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## **The Rice Genome revealed: DNA, diversity and development**

### *Introduction*

Desidero presentare i miei saluti alle autorità politico-istituzionali, alle autorità del mondo della ricerca scientifica qui presenti e a tutti i convenuti.

Ringrazio l'Accademia Nazionale delle Scienze per il cortese e molto gradito invito a partecipare in qualità di relatore al Convegno. Sono onorato di potermi rivolgere a questa illustre platea.

### *Population growth (slide 1)*

Il convegno verte sul tema «Biodiversità e Agricoltura». Tale binomio rappresenta un nodo fondamentale, di estrema importanza per il futuro. Di fatto, le previsioni odierne indicano che, entro venticinque anni, le risorse alimentari dei paesi in via di sviluppo, per evitare la morte di inedia delle loro popolazioni, dovranno essere aumentate di circa il 50%.

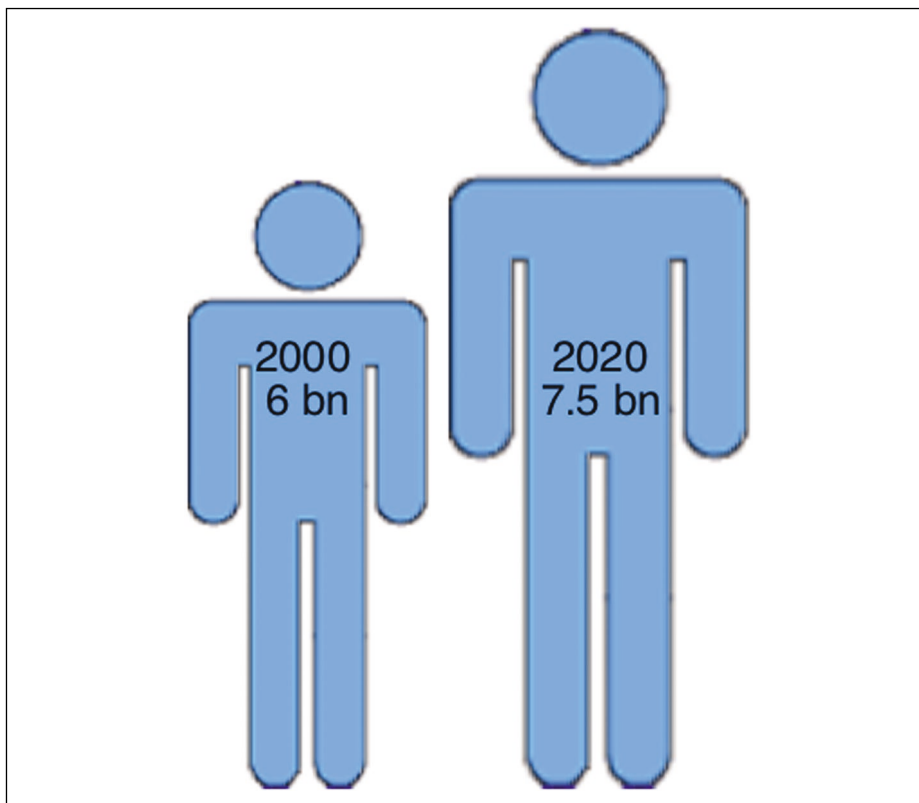
Il raggiungimento di tale obiettivo sarà possibile e sostenibile *solo* attraverso lo sviluppo di nuove varietà agricole resistenti alle diverse patologie, e di produttività superiore.

La protezione e conservazione della diversità genetica agricola (agrobiodiversità) rappresentano quindi i prerequisiti essenziali per il futuro alimentare d'interesse popolazioni.

La mia presentazione odierna descrive come la ricerca sul genoma, nelle sue applicazioni, può, potenziando le tecniche di miglioramento, aumentare la produttività agricola e di conseguenza la sicurezza alimentare.

Mi dispiace di non poter condurre la mia intera presentazione in italiano ma, al termine del mio intervento, non esitate comunque a presentare le vostre domande in Italiano.

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Slide 1 - Population growth. The UN's median estimate suggests that world population will grow to 7.5 billion by the year 2020.

*Rice Genome: Timeline* (slide 2)

In December 2002, six years ahead of the original objective, the entire sequence of the rice genome was announced by a consortium of research institutions from ten countries. These researchers have opened the book of life for the world's most important crop plant. Rice feeds more than half of the world's population. The huge and collaborative exercise to complete the rice genome, coordinated by the National Institute of Agrobiological Sciences in Japan, has been a tremendous scientific achievement. This paper will explore some of the ramifications of the new era in research that they open up. Unlocking the secrets of the rice genome offers an insight into far more than rice alone. It also opens up several other fields for further exploration. Most importantly, it offers the opportunity to make use of the vast stores of crop diversity held in genebanks and growing in farmers' fields, and makes it more important than ever that we conserve those resources.



Slide 2 - A family threshes the rice harvest in West Sumatra. Photo I. deBoreghyi/IPGRI.

*Rice Diversity* (slide 3)

It is well recognized that the basis of all agricultural improvement is genetic diversity. From the very beginnings of agriculture, which for rice is probably some 6000 years ago, farmers have exploited naturally occurring diversity. For millennia farmers made use of this diversity to select the crops that performed best for them under their particular circumstances. More recently, very recently if one considers the long history of rice growing, research scientists have entered the picture with rigorous breeding programmes designed to get the maximum harvests from the crop. Even the research scientists, however, depended on the diversity that existed in natural populations.



Slide 3 - Rice diversity. A display of old traditional rice varieties in Nepal. By a recent count there were more than 106,000 samples of rice diversity held in genebanks. Photo A. King/IPGRI.

*IBPGR: Collection and Conservation* (slide 4)

IPGRI came into being 30 years ago as the International Board for Plant Genetic Resources hosted by FAO. Its original mandate was to collect and preserve plant genetic diversity in so-called genebanks. The need was extremely urgent, because although modern agriculture in general and plant breeding in particular depend absolutely on genetic diversity, the very success of modern varieties threatens the existence of that diversity. Successful varieties, ones that produce a higher yield, are naturally adopted over a wide area. But as they spread, these modern varieties can displace tens or hundreds of older varieties, which farmers no longer grow because they cannot compete with the new variety. And yet these old varieties are a massive storehouse of genetic diversity, which breeders are sure to need in the future to meet new challenges.



Slide 4 - Collection and conservation. The genebank of the Chinese Academy of Agricultural Science holds more than 64,000 different kinds of rice. Photo IBPGR.



So IBPGR, which later became IPGRI, an independent centre supported by the Consultative Group on International Agricultural Research, helped national programmes and international agricultural research centres to collect and preserve diversity in genebanks. And breeders, at the international agricultural research centres and in private industry, called on those samples in search of the diverse characteristics they needed.

*IPGRI: Conservation through Use (slide 5)*

Later it became clear that conservation on the farm was an equally important aspect of conserving genetic diversity, because only on the farm would varieties continue to be exposed to the selection pressures that moulded their performance to match changing conditions. IPGRI branched out into on-farm conservation and, especially, into conservation through use.

In Nepal, for example, IPGRI projects have helped mountain farmers to develop a market for their traditional varieties. As a result, the traditional varieties



Slide 5 - Conservation through use. On the steep hillsides of Nepal, traditional varieties may be more useful than modern varieties, although they can still be improved by participatory breeding. Photo A. King/IPGRI.

are being more widely grown, and are improving the livelihoods of the farmers who grow them. Farmers are also working with researchers to blend traditional and modern varieties in an effort to breed even better «traditional» varieties. Or, to put it another way, to give modern varieties the characteristics they need to flourish in the marginal environments where traditional varieties are generally superior.

#### *Challenge Programme: Unlocking Crop Genetic Diversity*

IPGRI now stands ready for a new phase in the use of diversity to build a sustainable, improved agriculture. A CGIAR Challenge Programme called «Unlocking Genetic Diversity in Crops for the Resource Poor» plans to use the new discoveries of genomics, exemplified by the rice genome, to open the way to fresh approaches to the use of diversity for sustainable development.

Most of these approaches do not involve genetic engineering as it is currently understood. They are far more subtle, and more interesting, than that.

#### *Synteny*

Most of the possibilities arise from a phenomenon known as synteny. To put it at its simplest, synteny means that all the cereals, for example rice, wheat, barley and maize, share a very similar organization of their DNA. They contain roughly the same genes, in roughly the same order, as one another. If, for example, the genes for making more efficient use of phosphorus, a nutrient that is in short supply in many tropical soils, are found at a particular spot in the rice genome, near another cluster of genes, then they are likely to be near the same cluster of genes in the other cereals. Indeed, synteny can go further than that. From what is already known it seems that large chunks of the DNA of all plants is organized along very similar lines.

The implications are profound. If scientists work out the function of a stretch of DNA in one plant, they can quickly transfer their knowledge to other plants. This means that information gathered from a detailed study of the rice genome can be applied to many other crops, making rice more than a mere model.

#### *Marker Assisted Selection*

Another example is known as marker assisted selection. One of the bottlenecks in plant breeding is the time taken to see whether a particular desired trait has been passed to future generations. An apple tree may take seven or eight years before it bears fruit that can be assessed to see if the fruit has inherited the right qualities from the breeding crosses. Not just time, but resources. Traditional plant breeding is a numbers game, and marker assisted selection can drastically increase the efficiency of breeding.

Without knowing the genetic details of a particular trait, molecular biologists can work out that it is very closely associated with a particular DNA sequence known as a «marker». They can then screen the offspring of a cross in the laboratory for the presence of the markers, eliminating those that do not contain them. This makes the assessment of a cross much more efficient, because resources do not need to be devoted to offspring that do not contain the desired markers.

For rice and other annual crops, there is already a significant increase in efficiency because only offspring that are potentially of interest are grown and examined in more detail. For longer lived plants, such as fruit trees and the like, there are tremendous savings in time too.

### *Genetic Profiling*

Another approach that the sequence makes possible is the use of genetic profiling. This advanced technique places thousands of DNA samples on a glass slide, a so-called «DNA chip». The activity of each of the thousands of spots on the slide can be rapidly and accurately measured to give a profile of the genetic activity of the sample in question.

DNA chips have been widely used in medicine where, for example, they have shown that what doctors previously thought was a single disease, for example a leukaemia, was in fact two or more diseases, each with a different profile of gene activity and each responding to therapy in different ways. With this information doctors can now ensure that patients get the appropriate treatment.

In plant science, DNA chips might be used to ask the differences between a plant that has enough water and one that is stressed by drought, or to compare two varieties, one of which tolerates drought stress better. From such snapshots of genetic diversity – the same genes under different conditions, and different genomes that respond in different ways – we will be able to identify the responsible biochemical pathways and use that information to breed and select better varieties.

### *Drought*

Drought is, indeed, the main focus of the first phase of the Challenge Programme. In order to demonstrate that this approach to unlocking genetic diversity works, most efforts will focus on this one key characteristic.

Water is absolutely vital to agriculture, and much of the work of the CGIAR research centres is aimed at growing more grain with less rain. Genomics science can speed the achievement of better drought-resistant varieties.

Because of the similarities between the genomes of different species, the more scientists study the genomes of these species, the more useful all genomic information becomes. Knowledge peculiar to one species can, thanks to genomic science, synteny, and the shared evolutionary history of all plants, be applied to all other species.



The power of genomics can also influence improvement through genetic engineering. As we learn more about the genomes of different species, it is becoming clear that there are fundamental similarities in the way that they work.

This means that it is becoming possible to change genomes not by transferring genetic information (DNA) but by transferring intellectual information, not genetic engineering but knowledge management.

For example, it might be that in a particularly high-yielding rice variety, the ability to store food in the grain is controlled by a given set of genes. A crude genetic engineering approach might be to try and snip those genes out of rice and insert them into wheat, in the hope of boosting the productivity of wheat. A more subtle approach is to take the information from rice and use it, along with knowledge of synteny and genetic markers, to look for the same set of genes in wheat. This is where the genebank samples will again be very helpful, as it is a relatively simple matter to screen thousands of samples, if one knows what to look for. Having found the genes in the target crop, one could then adopt a variety of approaches to obtain the increased productivity one seeks without actually having to move DNA from one species to another. This is not simply a dream. Similar work has already resulted in new varieties of maize that are more nutritious as a result of directly adjusting maize's own genes, rather than importing the genes from another species. The scientists responsible are now looking – in rice – for other possibilities to use what has been called a «kinder, gentler» genetic engineering.

Regardless of the merits of the arguments for and against genetic engineering, such an approach can speed-up crop improvement, both through classical breeding and through genetic engineering, the latter especially in crops in which it is very difficult or impossible to breed because they are sterile, such as for example bananas.

These are some of the elements of the Challenge Programme on Unlocking Genetic Diversity. The Challenge Programme is a global partnership. Initially, eight CGIAR centres are linked with 7 other institutes, including The Beijing Academy of Sciences and the National Institute of Agrobiological Sciences in Japan, who were the powerhouses behind the rice genome sequence. There will also be other partners in private industry and academe.

#### *Need for Conservation*

The Challenge Programme can make a difference, but only if the raw materials of crop improvement remain available. That is why, even as research moves forward, it is vital to support the continued conservation of crop diversity in genebanks, on farms, and in wild areas.

Italy, as the capital of the United Nations' agricultural agencies, and as host of IPGRI, has already made a huge contribution to the elimination of hunger. Italian scientists have made important contributions to the conservation and use of genetic diversity and to the development of modern molecular biology and genome studies.

Hopefully Italy will continue and even increase its strong support to the conservation and use of plant genetic resources. It is also hoped that Italian scientists will join the Challenge Programme and bring their expertise, experience and flair to the important task of unlocking genetic diversity for sustainable development.

#### *Millennium Development Goals*

The world has come a long way since the first shoots of the green revolution in the 1960s. World population has doubled in that time. Despite that, publicly funded agricultural research has helped to ensure that the proportion of people in hunger has almost halved. Nevertheless, the absolute number of hungry people, around 840 million at the last estimate, has increased slightly. That is something we all need to work to eliminate. The Millennium Development Goals aim to halve hunger and poverty, and to do so in an environmentally sustainable manner, by the year 2015. Only by making full use of genomic research and genetic diversity can we hope to do so. The rice genome, wonderful as it is, is just the beginning. With the continued strong support of Italian scientists and the Italian government, meeting the Millennium Development Goals can become a reality.

Vi ringrazio per la vostra attenzione.