

# Plant genomics *and biotechnology*

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A note by

## Ana Cristina Miranda Brasileiro

“ **WORLD POPULATION GROWTH**, especially in poor countries, the continuous degradation of arable land, reduced access to potable water and climate change are substantial challenges for agricultural production and food security. Many efforts have been made to date to improve the tolerance of crop plants to various abiotic stresses, including drought, salinity, cold and pollution by heavy metals. However, the improvement of tolerance characters is very difficult in classic breeding programmes.

Better knowledge at the molecular level of the genes involved in resistance/susceptibility to abiotic stresses should aid in the development of new varieties that are better adapted to environmental constraints. The adaptation of plants to various abiotic stresses is a complex phenomenon with the direct or indirect involvement of numerous genes in the signal perception and transduction chains and in the mechanisms regulating other genes.

Functional genomics techniques now make it possible to analyse an entire plant as a system and lead to better understanding of the biological function and interactions of the genes expressed under certain stress conditions, such as shortage of moisture and salinity. Embrapa has a long tradition of research on plant improvement and the conservation of genetic resources and has an avant-garde leadership position in scientific research of plant genomics in Brazil.

A project of joint interest entitled 'Functional genomics of the response to abiotic stresses in rice' was therefore run within the framework of Labex Europe. It was conducted jointly by Embrapa and the DAP ('Plant development and improvement') joint research unit for four years (2002-2006) as part of the BIOTROP programme (Biotechnology and plant genetic resources) in Montpellier. The main aim of the project was to identify and characterise the genes involved in the response to abiotic stresses—drought and salinity—using rice as a model plant for cereals. ”

**Ana Cristina Miranda Brasileiro (Embrapa, Brazil)**

## 'A process has been launched'



**Jean-Christophe Glaszmann**, is now the Director of the 'Biological Systems' (BIOS) Department at CIRAD. The

Brazilian scientist was hosted by one of his teams for four years. He gives us his view of Labex Europe.

### 1. Did you work in collaboration with Brazil in general and with Embrapa in particular before a Labex scientist joined your team?

CIRAD has worked with Embrapa for a long time in various fields such as the varietal improvement of rice, the genetics of eucalyptus and natural resource management in Amazonia. But Embrapa, like CIRAD but on an even larger scale, is a complex body with specialised centres—some devoted to certain species and others to themes. Our relations were little coordinated and above all more opportunist than strategic.

### 2. What conclusions do you draw from the experience? What has this collaboration contributed to your team?

Making a list of all the interactions and collaborative work undertaken would take too long. It covers the genetics and genomics of more than ten crops; projects have been developed and some—not enough yet—have received international funding. A movement has been got under way. We have organised meetings in Montpellier or Brasilia several times and the two communities have got to know each other. As regards subjects that might result in collaboration, French scientists now know where to go and who to contact at Embrapa and vice versa.

# Identification of the genes involved in the response to abiotic stresses in rice

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The project of joint interest 'Functional genomics of the response to abiotic stresses in rice' was conducted for four years within the framework of the BIOTROP programme (CIRAD, Montpellier). The main aim was to identify and characterise the genes involved in the response of rice to drought and salinity. The conclusions of the work are as follows:

■ The project is considered as a pilot operation by the CIRAD plant genomics team as a number

of the methodologies used then enabled the team to launch other functional genomics projects. Without being exhaustive, projects include a hydroponic system for large-scale osmotic and saline treatment, obtaining and validating subtractive banks, marking probes for microarrays, etc.

■ A total of 101 rice genome sequences were identified as having differential, early expression in response to moisture stress. These candidate genes code the proteins involved in the response to abiotic stress such as signal transduction, oxidative stress and adaptive processes. Two possible genes were also identified as coding proteins involved in the adaptive response of radicular architecture to osmotic stress. This had not been described previously in rice.

■ Of the 43 candidate genes validated by RT-PCR and by study of the association between radicular architecture (phenotyping), the four most interesting ones were selected for the final stage of validation by transformation.

■ Validation of the biological function of the candidate genes was continued by the construction of RNAi type vectors for the four candidate genes and the use of *Agrobacterium* to introduce them in transgenic rice plants ('Nipponbare' and 'Nona Bokra' varieties). The T1 lines of these plants are currently being subjected to molecular analysis to confirm the suppression of the respective genes.

■ In the final stage of this work, the genetically modified rice lines bred will be phenotyped under controlled conditions in greenhouses in Brazil and Vietnam to evaluate the phenotypic effects of the suppression of the expression of the four candidate genes and thus confirm their role in plant response to moisture and saline stresses.

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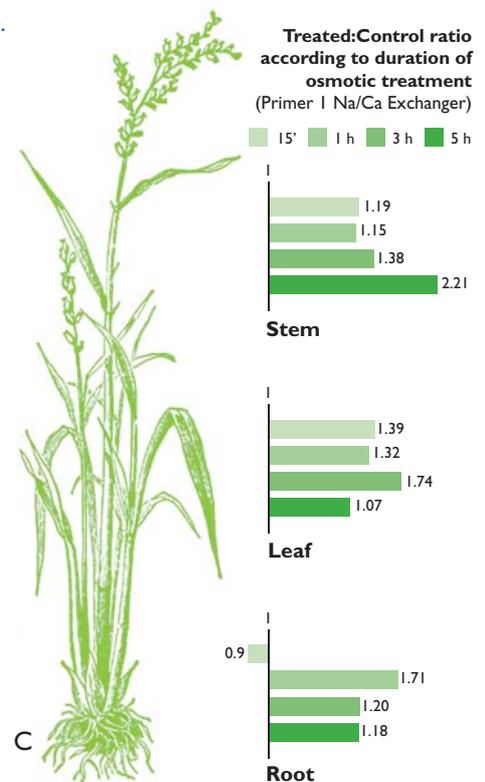
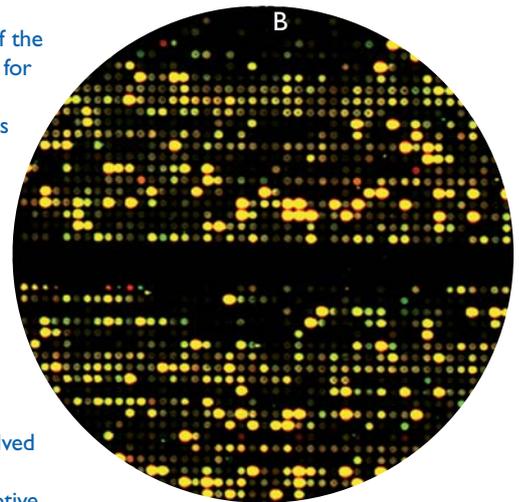
## Identification of the genes involved in the response of rice to osmotic shock (100 mM mannitol)

① Photo A - *cv.* 'Nipponbare' rice plants cultivated under hydroponic conditions 6 days after their transfer to a nutrient solution containing or not 100mM mannitol

② Cloned inserts corresponding to transcripts of the genes expressed differentially between the two treatments (SSH method)

③ Photo B - Display of transcripts over- (red) and under-expressed (green) under osmotic shock by microarray analysis on a glass slide (performed on the IGH transcriptomic platform)

④ Figure C - The regulation of the candidate genes by osmotic stress is confirmed by Q-RT PCR before functional validation by the analysis of mutants and/or overexpressors.



## 3. Now that the Brazilian scientist has returned home, is there any follow-up and/or consequences in terms of partnerships between your team and Brazilian institutions?

We have set up the *Consortium International en Biologie Avancée* (CIBA, International Advanced Biology Consortium). This performs regular monitoring and the people who run it are from our unit. In addition, Ana Brasileiro is a member of the programme committee of the CIRAD Biological Systems department. Some projects are running and others are being prepared.

Finally, the initiative will last if it is in the teams' interest, if they can secure funding, if they can find partnerships of a new type—triangular ones with African partners for example—and above all if a flow of students becomes established to strengthen links and to lay the foundation for new networks in the future.

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## The Brazilian scientist hosted

Ana Brasileiro, research scientist (Embrapa Genetic Resources and Biotechnology Department, Cenargen) spent nearly four years (May 2002 – April 2006) with the PIA joint research unit in molecular biology and genomics, working on the functional analysis of the tolerance of rice to drought and salinity.

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## The host laboratory

DAP (Développement et Amélioration des Plantes, Plant Development and improvement) joint research unit (formerly PIA, Polymorphismes d'intérêt agronomique, joint research unit) (CIRAD, Montpellier SupAgro, INRA, UM2) 68 scientists

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