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*Il X Simposio internazionale sulla Genetica dei frumenti (X International Wheat Genetics Symposium - IWGS) è stato – degnamente e con successo – ospitato in Italia, a Paestum, organizzato da un Comitato presieduto dal Dr. Norberto Pogna, dell'Istituto Sperimentale per la Cerealicoltura di Roma.*

*La serie di questi Convegni si aprì nel 1958 a Winnipeg, Manitoba, Canada, e tutte le edizioni sono state fondamentali pietre miliari del percorso scientifico e applicativo e sicure frecce per l'avanzamento delle conoscenze e delle innovazioni realizzate in un gruppo di specie che hanno accompagnato la storia e favorito lo sviluppo del genere umano.*

GIAN TOMMASO SCARASCIA MUGNOZZA \*

## **Welcoming Address and Introduction to the Session «Cytogenetics and Germplasm Evaluation»**

Ladies, Gentlemen, Dear Colleagues, Mr. Chairman,

I think that today I am one of the few chairmen who participated in the previous International Wheat Genetics Symposia (IWGS). In fact, I had the privilege of chairing (substituting Prof. M.S. Swaminathan) the VI Symposium in Kyoto, in 1983. Therefore, I take this opportunity to address a warm welcome to the chairmen and organizers who are here today and were present in the previous IWGS and thank the scientists and colleagues who contributed in making the IWGS successful events.

In this respect, I would like to propose to our chairman Dr. Pogna to consider, among the themes to be debated by this meeting, the opportunity of nominating an

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Editorial Board responsible for the historical review and critical examination of the progress and advance in knowledge, realization and results from all the IWGS, which have covered almost half a century starting from 1958 to present.

I believe it is appropriate, in a period of dangerous cuts, in many countries, in scientific research in agriculture, that the public opinion, the stakeholders, and public authorities acknowledge the efforts made by scientists, experts and farmers towards the welfare of humankind and how much this commitment is a guarantee for a positive advancement towards further goals and for an equitable and pacific development of humanity.

With this trust, dear colleagues, and on behalf of the Italian National Academy of Sciences I renew to you, participants of the 10<sup>th</sup> IWGS, my sincere appreciation for your work and welcome you and wish you a fruitful and pleasant stay in Italy.

Dear colleagues,  
cytogenetics and germplasm of *Triticum* and related species are the themes of one session.

Cytogenetics and germplasm evolution have been, together with mutagenesis and mutation breeding in *durum*, the research areas in which I have been working, with groups of colleagues and also in international organizations, during my scientific career.

Cytogenetics, as all other fields dealing with analysis and manipulation of the genome of plants of agricultural relevance such as wheat, has remarkably benefited from the substantial advancements in the area of molecular biology occurred in the last recent years. They have in fact succeeded in providing scientists and breeders with such an array of technical and methodological tools that their work has become perhaps more sophisticated and complex, but certainly more accurate, finely targeted and greatly rewarding in terms of both basic knowledge and practical achievements.

The recent progress in wheat cytogenetics, enabled by the molecular level of analysis, has offered the possibility to complement, and in some instances efficiently replace, classical cytogenetic approaches (e.g. meiotic pairing analysis, aneuploid-based mapping) and markers (e.g. telocentric chromosomes, C-bands), with tools which provide a much higher resolution insight of structural and behavioral characteristics of chromosomes. To this regard, one of the most impressive developments has been that of molecular cytogenetic techniques such as non-radioactive *in situ* hybridization (ISH) and, in particular, fluorescence *in situ* hybridization (FISH). By means of this technique, in fact, using cloned DNA sequences or total genomic DNA as probes on somatic and meiotic chromosomes or even on extended DNA fibers, a variety of research work can be carried out, including identification of chromosomes and chromosome segments, analysis of intergenomic relationships and of wheat-alien gene transfers, as well as fine physical mapping of even low-copy DNA sequences and genes.

And I have to underline the very interesting, recent progress, also for the wheat genome, in sorting out individual chromosomes by flow-cytometric approaches of which Prof. *Dolezel* will soon report.

In combination with such advanced cytogenetic methods, the dramatic extension of genetic maps of many crop plants, including wheat, enabled by the use of a plentiful and diversified array of molecular markers, as well as the results from comparative genomic analysis, which clearly show substantial gene and marker synteny between the genome of wheat and those of even distantly related *Triticeae* and even *Poaceae* species greatly contribute to expand the number and type of diagnostic and selection tools at hand for a highly comprehensive characterization and finely-tuned manipulation of the wheat genome.

I want, however, to recall how much we are indebted to the outstanding work of the late Prof. *Sears*, who has provided wheat scientists with a unique set of aneuploid stocks which, among other things, represent powerful tools for locating genes and markers to a specific chromosome or even chromosome arm. And, to this regard, I also want to mention the great contribution given to the development of additional important sets of wheat aneuploid lines, firstly at PBI, Cambridge and then at Norwich by Tony *Worland*, who unfortunately left us not long ago. In this context we must remember also the results obtained in Japan by Prof. *Kihara* and his school and by Prof. *Feldman* and his colleagues in Israel, etc.. In terms of extremely useful materials for physical mapping of genes and markers to specific chromosome segments, we have then to add the deletion stocks developed, in collaboration with Prof. *Bikram Gill*, by Prof. *Endo*, who will illustrate part of his work during this session.

We cannot forget to mention that E. *Sears*, besides being the father of wheat cytogenetics in general, must be recalled as the father of *Chromosome Engineering*, i.e. of that strategy which, by use of cytogenetic methodologies, enables controlled introduction of chromosomal segments of reduced entity from various *Triticeae* species into cultivated wheat. Thanks to *Sears*' isolation of the *ph1* mutant of Chinese Spring (1977), to which soon after (1978) followed the isolation of a corresponding one in *T. durum* by scientists working at the Casaccia Research Center, particularly Drs. *Benito Giorgi*, *Carla Ceoloni*, and others. The great success of chromosome engineering remains, I think, the one based on manipulations of the wheat pairing control system and, in particular, on the use of mutations for the main homoeologous pairing suppressor gene *Ph1*.

In this context we can quote also the long work carried out at Bari University by Prof. *A. Blanco* in the interspecific hybridization of tetraploid lines (with and without the *Ph* gene) with species of *Aegilops* and *Dasypirum* in order to introgress useful genes into cultivated wheat.

The strategic use of *Ph1* system has allowed a few dedicated wheat cytogeneticists, including Prof. *Lukaszewski* and Prof. *Carla Ceoloni* (Casaccia Center and Viterbo University), to achieve really meaningful results in terms of finely engi-

neered wheat lines that have a true potential for breeding purposes. The work of C. Ceoloni, in particular, is rather unique in that she has succeeded in successfully applying it to a species, i.e. *durum wheat*, which for its inherent characteristics, is much less tolerant than the hexaploid common wheat or triticale to chromosome manipulations. Actually, as you can see in the poster session as a result of the work by the Ceoloni group, the first variety, to my knowledge, of durum wheat is soon going to be released carrying a small chromosomal segment, with two useful genes from an alien donor species (*Thinopyrum ponticum*), which not only does not upset the recipient genome but confers to it remarkable added value.

In conclusion, classical as well as modern cytogenetic strategies, which imply even complex manipulation of the wheat and alien genomes, appear to be very effective for a wheat breeding able to tackle the present and future challenges and to lead to meaningful practical achievements.

This was, to some respect, *the dream, indeed the far-seeing perception of pioneer, that illuminated scientists*, such as McFadden and Sears in USA but also Prof. N. Strampelli in Italy, who, since the beginning of the last century, had stated the great and innovative potential associated with the exploitation of alien variability for wheat improvement. Aiming at the same goal, in the second half of the 20<sup>th</sup> century Prof. F. D'Amato, from Pisa University, always believed and stimulated work in the field of cytogenetics as fundamental for basic and applied research. While awaiting for further progress in the area of direct gene transfer via transformation methodologies, and even when this will be more readily accessible and more effective than at present, it seems reasonable to believe that there is and there will be sufficient place and good reason for both the chromosome and the genetic engineering approaches to contribute to *wheat germplasm enhancement*. In fact, if useful gene pools for the former are virtually unlimited, still there is enormous potential in those of the more closely related *Triticeae* species which looks worth being fully unleashed and profitably used.

Indeed, a judicious combination of traditional as well as unconventional avenues, some already quite set up, such as the chromosome engineering approach, and others going to reach the “finishing straight” in the forthcoming years, definitely appears the most effective strategy to follow for a modern plant breeding to be able to tackle the present and future challenges.

In this connection, some quick thoughts on germplasm evaluation are appropriate. There is plenty of evidence that users of genebanks want more evaluation of accessions and want the results to be made available. Virtually every survey shows this (see e.g. Hodgkin et al., 2003). This is particularly the case for evaluation of biotic and abiotic stress resistance (i.e. resistance to pests, diseases, drought, cold, water salinity, etc.)

Of course, core collections provide a way of handling the large numbers of accessions in collections, and providing users with the amount of information they would like. Core collection approaches are likely to be particularly useful where we

want to combine evaluation of complex traits with molecular characterization. Work with peanut has clearly shown that core collections are very cost effective ways of looking for accessions with specific useful traits such as disease resistance (Holbrook and Anderson, 1995 - Crop Science, 35: 1700-1702; and I think more recent articles also by Holbrook).

But, a major question confronting those involved in evaluation is the most efficient and most effective use of molecular tools as part of any evaluation programme. It is now possible to use molecular markers to characterize very large numbers of accessions (e.g. the whole lettuce germplasm collection at Wageningen has been characterized using AFLPs and microsatellites). The question is how can molecular markers be used most effectively within the context of germplasm evaluation. Should we be looking for molecular markers linked to variation in useful traits or variation in specific important traits like disease and pest resistance? And, if so, how might this best be done? Alternatively, should we use molecular markers simply as more or less anonymous characterization tools using AFLPs for example?

Nevertheless, as a matter of fact, the work on synteny of the grass genome has provided very exciting new insights into gene control and location and enabled us to locate genes for important useful traits in the different *gramineae* genomes. This means that we can use synteny to assist with evaluating and understanding the genetics of important useful traits in germplasm accessions.

I am sure that good answers and intelligent perspectives will come out from the reports of the speakers of this session. A session which starts with the report of Prof. *Dolezel*, whom I invite to take the floor.