# The Rice Functional Genomics platform

## An international hosting platform for the elucidation of gene function using rice as a model species

http://www.refuge-platform.org

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## What is Refuge?

REFUGE (The RicE FUnctional GEnomics platform) is a hosting platform, based in Montpellier, Agropolis-Lavalette campus, France open to the international plant science community.
REFUGE is funded by Agropolis Fondation (http://www.agropolis-fondation.fr/) and set up by the DAP (http://umr-dap.cirad.fr/) and GDP (http://lgdp.univ-perp.fr/) units.
REFUGE offers an access to the know-how and bioinformatic, biological, and molecular resources allowing hosted scientists, non rice specialists, to use rice as a model system to elucidate gene function through functional genomics strategies. Hosting of the scientists is typically carried out through one to several visits (from one week to 3 months) on the platform, REFUGE taking care of the materials produced between two visits. REFUGE wishes to become an experience-sharing site for Scientists from the North and the South.

## Objectives

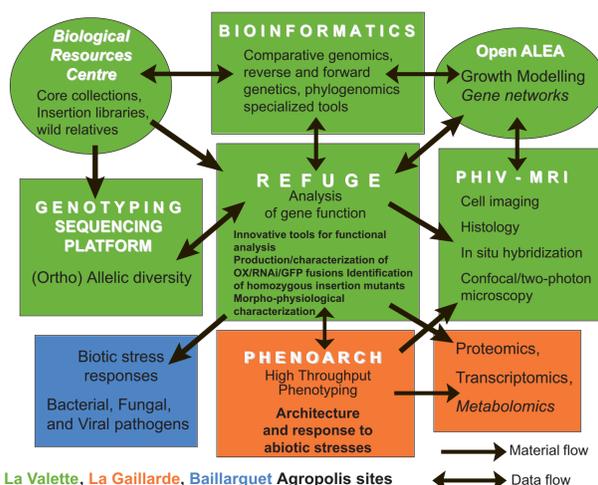The main objectives of the REFUGE platform are :
- **To enhance** the capacities of the Agropolis DAP and GDP units in hosting visitors of the international plant science community to carry on in rice the functional analysis of genes of agronomic importance, with a focus on plant development and stress response genes (Examples of hosted research projects are listed in Table 1).
- **To share** performing infrastructures, biological resources, bioinformatics and molecular tools and know-how unique in the public sector in Europe for the production and characterization of transgenic rice and insertion lines to support investigation on gene function.
- **To implement quality** in research on the platform notably through traceability of the molecular and biological materials and associated data (Figure 1).
- **To further optimize** functional genomics tools aiming at accurate DNA integration and RNA inactivation in implementing homologous recombination (HR) and artificial microRNAs (amiRNA) technologies.
- **To be an entry** node to the network of Agropolis platforms to further investigate the function and diversity of these genes and phenotyping of materials (Figure 2)

## The REFUGE Know-hows

- Bioinformatic searches
- Preparation of T-DNA vectors (inducible or constitutive overexpressor (OX) HpRNAi and amiRNA vectors, reporter gene fusions)
- High Thoughput production of rice transformants
- Molecular characterization of the transformants (Q-PCR, northern, Southern, western)
- Genotyping of insertion lines from local and international collections
- Growth, crossing and phenotyping (morphology, salinity , drought) in containment greenhouse
- Allelic variation in diversity panels (core collections)
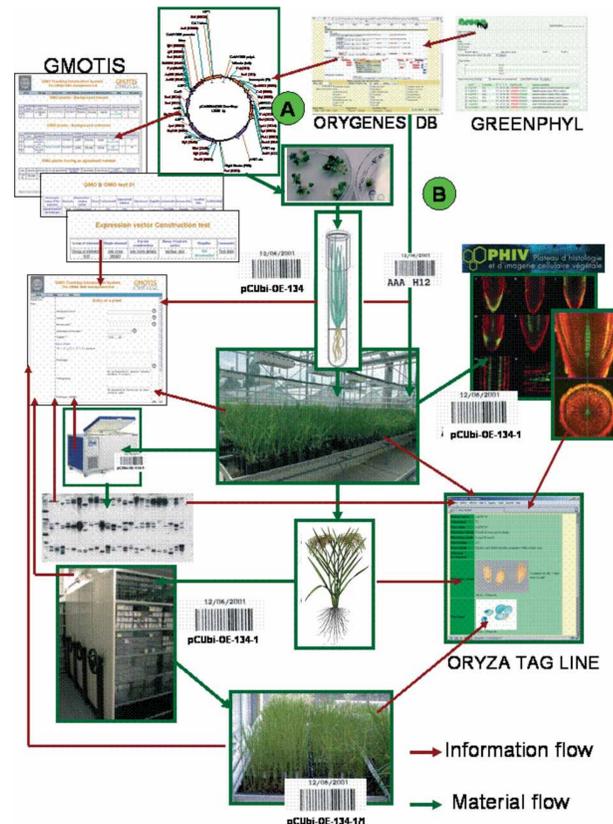- Access to Cell imaging and Genotyping platforms.



**Figure 1:**
Flow of information and materials on the REFUGE platform: The rice ortholog of an Arabidopsis gene is identified through the phylogenomics prediction tool GreenPhylDB. A. Overexpression, RNAi and GFP fusion vectors are prepared and the information related to the construct stored in GMO-TIS. Primary transformants are produced using a barcode ID that will also label the tissues collected and samples of isolated DNA/RNA samples and T1 seed stock. The GMO and related molecular characterization is documented in GMO-TIS.

Information on harvesting, destruction of substrate and plant residues through autoclaving is integrated in a central database. When T1 seeds are sown, new barcode IDs Similarly follow the materials. Information resulting from phenotype and molecular charcaterizations are gathered in the central database and transfered in the phenotype database Oryza Tag Line. GFP expression in tissues and changes in tissue organization , protein can be investigated in the nearby PHIV MRI platform. B: An insertion line is identified in the local or international collections through OrygenesDB. T1 seeds are sown and similarly followed by a barcode ID to identify an homozygous mutant exhibiting rearrangement at the target locus and WT siblings. T2 homozygous lines are examined for morphophysiological changes and later challenged with a range biotic and abiotic stresses and finely phenotyped in other Agopolis platforms (e.g.PHENOARCH).

### Table 1

| Visitor | Laboratory | Topic | Growth of insertion lines | Crossing | Construction of RNAi and GUS vectors | Genotyping | Phenotyping | Rice genetic transformation | Cotransformation | Analysis of promoter-gfp or gus-A fusions | Thesis | Publication | Patent |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Mehdi Jabnoune | BBMP, Montpellier, France H. Sentenac | HKT genes | x | x | | | | | | | x | x | |
| Odile Faivre Rampant | PTP Lodi, Italy | WRKY gene family | x | | | | | | | | | x | x |
| Le Quang Hoa | U. Polytechnique Hanoi, Vietnam | Salt tolerance | | | x | x | | | | | | x | |
| Michela Osnato | U. Milano, Italy (Pr L. Rossini) | Regulators of Bkn3 | | | x | x | x | | | x | | x | |
| Glossia Cabral | EMBRAPA, Brazil | Apomixis | x | | | | | | | | | x | |
| Véronique Planchot | INRA, Nantes, France | Sucrose synthase | | | | x | | | | | | | x |
| Jordi Quilis | CSIC Barcelona, Spain (Dr San Segundo) | Plant defense against fungal diseases | x | | | | | | | | x | x | |
| Helen Parker | U. Nottingham, UK (Pr M. Bennett) | Aux-1 and lax3 genes | | | | x | | x | x | x | | x | |
| Nampeung Anukul | U. Nottingham, UK (Pr M. Bennett) | Folate biosynthesis gene | | | | x | | | | | | x | |
| Reza Slahpoosh | MPIPMB, Postdam, Germa (Dr J. Kopka) | Invertase genes | x | | | | | | | | | x | |
| Farkhanda Khowaja | U. Aberdeen , UK (P-A. Price) | Osmotic adjustment | | | | x | | | | | | x | |
| Deyun Qui | ANU, Canberra (Dr J. Mawle) | EREChT gene family | x | | | x | | x | | | | x | |
| Alexander Johnson | ACIPG, Adelaide, Australia (Pr M. Tester) | Homeostasic genes | x | | | x | | | | | | x | |
| Rania Ben Saad | CBS Sfax, Tunisia (Dr A. Hassani) | Drought and salt tolerance | x | | x | x | x | | | | | x | |
| D. Sérène | INRA (Burkina Faso) | Analysis of silencing suppressors in rice | x | | | x | | | | | | x | |
| D. Thiélémé | Abidjan (Côte d'Ivoire) | Ryme resistance gene | | | | x | x | | x | | | x | |
| G. Djedatin | Cotonou (Bénin) | Identification of resistance genes | | | | x | x | | x | | | x | |

**Table 1:**
Programs hosted on the REFUGE platform in 2006-2008. The type of support provided in the platform ranges from simple allocation of containment greenhouse space and follow up of plant growth to a full supervision encompassing bioinformatics, vector construction, transformation and molecular characterization of OX/RNAi/ GFP-GUS fusions, and genotyping of insertion lines.

## Who can submit and how to submit a proposal?

The REFUGE platform is open to the international plant science community.
The REFUGE platform provides supervision of the hosted scientists and students and covers bench fees.
Visitors have to find their own travel and subsistence funds. However, REFUGE can provide support to scientists, notably from South countries, to find an appropriate funding source for travel and subsistence.
Due to the limited hosting capacities, research projects carried out in the platform have to be selected on the basis of their intrinsic qualities, feasibility and training dimension.
Selection is made by a scientific committee consisting in scientists of the DAP and GDP units, of other Agropolis units and of international labs.

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**Figure 2:**
Interrelationships between the REFUGE international hosting platform and the other existing Agropolis platforms. The BIOINFORMATICS platform provides support for ortholog prediction, identification of insertion lines, definition of primers, comparative genomics through genetic maps of markers/QTLs anchored on physical maps of fully sequenced genomes. Sub cellular localization of gene products, protein trafficking and interactions are further investigated on the PHIV MRI cell imaging platform, as well as changes in tissue organization in mutant/OX vs WT through two-photon imaging. PHIV MRI is linked to the Open ALEA platform which elaborates models of shape formation in meristems and investigate gene networks. Selected mutant/OX as well as of diversity panels representing allelic variation in the gene(s) under investigation -determined on the GENOTYPING-SEQUENCING (UMR DAP-DiAPC) platform using resources of the future unified Biological Resources Centre, can be further finely phenotyped on the PHENOARCH (UMR LEPSE) high throughput phenotyping platform. Phenotyping for biotic stress response can be achieved in Baillarguet and La Valette (UMR BGPI and GDP) for fungal, bacterial and viral pathogens.

To submit a proposal, go to the REFUGE web site http://www.refuge-platform.org to upload your application that will be readily examined by the scientific committee.
Further details at refuge.agropolis-fondation@cirad.fr

Centre de coopération internationale en recherche agronomique pour le développement

Conception et réalisation: Cirad - Bios Septiembre 2009