *C. heterostrophus* mature asynchronously (Guzman *et al.* 1982) and at the magnifications used for dissection it was not possible to distinguish barren asci from fertile asci at an early stage of development; therefore, only asci that had at least one mature ascospore were recorded. (Maturation of viable spores within an ascus is synchronous.) For crosses reported in Table 4, ascospores were released by suspending the asci in 5% β-glucuronidase (v/v of water; type H-2S, Sigma Chemical Co., St. Louis, MO); all asci were counted. T-toxin production by ascospore progeny was assessed using a whorl assay (Klittich and Bronson 1986).

Crosses for cytological observations were incubated at 25°C and examined at 2-day intervals between 11 and 21 days after crossing. Pseudothecia were fixed, hydrolyzed, and stained with iron-hematoxylin (Raju and Newmeyer 1977).

TABLE 1. Strains of *C. heterostrophus* used in this study

	Genotype
Laboratory strains	
B30 siblings	
B30.A3.R.1	*TOX1 ALB1 Cyh1S MAT1-1*
B30.A3.R.2	*TOX1 ALB1 Cyh1R MAT1-2*
B30.A3.R.11	*TOX1 alb1 Cyh1S MAT1-2*
B30.A3.R.20	*TOX1 alb1 Cyh1S MAT1-1*
B30.A3.R.65	*TOX1 ALB1 Cyh1S MAT1-2*
B30.A3.R.85	*tox1 ALB1 Cyh1S MAT1-1*
B30.A3.R.87	*tox1 ALB1 Cyh1S MAT1-2*
B30.A3.R.89	*TOX1 ALB1 Cyh1R MAT1-1*
K22 siblings	
K22.R.1	*tox1 ALB1 Cyh1S MAT1-1*
K22.R.14	*TOX1 ALB1 Cyh1S MAT1-2*
K22.R.25	*tox1 ALB1 Cyh1S MAT1-2*
K22.R.30	*TOX1 ALB1 Cyh1S MAT1-1*
K38 siblings	
K38.R.5	*tox1 ALB1 Cyh1S MAT1-1*
K38.R.13	*TOX1 ALB1 Cyh1S MAT1-1*
K38.R.14	*TOX1 ALB1 Cyh1S MAT1-2*
K38.R.16	*tox1 ALB1 Cyh1S MAT1-2*
Field isolates*	
Hm86	*TOX1 ALB1 Cyh1S MAT1-2*
Hm540	*tox1 ALB1 Cyh1S MAT1-1*
Hm813	*tox1 ALB1 Cyh1S MAT1-2*
Mon1	*TOX1 ALB1 Cyh1S MAT1-1*

*Hm86 and Hm540 are isolates from North Carolina. Hm813 and Mon1 are from Japan and Montana, respectively.

Results

The fertility of laboratory strains crossed in all possible combinations with respect to alleles of *Tox1* and mating type is reported in Table 2. Crosses homozygous at the *Tox1* locus were always more fertile than heterozygous crosses. In homozygous crosses, asci with eight mature, viable spores were most common, ranging from 35% to 47% of those asci containing mature spores. There was no detectable difference in spore abortion between crosses homozygous for the *TOX1* allele and crosses homozygous for the *tox1* allele. In heterozygous crosses, the frequency of eight-spored asci dropped to 3–17% of the population and asci with only four mature spores (four-spored asci) predominated (52–73%). Results were similar in three sets of siblings (B30, K22, and K38), representing further levels of inbreeding to increase isogenicity between *TOX1* and *tox1* strains. Crosses homozygous and heterozygous at the *Cyh1* locus and at the *Alb1* locus were also examined to see if these loci were similarly associated with an effect on fertility. No association was found; all crosses had

TABLE 2. Fertility of crosses homozygous and heterozygous for the *Tox1* locus among closely related laboratory strains of *C. heterostrophus*

Parental strains*	Genotype	No. of asci examined	% of asci with indicated no. of mature ascospores†							
			1	2	3	4	5	6	7	8
B30 siblings										
1 × 65	*TOX1*×*TOX1*	51	0	2	6	16	4	22	16	35
85 × 87	*tox1*×*tox1*	66	0	5	5	17	3	20	6	45
1 × 87	*TOX1*×*tox1*	61	0	18	10	52	0	5	2	13
85 × 65	*tox1*×*TOX1*	32	0	6	6	66	0	13	3	6
1 × 65	*Cyh1S*×*Cyh1S*	30	0	3	0	27	3	20	7	40
89 × 2	*Cyh1R*×*Cyh1R*	30	0	3	3	27	0	13	10	43
1 × 2	*Cyh1S*×*Cyh1R*	30	0	3	0	23	0	23	17	33
89 × 65	*Cyh1R*×*Cyh1S*	30	0	0	3	23	7	13	7	47
1 × 65	*ALB1*×*ALB1*	30	0	0	3	13	20	13	17	33
20 × 11	*alb1*×*alb1*	30	0	0	3	20	7	3	27	40
1 × 11	*ALB1*×*alb1*	36	0	0	3	19	6	17	11	44
20 × 65	*alb1*×*ALB1*	30	0	7	0	10	3	17	13	50
K22 siblings										
30 × 14	*TOX1*×*TOX1*	54	0	0	6	7	11	22	15	39
1 × 25	*tox1*×*tox1*	56	0	4	0	13	9	18	13	45
30 × 25	*TOX1*×*tox1*	52	0	8	6	62	0	10	8	8
1 × 14	*tox1*×*TOX1*	53	2	6	13	53	4	9	0	13
K38 siblings										
13 × 14	*TOX1*×*TOX1*	30	0	0	3	20	3	10	17	47
5 × 16	*tox1*×*tox1*	30	0	0	3	27	7	10	13	40
13 × 16	*TOX1*×*tox1*	30	0	13	3	63	3	0	0	17
5 × 14	*tox1*×*TOX1*	30	0	13	0	73	0	3	7	3

*For simplicity, strains in each set of siblings are identified only by their random-spore number. For example, B30 sibling 1 is B30.A3.R.1. Parents in all crosses are listed in the order *MAT1-1* × *MAT1-2*. The number of pseudothecia examined per cross ranged from 3 to 12.

†Only asci with at least one mature ascospore were counted.

spore abortion patterns similar to the crosses homozygous for *Tox1* (Table 2). In all crosses, asci with even numbers of mature spores were more common than asci with odd numbers.

The pattern of spore loss in crosses heterozygous for *Tox1* was examined by observing segregation for T-toxin production (Table 3). Although the overall segregation ratio was 1:1 (*TOX1*:*tox1*), ascospore loss was not random. Among four-spored asci, segregation was almost exclusively 2 *TOX1* : 2 *tox1* (98%), confirming a similar report of nonrandom loss by Taga *et al.* (1985).

Attempts to break the association between *Tox1* and the factor reducing fertility in heterozygous crosses failed. Random progeny from an additional cross of B30.A3.R.1 (*TOX1*) and B30.A3.R.87 (*tox1*) were tested for toxin production and relative fertility in crosses homozygous and heterozygous for *Tox1* with the appropriate B30 strains (B30.A3.R.1, B30.A3.R.65, B30.A3.R.85, B30.A3.R.87). Among 50 *TOX1* and 50 *tox1* progeny examined, no recombinants were found.

The tight linkage in the laboratory strains suggested that *Tox1* and the factor reducing fertility may exist in the same coupling phase in naturally occurring field isolates. Race T and race O field isolates that had been demonstrated to have *TOX1* and *tox1*, respectively, (M. Taga, C. R. Bronson, and O. C. Yoder, unpublished data) were crossed in homozygous and heterozygous combinations with the laboratory strains (Table 4). The fertility of homozygous crosses between field isolates and the laboratory strains was much lower than for homozygous crosses among the laboratory strains. However, the pattern of additional spore loss in heterozygous crosses was similar; i.e., a large portion of the asci appeared to abort four spores. Asci having no mature spores increased substantially, although it was not possible in this procedure to distinguish asci that were barren from those containing immature spores. Segregation in 38 of 46 four-spored asci (83%) from additional heterozygous crosses of Hm540 with laboratory strains was 2:2 for alleles of *Tox1*. Six race T isolates, including Hm86

TABLE 3. Segregation of alleles of the *Tox1* locus in individual asci from crosses between laboratory strains of *C. heterostrophus**

Viable ascospores† *TOX1*:*tox1*	% of asci
2:0	7
0:2	7
3:0	1
2:1	4
1:2	5
2:2	55
4:0	1
4:2	1
3:3	1
2:4	6
4:3	1
3:4	1
4:4	9

*Pooled data for crosses of B30.A3.R.1 × B30.A3.R.87 and B30.A3.R.85 × B30.A3.R.65 (Table 2).

†Total ascospore ratio was 179 *TOX1* : 181 *tox1*.

TABLE 4. Fertility of crosses homozygous and heterozygous for *Tox1* between field isolates and laboratory strains of *C. heterostrophus*

Parental strains*	Genotype	No. of asci examined	% of asci with indicated no. of mature ascospores								
			0†	1	2	3	4	5	6	7	8
Hm813×85	*tox1*×*tox1*	115	39	3	17	10	20	1	3	3	6
Hm813× 1	*tox1*×*TOX1*	136	69	3	18	5	5	0	0	0	0
Hm540×87	*tox1*×*tox1*	155	46	6	19	7	21	0	0	0	0
Hm540×65	*tox1*×*TOX1*	148	76	3	14	2	5	0	0	0	0
Hm86× 1	*TOX1*×*TOX1*	75	13	3	7	9	23	0	13	8	24
Hm86×85	*TOX1*×*tox1*	94	48	1	14	6	22	1	3	2	2
Mon1×65	*TOX1*×*TOX1*	137	20	2	3	6	31	3	10	7	17
Mon1×87	*TOX1*×*tox1*	141	40	1	16	6	28	0	1	1	6

*Laboratory strains are B30 siblings and are identified only by their random-spore number.
†May include asci with immature spores as well as asci with aborted spores.

and Mon1, had previously been tested in crosses with *tox1* laboratory strains (Taga *et al.* 1985). Among four-spored asci, segregation for T-toxin production was 80 to 95% 2:2. These results are consistent with the hypothesis that the *TOX1* and *tox1* field isolates differ by the same factor in the same coupling phase as the *TOX1* and *tox1* laboratory strains.

Cytology

Cytologic observations of homozygous (B30.A3.R.1(*TOX1*) × B30.A3.R.65(*TOX1*)) and heterozygous (B30.A3.R.1 (*TOX1*) × B30.A3.R.87(*tox1*)) crosses revealed that ascospore loss in heterozygous crosses was due to abortion of the spores after delimitation. Meiosis and ascospore delimitation occurred similarly in both types of crosses, yielding eight small, filiform spores lacking cross walls. In the homozygous cross, most asci became packed with a tight coil of maturing spores (Fig. 1A). In the heterozygous cross, the coils were usually looser (Fig. 1B) and poorly staining degenerated spores were often seen wrapped among the maturing spores or loosely crinkled in the ascus (Fig. 1B, 1C). Degenerated spores were occasionally detected during dissection of living material. Attempts to germinate them invariably failed. The frequency of asci in which all spores had aborted was higher in the heterozygous cross than in the homozygous cross.

The shape and arrangement of *Cochliobolus* ascospores in the ascus precluded reliable counts of mature spores in fixed, intact asci. Dissection of living material demonstrated a correlation between the tightness of the coils and the number of mature spores present, but counts based on the tightness of coiling were not accurate, especially when the number of mature spores exceeded four. This was in part because the length of the spores tended to be inversely proportional to the number of mature spores in the ascus.

Attempts were made to observe pachytene nuclei cytologically (N. B. Raju and C. R. Bronson, unpublished data). *Cochliobolus heterostrophus* chromosomes appeared smaller than those of *Neurospora crassa* and were difficult to count. We were unable to confirm the reports by Guzman *et al.* (1982) that *C. heterostrophus* has eight chromosomes or reliably detect a difference in chromosome pairing between homozygous and heterozygous crosses.

Discussion

These results show that crosses of *C. heterostrophus* heterozygous at the *Tox1* locus undergo a high frequency of nonrandom ascospore abortion. Differences in parental genotype at this locus could account for much of the variation in fertility observed by previous workers for crosses among laboratory strains. The fertility of crosses heterozygous for *Tox1* among laboratory strains was similar to that reported by Taga *et al.* (1985), with the majority of asci having four or fewer mature spores. The fertility of homozygous crosses was similar to reported fertility for crosses between unspecified C-strain genotypes by Leach *et al.* (1982*a*), but less than reported fertility in homozygous crosses (80% eight-spored asci) by Guzman *et al.* (1982). The ascospore counts by Guzman *et al.* (1982) were estimates based on the tightness of coiling in stained, intact asci (O. C. Yoder, personal communication) and thus may not reflect higher fertility than that reported here. The reason for the low fertility of homozygous crosses is not known, but the loss appears to be more or less random except for the tendency to recover more even-spored than odd-spored asci.

Heterozygosity for *Tox1* could also account for the differences in fertility observed in crosses among field isolates (Yoder 1976; Yoder and Gracen 1975). Tests of field isolates were hampered by their low fertility, but the race T and race O isolates appeared to differ by the same factor in the same coupling phase as in the laboratory strains. This conclusion is supported by the demonstration that the *Tox1* locus and the abortion-inducing factor are tightly linked in the laboratory strains. It is likely that the field isolates used by Yoder (1976) and Yoder and Gracen (1975) in their studies of the inheritance of toxin production, and by Leach *et al.* (1982*a*) in the development of the C-strains, also differed by this factor.

The reasons for the low fertility in homozygous crosses involving field isolates are not clear. It is noteworthy that fertility tended to be higher in crosses of laboratory strains to race T rather than race O field isolates. The C-strains were developed by backcrossing *tox1* from a race O field isolate into a race T field isolate (Leach *et al.* 1982*a*). The C-strains may have more similarities to race T than to race O field isolates.

Interpretation

The observations to date on ascospore abortion in crosses of *C. heterostrophus* heterozygous for *Tox1* are consistent with the hypothesis that *TOX1* and *tox1* strains differ by a chromosome rearrangement, possibly a reciprocal translocation, with one of the breakpoints at or near *Tox1*.

Two factors, chromosome rearrangements (Perkins 1974) and spore killers (Turner and Perkins 1979), are known to cause ascospore abortion in *Neurospora* and other fungi when

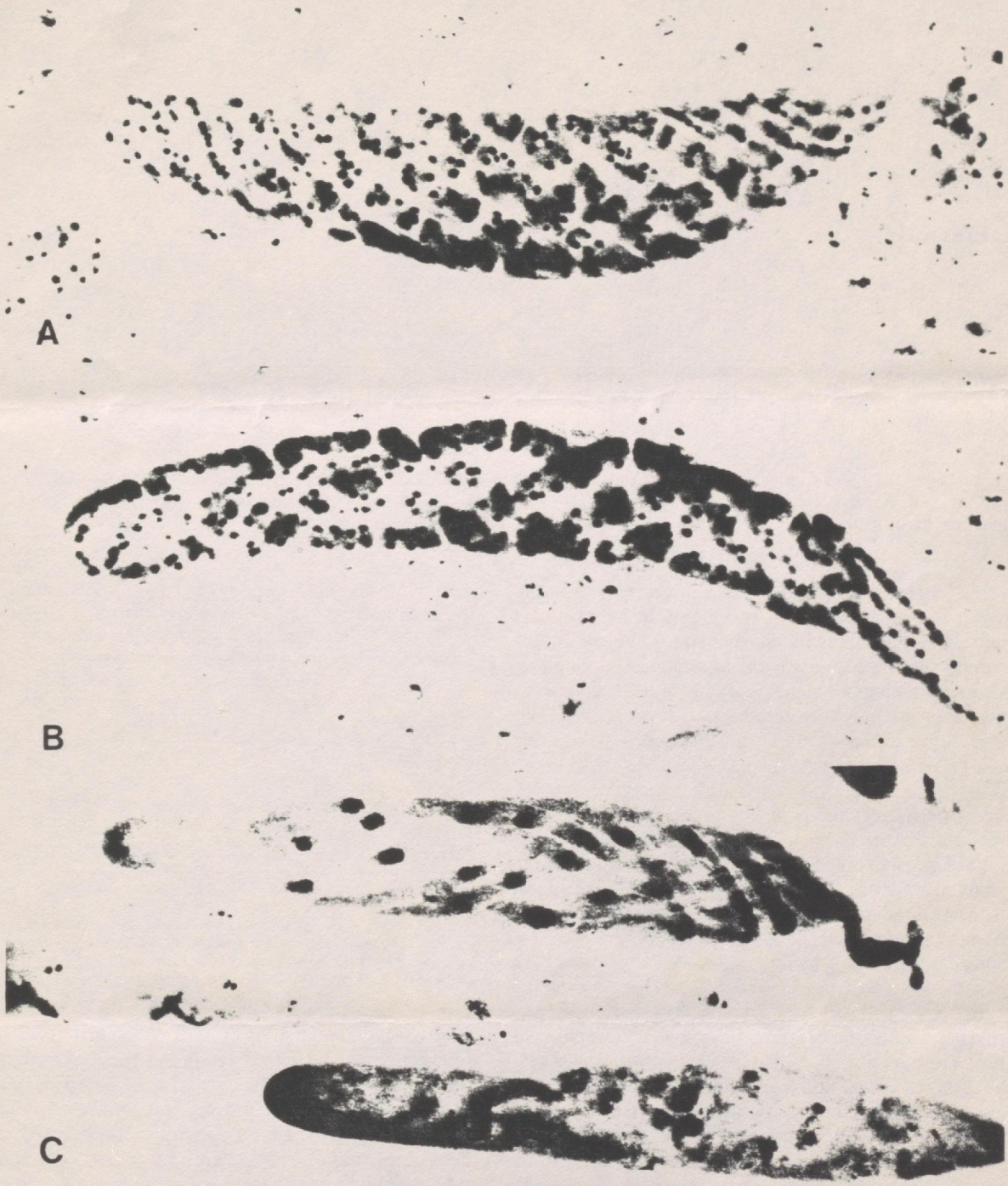

FIG. 1. Iron-hematoxylin stained asci of *Cochliobolus heterostrophus* (magnification 725×). (A) An ascus from a 17-day-old cross of *TOX1* × *TOX1* (1 × 65). The ascus is tightly packed with six to eight filiform ascospores. Each ascospore is multiply segmented and multinucleate. (B) Asci from a cross of *TOX1* × *tox1* (1 × 87) (17 days). The top ascus contains four loosely coiled ascospores. Four other ascospores have aborted and degenerated. All eight ascospores have aborted in the lower lightly stained ascus. (C) Asci from a 15-day-old cross of *TOX1* × *tox1*. The top ascus shows eight immature binucleate ascospores some of which may or may not mature. The two lower asci have aborted at or shortly after ascospore delimitation. Photographs were contributed by Namboori B. Raju of Stanford University.

heterozygous. In crosses heterozygous for a spore killer (that is, Sk^K (killer) × Sk^S (sensitive)), only ascospores receiving the killer allele survive. No killing occurs in homozygous crosses (Sk^K × Sk^K or Sk^S × Sk^S). Since all crosses among laboratory strains in this study were among siblings, spore killers are effectively ruled out as the cause of abortion. Crosses heterozygous for a rearrangement, on the other hand, produce both normal and rearrangement progeny and ascospore abortion is expected in heterozygous crosses among siblings.

Perkins (1974) has documented the effects of various rearrangements on the viability of meiotic products in *Neurospora*. In heterozygous crosses the frequencies of asci with various patterns of viable and inviable spores are characteristic

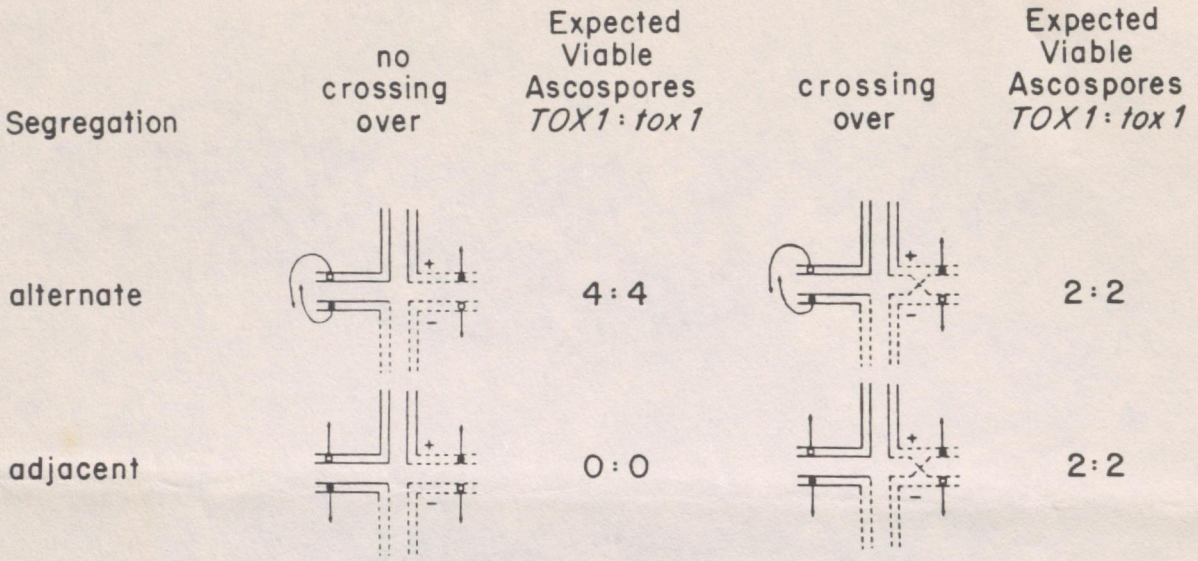

FIG. 2. Expected ascus types from a cross heterozygous for a reciprocal translocation with a breakpoint tightly linked to the virulence locus *Tox1*. The location of alternate alleles of *Tox1* is unknown. *TOX1* (+) is shown on a rearranged chromosome based on the hypothesis that race T arose by mutation from race O. The *tox1* allele (−) is shown on the homologous chromosome.

of the type of rearrangement and the frequency of crossing over between the breakpoints for inversions or between the breakpoints and centromeres for translocations. Viable spores may be normal sequence, rearrangement sequence, or duplications. Spores containing deficiencies are inviable. The patterns of ascospore abortion in rearrangement heterozygotes of *Cochliobolus* should be similar to those in *Neurospora*.

Crosses of *C. heterostrophus* heterozygous for *Tox1* show decreases in the frequency of 8:0 asci (mature, viable : aborted, inviable spores) and increases in the frequency of 4:4 asci and 0:8 asci. Among the four viable spores of 4:4 asci, segregation is almost exclusively 2:2 for alleles at *Tox1* and the abortion inducing factor. Data of Taga *et al.* (1985) suggest that the four aborted spores are nonsister meiotic products. Two types of rearrangements could account for these observations: a long inversion or a reciprocal translocation with long interstitial regions between the breakpoints and their respective centromeres.

The expected results of a cross heterozygous for a reciprocal translocation are shown in Fig. 2. In the absence of crossovers, asci will segregate either 8:0 (parental ditypes) or 0:8 (nonparental ditypes), depending on whether first division segregation is alternate or adjacent, respectively. Asci in which there has been a crossover between one of the breakpoints and its associated centromere (tetratypes) will segregate 4:4 due to the abortion of nonsister meiotic products containing deficiencies. In such asci the viable ascospores will comprise two sets of mitotic twins; one set will be normal sequence and the other rearrangement sequence. Segregation of markers tightly linked to centromeres or either of the breakpoints will be 2:2. The relative proportions of 8:0, 4:4, and 0:8 asci will be 1/6, 2/3, and 1/6, respectively, assuming one or both breakpoints are far from their centromeres and 100% of asci in homozygous crosses segregate 8:0. The expected results of a long inversion in which there is good pairing within the inversion are the same, since the breakpoints are effectively unlinked.

The observations of crosses heterozygous for *Tox1* fit reasonably well with the patterns expected for a reciprocal translocation or inversion if one takes into account the low fertility of the homozygous crosses. Predicted ascus frequencies for heterozygous crosses involving these rearrangements are shown in Table 5. Calculations were based on the observed fertility of homozygous crosses among laboratory strains. The reciprocal translocation hypothesis is preferred at present. Reciprocal translocations are the most common class of rearrangements in *Neurospora*, with several known to yield high frequencies (approximately 67%) of 4:4 asci (Perkins and Barry 1977; Perkins *et al.* 1982). There are relatively few reports of inversions. The identification and mapping of markers near *Tox1* in both *TOX1* and *tox1* strains should indicate the presence of a rearrangement and determine its form if it exists.

If the chromosome rearrangement hypothesis is correct, it is clear that *Tox1* must be tightly linked to one of the rearrangement breakpoints. No recombinants between *Tox1* and the abortion-inducing factor were detected among 112 progeny of laboratory strains. The observation that nearly all four-spored asci (98%) in heterozygous crosses segregated 2:2 for *Tox1* is also consistent with this hypothesis. (Loci unlinked to a breakpoint or a centromere are expected to segregate 2:2 in 67% of

TABLE 5. Predicted frequencies of asci with various numbers of viable spores in crosses of *C. heterostophus* heterozygous for either a reciprocal translocation or a long inversion

Type of cross	% of asci with indicated no. of mature ascospores			
	1 and 2	3 and 4	5 and 6	7 and 8
Observed*				
Homozygous	2	20	23	55
Heterozygous	11	68	8	13
Expected†				
Heterozygous	23	58	6	13

*Pooled data for crosses among B30, K22, and K38 siblings homozygous or heterozygous for *Tox1*.

†Expected frequencies are for a long inversion or a reciprocal translocation with a long interstitial interval(s) between the breakpoints and their respective centromeres. Frequencies were calculated assuming the observed fertility of homozygous crosses and adjusted to include only asci with at least one mature spore.

four-spored asci.) Exceptions to 2:2 segregation may be due to abortion unassociated with *Tox1*, as seen in homozygous crosses. Cloning and restriction mapping of *Tox1* alleles and flanking regions should help to identify the putative breakpoints.

If mapping studies do not demonstrate a rearrangement near *Tox1*, it is possible that abortion is due to synthetic lethals, i.e., genes that affect viability only in specific combinations (Dobzhansky 1946). To obtain the patterns of spore abortion observed in crosses heterozygous for *Tox1*, two loci (A and B) must interact such that AB and A′B′ ascospores are viable, but not AB′ or A′B ascospores. The locus showing nonrandom segregation (*Tox1*) must be tightly linked to one of these loci (or itself be one of the loci) and the other locus must be effectively unlinked. Though such interlocus interactions are conceivable, the author knows of no reports of synthetic lethals of this type (Thompson 1986).

The rearrangement hypothesis may help explain the behavior of race T strains in nature. Leonard (1973) proposed that race T arose by mutation from race O. Race T subsequently increased in frequency on T-cytoplasm maize, culminating in the 1970 southern leaf blight epidemic (Hooker 1972), then declined rapidly when T-cytoplasm maize was replaced with normal cytoplasm maize. Genetic studies have shown that the reduced fitness of race T compared with race O on normal cytoplasm maize is tightly linked to *Tox1* (Leonard 1977; Klittich and Bronson 1986). Results presented here suggest that the mutational event that created *TOX1* may have been a chromosome rearrangement. If so, the reduced fitness of race T compared with race O is consistent with observations in related Ascomycetes that rearrangements are at a disadvantage. Rearrangements are common among laboratory mutants of *Neurospora* and *Sordaria* (Perkins 1985), but are rarely detected in nature. The reason for the failure of new chromosome arrangements to become established is not known.

Acknowledgment

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DEVELOPMENT OF GENETIC RESEARCH IN THE U.S.S.R.

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Institute of Cytology and Genetics, Siberian Branch of the U.S.S.R. Academy of Sciences, Novosibirsk, U.S.S.R.

Shumny, V.K. 1988. Development of genetic research in the U.S.S.R. Genome.

Two periods of the development of genetic research in the U.S.S.R. with reference to its current trends of plant and animal genetics, cytogenetics and molecular genetics are reviewed.A short list of priority areas is arrived at: the maintenance and use of unique gene pools of plants and animals; the domestication of animals and cultivation of new plants; the development of programmes for mathematical treatment of genetic data banks.It is suggested to consider them within the framework of international projects. The idea is to promote the collobora-tive efforts of scientists on an international scale.

Key words: genetics in the U.S.S.R., current trends, internatunal cooperation.

Concern and responsibility for development of science is an indispensable part of policies of any country, including the USSR. For this country, the role of science in the economic and social life of society is of special importance, since it is becoming a powerful creative factor in the processes of restructuration, modernization of technology, management, and economy.

This is also true for genetics, because its achievements bear directly on such important spheres of human activity as agriculture, medicine, ecology etc.

It would not be an exaggeration to say that the future of mankind depends greatly on the level of genetic knowledge. This by itself predetermines the priority of this field of science, the prognosis of its development and possible spheres of application.

That is why it is natural that the main peculiarity of the state policy of the USSR in the field of genetics is the promotion of deep fundamental research in all directions of its modern development.

However, in order to evaluate objectively its contribution to world genetics, its contemporary state, achievements and trends, it is necessary to go back to its sources, and to make a brief historical outline, in which it is worth distinguishing two main stages of development of genetics in the USSR.

The 1st stage includes the time till 1948 and is characterized by an intense development of genetics in all its fields. It is enough to name the outstanding scientists who have largely contributed to the foundations of Soviet and world genetics.

First of all, it was Nikolai Vavilov, whose 100th anniversar was celebrated in 1987. He has discovered the law of homological variation which has a great predictive power even nowadays (Vavi-

lov, 1922). The high degree of homology of genes of related species, maintenance of similar gene orders in some groups of organisms, especially mammals, have been confirmed. This law gave a stimulus to development of a new, rapidly advancing trend, the comparative genetics, which investigates similarity and differences in the heredity and variation in organisms of different systemic groups, at all levels of organization - from the analysis of nucleotide and aminoacid sequences to complex morphophysiological and productive characters.

Another Vavilov's great contribution to genetics was the discovery of centres of origin of cultivated plants, which made it possible not only to understand the principles of botanic and geographical distribution of cultivated plant resources, but also to perform consciously their search and create genetic collections (Vavilov, 1926). The importance of this work still exists, as we shall see below.

Next, I would like to name Sergei Chetverikov, whose ideas and experiments have greatly influenced the development of world genetics.

Having demonstrated the enormous reserves of genetic polymorphism of Drosophila populations and estimated its role in the evolution, he has founded a new trend - population genetics (Chetverikov, 1926) which later on was largely developed in the works of geneticists in USSR and abroad.

Nikolai Koltzoff as early as 1927, in his work "Physico-Chemical Basis of Morphology" (Koltzoff, 1928), proposed the idea of self-reproduction of molecules of heredity, thus laying the basis of the future molecular genetics and biology. These ideas were developed further on by his disciple N.V.Timofeeff-Resovsky

(1939), who, together with M.Delbruck and K.Zimmerman, tentatively estimated the size of a gene on the basis of data of radiation genetics; this size turned out to be close to that of protein molecules known at that time. Thanks to this, Delbruck has formulated the idea of gene as a macromolecule, and Schrödinger (1944), having developed this idea, stated directly that a mechanism of coding of genetic macromolecules must exist.

Next to this, S.M.Gerschenson in late 30ies found a mutagenic effect of alien DNA on some loci in chromosomes of Drosophila. Further on, it was demonstrated that this phenomenon was similar to genetic instability caused by insertion of migrating fragments of genetic material (Gerschenson, Alexandrov, Maluta, 1975).

Alexandre Serebrovsky, together with Nikolai Dubinin, in 1929 discovered the phenomenon of complementation, and developed, on its basis, the theory of divisibility of a gene and linear distribution of its elements (Serebrovsky, Dubinin, 1929).

Undoubted are the merits of Prof.Yu.Philipchenko (1934) in the development of genetics of quantitative characters, S.Navashin (Navashin, Gerasimova, 1935), G.Levitsky (1924) in the development of cytogenetics, S.Davidenkov (1932) in human genetics, and G.Nadson and G.Filippov (1925) in the discovery of mutagenic effect of ionizing radiation.

The list of famous names of Russian genetics who have made great contributions to the foundations of world genetics, could be continued. It was natural that great scientific schools were formed around them, which represented various fields of genetics and worked actively till 1948.

Thus, with this brief outline we demonstrated the powerful

start of Soviet genetics, the birth of a series of original trends; the formation of important scientific schools, and obtaining of brilliant results. At the same time, it seems worth underlining the formation of the traditions of genetics in the USSR, which may be characterized by two main features:

(1) interpretation of genetic phenomena from general biological point of view, and first of all from evolutionary positions;
(2) interdisciplinary integration in the investigation of big problems.

These features were reflected with a special brightness in the works of Vavilov, which combined problems of evolutionary genetics and breeding and united the efforts of botanists, physiologists, phytopathologists, geneticists, biochemists and geographers.

Naturally, these traditions have their continuation and development in modern genetics.

However, as you know, there was a long gap in the development of genetics in the USSR. It was connected with the activities of T.Lysenko and his supporters who usurped and monopolized, on Lamarquist basis, the leadership in biology, which resulted in decay of genetic research and teaching of young geneticists at the universities.

It is not necessary to dwell upon this negative period which has been given objective official estimation. We greatly regret to have had such a bad time in the history of our science.

The renaissance of genetics in USSR began with the organization, in 1956, of the Laboratory of Radiation Genetics headed by N.Dubinin, and, in 1957, of the Institute of Cytology

and Genetics in Novosibirsk, whose organizer and first director till 1959 was N.Dubinin, and from 1959 to 1985, D.Belyaev. I have been working in this institute since 1958, and I have the honour to be its Director now.

Somewhat later on, other genetic institutes were re-established in Moscow, Leningrad, Kiev, and Minsk. Some universities, and first of all the Leningrad University, began to produce new generations of Soviet geneticists in middle sixties.

Even this brief list of events demonstrates that the renaissance of genetics in the USSR has been a painful and complicated process which is being continued now, at an increasing rate.

Realising the increasing role of genetics in the economy, agriculture, medicine and ecology, the Soviet government issued, during two last decades, some important documents, which concerned the foundation of new centres of genetics, for further development of fundamental research. During these years, the system of genetic training and the experimental facilities have been improved.

The Academy of Sciences of the USSR considers fundamental research in various fields of genetics, from genetic engineering and biotechnology to preservation of genetic pools of plants, animals and microorganisms, as one of priority directions.

How do we understand the strategy of development of genetics to-day and in the future? The knowledge of the structure and function of the gene has resulted in development of genetic engineering and biotechnology using bacterial systems and beginning to use eukaryotic systems. This, in its turn, made it possible to approach the direct study of the structure and function of genomes of higher organisms and their reorganisation by means

of molecular biologic techniques. To-day, obtaining transgenic plants and animals has become a reality. The geneticists came close to the complete decoding of genomes of the most thoroughly studied and economically most important plants and animals, including man.

We believe that in the nearest future the most important will become the problem of interactions between genomes in biocenoses, investigation of natural biological systems, and construction of artificial communities of different kinds and species of organisms which are necessery to man and optimum for nature.

Such is, according to our view, the general tendency of development of genetics based on the closest integration of general biological and physico-chemical ideas and techniques.

In connection with what was told above, the concept of development of genetics in the USSR has been worked out.

Its general purport is as follows:

(a) intense development of fundamental research in all principal fields of genetics;

(b) maximum possible integration of purely genetic and molecular-genetic approaches in the studies of pro- and eukaryotic genomes, and their reorganization in the directions necessary for research and practice;

(c) organization of national programs for solution of big genetic problems, which would cover all stages, from the fundamental research to application of its results.

In this concept, the last two items require a special detailed analysis, while the first one is an indispensable part of the state policy.

As it was mentioned already, characteristic of Soviet geneticists, beginning from Vavilov, Chetverikov, Timofeeff-Resovsky

and Schmalhausen etc., has always been an evolutionary approach to understanding and interpretation of genetic phenomena, and the priority of the biological problem in planning genetic experiments. The modern generation of geneticists is continuing this tradition on the basis of maximum possible integration of evolutionary genetic and molecular biological approaches to the study of all genetic events. That is why we believe that there must be a parallel development of both genetic engineering and evolution and population genetics of plants and animals, as well as studies of fine genetic structure of higher animals and man.

This program method of science development in the USSR is aimed at combination of all levels of research and at application of results of fundamental research to respecive branches of economy.

This method is based on large-scale national programs, including those in genetics.

As examples thereof, one could point to programs in genetic basis of plant and animal breeding, biotechnologies, "Oncogen", "Human Genome" etc.

Below, I will try to give a brief analysis of the modern state of various fields of genetics in the USSR and prospects of their development for the nearest decades.

The most important scientific school was created by Vavilov and his disciples and followers Philipchenko, Karpechenko (1927) and many others, in plant genetics. And to-day, an intense study of the law of homologous variation, centres of origin of cultivated plants, and a constant replenishment and maintenance of the genetic collection, are continued. Karpechenko's classical works on Raphanobrassica, in which the mechanisms of restoration of fertility in intergeneric hybrids had been discovered, were developed

large series of studies on cereals carried out by Pisarev, Tsitsin and others. By now, unique combinations of Triticale, wheat-agropyron and wheat-aegylops, barley-wheat and barley-rye hybrids have been produced (Tsitsin, 1978; Shumny, Pershina, Belova, 1982). This trend of genetics which is traditional for us, is successfully developed also on other plant species and genera with the aim of obtaining suitable initial material for studies in genetic and breeding.

Now, research is being carried out also in radiation and chemical mutagenesis in plants. Its basis had been laid by Nadson and Filippov, and then developed by Rapoport, Lobashev, Shkvarnikov and others (Nadson, Filippov, 1925; Rapoport, 1947; Lobashev, 1934; Shkvarnikov, 1935).

Without going on with enumeration of results I will only tell that the front of researches on plant genetics in the USSR is rather wide and covers all the main directions.

Nowadays, when programs of development of this field of genetics are worked out, the special importance is given to integration of classical methods of induction of hereditary variation and cytogenetic analysis, with new methods of genetic, chromosomal and cellular engineering for investigation and reconstruction of plant genome.

In the field of molecular genetics, the main attention is paid to comparative studies of the structural organization of genomes, analysis of their regions containing structural genes and other actively functioning chromosome regions. Molecular analysis of genomes of different cereal species makes it possible to find changes at the level of separate DNA sequences occurring in the process of species divergence in evolution (Shumny, Vershinin, 1988). Compilation of genome libraries of cultivated

cereal species is begun, which permits to have a set of necessary genes as the initial material for genetic engineering and production of transgenic plants.

On the other hand,we pay a great attention to detailed studies of genetic structure of some functionally essential traits of plants which are important for breeding, by means of traditional methods, since it is only a detailed knowledge of the structure of such traits that can open ways of identification and cloning of genes and production of transgenic plants.

Thus, we believe that it is only in the unity of general and special genetics, genetic and cellular engineering that the firm basis can be built, on which successes in the knowledge and reconstruction of eukaryotic genome are possible.

An important contribution has been made by Soviet geneticists to the research of genetic mechanisms of the evolution.Developing Chetverikov's ideas, Schmalhausen, in his work "Factors of Evolution (The Theory of Stabilizing Selection)" has considerably enriched population genetics and the theory of evolution (Schmalhausen, 1946). By now, our geneticists have greatly advanced in the understanding of evolutionary reorganizations by means of investigation of integral characteristics of genome organization. Such characteristics, which have complex systemic effects, include animal behaviour, stress resistance, neuroendocrine systems, photo-reactivity, reproduction etc. Developing this line of research and analyzing special evolutionary events occurring in extreme situations such as, e.g., the initial stage of domestication of wild animals, D.K.Belyaev formulated the concept of destabilizing selection, a new idea in the evolution theory which elucidated the role of selection for behaviour (Be-

lyaev, 1980).

A great contribution to animal genetics was made by Astaurov and his school with their works on sex regulation in silkworm. He was the first to solve the problem of artificial parthenogenesis, experimental production of animal tetraploids capable of reproduction (Astaurov, 1940).

His disciple V.Strunnikov developed this trend and worked out the genetics of silkworm, techniques of its artificial reproduction, sex regulation, and breeding on the basis of heterosis. Strunnikov is the author of a new idea of heterosis based on compensation gene complexes, which neutralize lethal and semilethal mutations (Strunnikov, 1987).

The initial period of development of Soviet genetics could be called, as Astaurov (1968) puts it,the period of formulation of general principles of phenogenetics. This means that the main interest of our investigations was concentrated on the laws of manifestation and phenotypical expression of genes, and therefore on the problems of their role in ontogenesis and of mechanisms of their action. This direction was developed by Chetverikov's disciples Timofeeff-Resovsky (1925), Romashov (Romashov, Balkashina, 1929), Rokitsky (1925) et al. Nowadays, this branch of genetics is also studied at molecular level. Thus, in the works of Korochkin, Konyukhov,Ivanov, on various objects, a system of tissue specific trans-processing genes controlling the formation of the molecular phenotype was described(Korochkin, Konyukhov, 1987).

It is natural, that apart from the evolutionary genetic and phenogenetic research which is traditional for the USSR, all the other directions of animal genetics: studies of the structure

and function of animal genomes, immunogenetics, physiological genetics, somatic cell genetics, and special genetics of some animal species, are also being investigated. A great importance is given to gene mapping in different species, first of all those used in agriculture. This is important both for animal genetic engineering, production of transgenic forms, and for improvement of breeding methods.

As an example of successful realization of this program one could point to a work carried out in the Institute of Cytology and Genetics on mapping of more than 50 genes of American mink (Serov et al., 1987).

Cytogenetics is also developed traditionally in the USSR. The greatest successes have been achieved by Soviet cytologists and geneticists in such fields as construction of chromosomes, cytogenetics of sex, cytogenetics of parthenogenesis and apomyxis, evolution of karyotypes of mammals and Diptera, genomic analysis of plants, structural and functional organization of polytene chromosomes, cytogenetic mapping, production of monosomic and substituted strains of plants and cell cultures,genetic control of meiosis, radiation genetics of mammals (Kiknadze,1972; Zhimulev et al., 1981).

In further plans of development of fundamental researches in the USSR, the following directions of cytogenetics were singled out as the most promising ones: study of the principles of structural and functional organization of prokaryotic and eukaryotic chromosomes, cytogenetic mapping of chromosomes, mechanisms of occurrence of chromosome rearrangements, meiosis and its genetic control.

During the recent years, researches in chromosome mapping

by means of use of hybrid cells of agricultural and laboratory animals were enlarged; techniques of construction of hybridomes as producers of monoclonal antibodies and valuable models for somatic cell cytogenetics were developed.

The traditions of development of molecular genetics in the USSR go back to the works of Koltzoff and his school as it was already mentioned. The most important results were obtained by Soviet scientists in molecular genetics of eukaryotic cells, first of all in discovery and study of the functional role of mobile genetic elements (Georgiyev, 1984).

A considerable contribution has been made by some laboratories to the elaboration of methods of site-directed DNA modifications, and, on this basis, methods of gene-directed mutagenesis, and decoding of molecular mechanisms of occurrence of structural mutations (Salganik, 1987).

In many research centres a large work has been done on cloning and studying individual genes of eukaryote organisms.

Even this short list of researches shows that in the USSR molecular genetics is developed in many directions.Studies are made on mapping and determination of the primary structure of human, animal, plant and bacterial genes, production of transgenic plants and animals, investigation of genes and gene complexes of the immunity system (Baranov, 1988), oncogens, genes of cell differentiation, neurogenes and other genes controlling the most important bodily functions. Very interesting are the studies on structural organization and biological role of the repetitive genome elements, including the mobile genetic elements, the laws of genome evolution. It is natural, that apart from the research on the structural organization of genome, studies

of regulatory elements of single genes and gene complexes will be deepened.

Such is the general outline of strategy of research in molecular genetics.

Above, I have mentioned the main tendencies in the main fields of genetics. As examples, some results in plant and animal genetics, phenogenetics of ontogenesis, cytogenetics and molecular genetics were told about. Naturally, the choice of strategy in the development of fundamental research in genetics is based on possibilities of each state, and on the availability of sufficiently trained people. However, these researches could also be united into large international programs, equally interesting for all the mankind.

Since all science, including genetics, is international in its nature, unification of efforts of scientists from all countries is necessary for joint solution of important problems, first of all those concerning the increase of food resources, medicine, and ecology. We are all for such a policy, and we are ready to take an active part in large international programs.

As possible proposals on our part, one might discuss the problem of collection, preservation and joint use of unique genetic pools of cultivated and wild plants and animals. The most part of the territory of the USSR has extreme environmental conditions, such as extremely low temperatures, droughts, short vegetation period etc. Naturally, due to this we have plants and animals possessing a valuable pool of genes resistant to the extreme environmental factors.

Each country possesses, apart from collections of world plant and animal resources, also unique native forms which are

of special interest for joint use.

As an example, I could mention the works done in our institute on collection of Siberian native plants and animals. Now, we have in our collection the Yakutian cow, Yakutian horse, Altai sheep etc. No doubt, they are valuable donors of genes of resistance to extreme conditions of Siberia, and in this respect they have no equals.

The time seems to have come for a common inventorization of plant and animal genetic resources, and for creation of a maximum complete genetic collection. The foundation of this work was made by Vavilov who created the first world collection of plant resources. Later on, similar collections were made in some other countries, and their replenishment is going on. No doubt, in each of these collection there is a unique part. If a general, universal collection is made, it would be possible to discover maximally complete genetic variation of each species of agricultural plants and animals, and, what is especially important, to see, which elements are lacking in it. This would permit us to continue the search for missing links of genetic variation and, further on, to induce their appearance by means of classical or modern genetics.

Thus, the preservation and use of genetic pools, especially unique genetic pools, should be put at the level of large international programs.

Finally, extremely important is the organization of a united international centre for preservation and study of genetic pools. Such a centre should rightly carry Vavilov's name. Soviet geneticists are ready to take an active part in its organization and work.

The famous Russian writer Lev Tolstoi once reproached scientists for doing little to introduce new agricultural plants and animals. This reproach seems right nowadays.

The process of domestication and introduction of new species is extremely long and complicated. In other words, such a work can be done only by means of large international programs.

However, the basis for carrying out such a work has been prepared. For example, a model of domestication has been worked out in the Institute of Cytology and Genetics in Novosibirsk, on foxes. To-day, the characters for which selection must be done in animal domestication, became known. Consequences of such a selection have been studied, and populations of domesticated animals have been obtained. However, this is only an initial model which makes it possible to start a serious long-term work on domestication of many important animal species. It would be more reasonable to develop this work in the framework of an international program. The same concerns new species of cereals, fodder and medicinal plants.

Some institutes of the Academy of Sciences of the USSR, including our Institute, could participate most actively in creation of banks of molecular genetic data and sets of software for computer analysis of large animal and plant genomes, including that of man, for simulation of large and complicated genetic systems controlling self-reproduction, ontogenesis, immunity, carcinogenesis, the cell as a whole, etc. In our Institute of Cytology and Genetics (Novosibirsk), there is a good basis for all these works. No doubt, creation of such banks with suitable software will accelerate considerably the realization of such large international programs as "Human Genome", "Oncogene" and others.

One of the most important though complicated problems for joint international research is that of population and ecological genetics of man. A continuons monitoring of technogenic influences on the environment must be carried on, which should include not only the estimation of present risk factors, but also the prediction of possible remote consequences for human health.

The Chernobyl accident, and many other accidents in other countries require from geneticist of all the world a solidarity in objective evaluation of consequences of the increasing anthropogenic influences on the environment.

Our leader, Mr. Gorbachov has proposed a conception of "new thinking". The main aspect of this is the common concern for the preservation of life, and for protection of environment suitable for human life.

An international solidarity of scientists, including geneticists, in solution of urgent human problems will be a good basis for the new thinking.

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DEVELOPMENT OF GENETIC RESEARCH IN THE U.S.S.R.

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Nikolai Koltzoff, as early as 1927, in his work "Physico-Chemical Basis of Morphology" (Koltzoff, 1928), proposed the idea of self-reproduction of molecules of heredity, thus laying the basis of the future molecular genetics and biology. These ideas were developed further on by his disciple N.V.Timofeeff-Resovsky

(1939), who, together with M.Delbruck and K.Zimmerman, tentatively estimated the size of a gene on the basis of data of radiation genetics; this size turned out to be close to that of protein molecules known at that time. Thanks to this, Delbruck has formulated the idea of gene as a macromolecule, and Schrö - dinger (1944), having developed this idea, stated directly that a mechanism of coding of genetic macromolecules must exist.

Next to this, S.M.Gerschenson in late 30ies found a mutagenic effect of alien DNA on some loci in chromosomes of Drosophila. Further on, it was demonstrated that this phenomenon was similar to genetic instability caused by insertion of migrating fragments of genetic material (Gerschenson, Alexandrov, Maluta, 1975).

Alexandre Serebrovsky, together with Nikolai Dubinin, in 1929 discovered the phenomenon of complementation, and developed, on its basis, the theory of divisibility of gene and linear distribution of its elements (Serebrovsky, Dubinin, 1929).

Undoubted are the merits of Prof.Yu.Philipchenko (1934) in the development of genetics of quantitative characters, S.Navashin (Navashin, Gerasimova, 1935), G.Levitsky (1924) in the development of cytogenetics, S.Davidenkov (1932) in human genetics, and G.Nadson and G.Filippov (1925) in the discovery of mutagenic effect of ionizing radiation.

The list of famous names of Russian genetics who have made great contributions to the foundations of world genetics, could be continued. It was natural that great scientific schools were formed around them, which represented various fields of genetics and worked actively till 1948.

Thus, with this brief outline we demonstrated the powerful

start of Soviet genetics, the birth of a series of original trends; the formation of important scientific schools, and obtaining of brilliant results. At the same time, it seems worth underlining the formation of the traditions of genetics in the USSR, which may be characterized by two main features:

(1) interpretation of genetic phenomena from general biological point of view, and first of all from evolutionary positions;

(2) interdisciplinary integration in the investigation of big problems.

These features were reflected with a special brightness in the works of Vavilov, which combined problems of evolutionary genetics and breeding and united the efforts of botanists, physiologists, phytopathologists, geneticists, biochemists and geographers.

Naturally, these traditions have their continuation and development in modern genetics.

However, as you know, there was a long gap in the development of genetics in the USSR. It was connected with the activities of T.Lysenko and his supporters who usurped and monopolized, on Lamarquist basis, the leadership in biology, which resulted in decay of genetic research and teaching of young geneticists at the universities.

It is not necessary to dwell upon this negative period which has been given objective official estimation. We greatly regret to have had such a bad time in the history of our science.

The renaissance of genetics in USSR began with the organization, in 1956, of the Laboratory of Radiation Genetics headed by N.Dubinin, and, in 1957, of the Institute of Cytology

and Genetics in Novosibirsk, whose organizer and first director till 1959 was N.Dubinin, and from 1959 to 1985, D.Belyaev. I have been working in this institute since 1958, and I have the honour to be its Director now.

Somewhat later on, other genetic institutes were re-established in Moscow, Leningrad, Kiev, and Minsk. Some universities, and first of all the Leningrad University, began to produce new generations of Soviet geneticists in middle sixties.

Even this brief list of events demonstrates that the renaissance of genetics in the USSR has been a painful and complicated process which is being continued now, at an increasing rate.

Realising the increasing role of genetics in the economy, agriculture, medicine and ecology, the Soviet government issued, during two last decades, some important documents, which concerned the foundation of new centres of genetics, for further development of fundamental research. During these years, the system of genetic training and the experimental facilities have been improved.

The Academy of Sciences of the USSR considers fundamental research in various fields of genetics, from genetic engineering and biotechnology to preservation of genetic pools of plants, animals and microorganisms, as one of priority directions.

How do we understand the strategy of development of genetics to-day and in the future? The knowledge of the structure and function of the gene has resulted in development of genetic engineering and biotechnology using bacterial systems and beginning to use eukaryotic systems. This, in its turn, made it possible to approach the direct study of the structure and function of genomes of higher organisms and their reorganisation by means

of molecular biologic techniques. To-day, obtaining transgenic plants and animals has become a reality. The geneticists came close to the complete decoding of genomes of the most thoroughly studied and economically most important plants and animals, including man.

We believe that in the nearest future the most important will become the problem of interactions between genomes in biocenoses, investigation of natural biological systems, and construction of artificial communities of different kinds and species of organisms which are necessery to man and optimum for nature.

Such is, according to our view, the general tendency of development of genetics based on the closest integration of general biological and physico-chemical ideas and techniques.

In connection with what was told above, the concept of development of genetics in the USSR has been worked out.

Its general purport is as follows:

(a) intense development of fundamental research in all principal fields of genetics;

(b) maximum possible integration of purely genetic and molecular-genetic approaches in the studies of pro- and eukaryotic genomes, and their reorganization in the directions necessary for research and practice;

(c) organization of national programs for solution of big genetic problems, which would cover all stages, from the fundamental research to application of its results.

In this concept, the last two items require a special detailed analysis, while the first one is an indispensable part of the state policy.

As it was mentioned already, characteristic of Soviet geneticists, beginning from Vavilov, Chetverikov, Timofeeff-Resovsky

and Schmalhausen etc., has always been an evolutionary approach to understanding and interpretation of genetic phenomena, and the priority of the biological problem in planning genetic experiments. The modern generation of geneticists is continuing this tradition on the basis of maximum possible integration of evolutionary genetic and molecular biological approaches to the study of all genetic events. That is why we believe that there must be a parallel development of both genetic engineering and evolution and population genetics of plants and animals, as well as studies of fine genetic structure of higher animals and man.

This program method of science development in the USSR is aimed at combination of all levels of research and at application of results of fundamental research to respecive branches of economy.

This method is based on large-scale national programs, including those in genetics.

As examples thereof, one could point to programs in genetic basis of plant and animal breeding, biotechnologies, "Oncogen", "Human Genome" etc.

Below, I will try to give a brief analysis of the modern state of various fields of genetics in the USSR and prospects of their development for the nearest decades.

The most important scientific school was created by Vavilov and his disciples and followers Philipchenko (1927), Karpechenko and many others, in plant genetics. And to-day, an intense study of the law of homologous variation, centres of origin of cultivated plants, and a constant replenishment and maintenance of the genetic collection, are continued. Karpechenko's classical works on Raphanobrassica, in which the mechanisms of restoration of fertility in intergeneric hybrids had been discovered, were developed

large series of studies on cereals carried out by Pisarev,Tsitsin and others. By now, unique combinations of Triticale, wheat-agropyron and wheat-aegylops, barley-wheat and barley-rye hybrids have been produced (Tsitsin, 1978; Shumny, Pershina, Belova, 1982). This trend of genetics which is traditional for us, is successfully developed also on other plant species and genera with the aim of obtaining suitable initial material for studies in genetic and breeding.

Now, research is being carried out also in radiation and chemical mutagenesis in plants. Its basis had been laid by Nadson and Filippov, and then developed by Rapoport, Lobashev, Shkvarnikov and others (Nadson, Filippov, 1925; Rapoport, 1947; Lobashev, 1934; Shkvarnikov, 1935).

Without going on with enumeration of results I will only tell that the front of researches on plant genetics in the USSR is rather wide and covers all the main directions.

Nowadays, when programs of development of this field of genetics are worked out, the special importance is given to integration of classical methods of induction of hereditary variation and cytogenetic analysis,with new methods of genetic, chromosomal and cellular engineering for investigation and reconstruction of plant genome.

In the field of molecular genetics, the main attention is paid to comparative studies of the structural organization of genomes, analysis of their regions containing structural genes and other actively functioning chromosome regions. Molecular analysis of genomes of different cereal species makes it possible to find changes at the level of separate DNA sequences occurring in the process of species divergence in evolution (Shumny, Vershinin, 1988). Compilation of genome libraries of cultivated

cereal species is begun, which permits to have a set of necessary genes as the initial material for genetic engineering and production of transgenic plants.

On the other hand,we pay a great attention to detailed studies of genetic structure of some functionally essential traits of plants which are important for breeding, by means of traditional methods, since it is only a detailed knowledge of the structure of such traits that can open ways of identification and cloning of genes and production of transgenic plants.

Thus, we believe that it is only in the unity of general and special genetics, genetic and cellular engineering that the firm basis can be built, on which successes in the knowledge and reconstruction of eukaryotic genome are possible.

An important contribution has been made by Soviet geneticists to the research of genetic mechanisms of the evolution.Developing Chetverikov's ideas, Schmalhausen, in his work "Factors of Evolution (The Theory of Stabilizing Selection)" has considerably enriched population genetics and the theory of evolution (Schmalhausen, 1946). By now, our geneticists have greatly advanced in the understanding of evolutionary reorganizations by means of investigation of integral characteristics of genome organization. Such characteristics, which have complex systemic effects, include animal behaviour, stress resistance, neuroendocrine systems, photo-reactivity, reproduction etc. Developing this line of research and analyzing special evolutionary events occurring in extreme situations such as, e.g., the initial stage of domestication of wild animals, D.K.Belyaev formulated the concept of destabilizing selection, a new idea in the evolution theory which elucidated the role of selection for behaviour (Be-

lyaev, 1980).

A great contribution to animal genetics was made by Astaurov and his school with their works on sex regulation in silkworm. He was the first to solve the problem of artificial parthenogenesis, experimental production of animal tetraploids capable of reproduction (Astaurov, 1940).

His disciple V.Strunnikov developed this trend and worked out the genetics of silkworm, techniques of its artificial reproduction, sex regulation, and breeding on the basis of heterosis. Strunnikov is the author of a new idea of heterosis based on compensation gene complexes, which neutralize lethal and semilethal mutations (Strunnikov, 1987).

The initial period of development of Soviet genetics could be called, as Astaurov (1968) puts it, the period of formulation of general principles of phenogenetics. This means that the main interest of our investigations was concentrated on the laws of manifestation and phenotypical expression of genes, and therefore on the problems of their role in ontogenesis and of mechanisms of their action. This direction was developed by Chetverikov's disciples Timofeeff-Resovsky (1925), Romashov (Romashov, Balkashina, 1929), Rokitsky (1925) et al. Nowadays, this branch of genetics is also studied at molecular level. Thus, in the works of Korochkin, Konyukhov, Ivanov, on various objects, a system of tissue specific trans-processing genes controlling the formation of the molecular phenotype was described (Korochkin, Konyukhov, 1987).

It is natural, that apart from the evolutionary genetic and phenogenetic research which is traditional for the USSR, all the other directions of animal genetics: studies of the structure

and function of animal genomes, immunogenetics, physiological genetics, somatic cell genetics, and special genetics of some animal species, are also being investigated. A great importance is given to gene mapping in different species, first of all those used in agriculture. This is important both for animal genetic engineering, production of transgenic forms, and for improvement of breeding methods.

As an example of successful realization of this program one could point to a work carried out in the Institute of Cytology and Genetics on mapping of more than 50 genes of American mink (Serov et al., 1987).

Cytogenetics is also developed traditionally in the USSR. The greatest successes have been achieved by Soviet cytologists and geneticists in such fields as construction of chromosomes, cytogenetics of sex, cytogenetics of parthenogenesis and apomyxis, evolution of karyotypes of mammals and Diptera, genomic analysis of plants, structural and functional organization of polytene chromosomes, cytogenetic mapping, production of monosomic and substituted strains of plants and cell cultures,genetic control of meiosis, radiation genetics of mammals (Kiknadze,1972; Zhimulev et al., 1981).

In further plans of development of fundamental researches in the USSR, the following directions of cytogenetics were singled out as the most promising ones: study of the principles of structural and functional organization of prokaryotic and eukaryotic chromosomes, cytogenetic mapping of chromosomes, mechanisms of occurrence of chromosome rearrangements, meiosis and its genetic control.

During the recent years, researches in chromosome mapping

by means of use of hybrid cells of agricultural and laboratory animals were enlarged; techniques of construction of hybridomes as producers of monoclonal antibodies and valuable models for somatic cell cytogenetics were developed.

The traditions of development of molecular genetics in the USSR go back to the works of Koltzoff and his school as it was already mentioned. The most important results were obtained by Soviet scientists in molecular genetics of eukaryotic cells, first of all in discovery and study of the functional role of mobile genetic elements (Georgiyev, 1984).

A considerable contribution has been made by some laboratories to the elaboration of methods of site-directed DNA modifications, and, on this basis, methods of gene-directed mutagenesis, and decoding of molecular mechanisms of occurrence of structural mutations (Salganik, 1987).

In many research centres a large work has been done on cloning and studying individual genes of eukaryote organisms.

Even this short list of researches shows that in the USSR molecular genetics is developed in many directions.Studies are made on mapping and determination of the primary structure of human, animal, plant and bacterial genes, production of transgenic plants and animals, investigation of genes and gene complexes of the immunity system (Baranov, 1988), oncogens, genes of cell differentiation, neurogenes and other genes controlling the most important bodily functions. Very interesting are the studies on structural organization and biological role of the repetitive genome elements, including the mobile genetic elements, the laws of genome evolution. It is natural, that apart from the research on the structural organization of genome, studies

of regulatory elements of single genes and gene complexes will be deepened.

Such is the general outline of strategy of research in molecular genetics.

Above, I have mentioned the main tendencies in the main fields of genetics. As examples, some results in plant and animal genetics, phenogenetics of ontogenesis, cytogenetics and molecular genetics were told about. Naturally, the choice of strategy in the development of fundamental research in genetics is based on possibilities of each state, and on the availability of sufficiently trained people. However, these researches could also be united into large international programs, equally interesting for all the mankind.

Since all science, including genetics, is international in its nature, unification of efforts of scientists from all countries is necessary for joint solution of important problems, first of all those concerning the increase of food resources, medicine, and ecology. We are all for such a policy, and we are ready to take an active part in large international programs.

As possible proposals on our part, one might discuss the problem of collection, preservation and joint use of unique genetic pools of cultivated and wild plants and animals. The most part of the territory of the USSR has extreme environmental conditions, such as extremely low temperatures, droughts, short vegetation period etc. Naturally, due to this we have plants and animals possessing a valuable pool of genes resistant to the extreme environmental factors.

Each country possesses, apart from collections of world plant and animal resources, also unique native forms which are

of special interest for joint use.

As an example, I could mention the works done in our institute on collection of Siberian native plants and animals. Now, we have in our collection the Yakutian cow, Yakutian horse, Altai sheep etc. No doubt, they are valuable donors of genes of resistance to extreme conditions of Siberia, and in this respect they have no equals.

The time seems to have come for a common inventorization of plant and animal genetic resources, and for creation of a maximum complete genetic collection. The foundation of this work was made by Vavilov who created the first world collection of plant resources. Later on, similar collections were made in some other countries, and their replenishment is going on. No doubt, in each of these collection there is a unique part. If a general, universal collection is made, it would be possible to discover maximally complete genetic variation of each species of agricultural plants and animals, and, what is especially important, to see, which elements are lacking in it. This would permit us to continue the search for missing links of genetic variation and, further on, to induce their appearance by means of classical or modern genetics.

Thus, the preservation and use of genetic pools, especially unique genetic pools, should be put at the level of large international programs.

Finally, extremely important is the organization of a united international centre for preservation and study of genetic pools. Such a centre should rightly carry Vavilov's name. Soviet geneticists are ready to take an active part in its organization and work.

The famous Russian writer Lev Tolstoi once reproached scientists for doing little to introduce new agricultural plants and animals. This reproach seems right nowadays.

The process of domestication and introduction of new species is extremely long and complicated. In other words, such a work can be done only by means of large international programs.

However, the basis for carrying out such a work has been prepared. For example, a model of domestication has been worked out in the Institute of Cytology and Genetics in Novosibirsk, on foxes. To-day, the characters for which selection must be done in animal domestication, became known. Consequences of such a selection have been studied, and populations of domesticated animals have been obtained. However, this is only an initial model which makes it possible to start a serious long-term work on domestication of many important animal species. It would be more reasonable to develop this work in the framework of an international program. The same concerns new species of cereals, fodder and medicinal plants.

Some institutes of the Academy of Sciences of the USSR, including our Institute, could participate most actively in creation of banks of molecular genetic data and sets of software for computer analysis of large animal and plant genomes, including that of man, for simulation of large and complicated genetic systems controlling self-reproduction, ontogenesis, immunity, carcinogenesis, the cell as a whole, etc. In our Institute of Cytology and Genetics (Novosibirsk), there is a good basis for all these works. No doubt, creation of such banks with suitable software will accelerate considerably the realization of such large international programs as "Human Genome", "Oncogene" and others.

One of the most important though complicated problems for joint international research is that of population and ecological genetics of man. A continuons monitoring of technogenic influences on the environment must be carried on, which should include not only the estimation of present risk factors, but also the prediction of possible remote consequences for human health.

The Chernobyl accident, and many other accidents in other countries require from geneticist of all the world a solidarity in objective evaluation of consequences of the increasing anthropogenic influences on the environment.

Our leader, Mr. Gorbachov has proposed a conception of "new thinking". The main aspect of this is the common concern for the preservation of life, and for protection of environment suitable for human life.

An international solidarity of scientists, including geneticists, in solution of urgent human problems will be a good basis for the new thinking.

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