'RICE CONNECTIONS'

'Connecting the biologies of rice disease resistance, drought tolerance and flowering times'

ABSTRACT

'Drought tolerance, disease resistance and flowering time are three major traits in crops that are biologically connected. However the molecular connection nodes linking them together are poorly understood. The Riceconnections projects aims at identifying such nodes in the model system involving rice using three approaches: phenotyping under laboratory and field conditions rice mutants, gene expression analysis under combined biological conditions and identifying proteins that are connecting regulation networks involved in different biological pathways.
The first major challenge was to develop protocols where two biological processes would take place simultaneously. This was done in the case of drought and flowering time and drought and disease resistance against the rice blast fungus (Magnaporthe oryzae). As expected from literature, drought severely impacted on flowering (delay) and disease susceptibility (increased). The complex combinational protocols developed in the project were used to produce RNA for RNASeq analysis. In the case of the impact of drought on flowering, the analysis showed that drought is abolishing the transcriptional regulation of some key regulators of flowering, explaining the observed delay in flowering. In the case of the negative impact of drought on disease resistance, the analysis showed that plant immunity is almost completely abolished. More unexpected, the analysis showed that the blast fungus is changing its pathogenicity program and adapts to this new environment. In order to identify proteins that are physically connecting regulation networks, we undertook a Y2H approach. First we built a Yeast-two-hybrid library from rice tissues under different conditions (disease, drought, flowering transition). This library was then used to screen for partners of 4 proteins (starting nodes used as baits) involved in either disease resistance, drought or flowering transition. More than 200 partner proteins were identified, some of which are common to several baits; such partners are potential connection nodes between distinct regulation pathways for flowering time, disease resistance and drought tolerance.'

Keywords : Quality

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Project leader : 'Jean-Benoit Morel'
Project leader's institution : 'INRA-INRAE'
Project leader's RU : 'BGPI-PHIM'

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GOAL

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ACTION

'WP1 To establish the phenotype for disease resistance, drought tolerance and flowering time of all rice lines in the project
WP2 To establish, using gene expression studies, the regulatory connections between the targeted biological pathways
WP3 To establish connections nodes, as identified by Yeast-two-hybrid approaches and cellular imaging, between the targeted biological pathways
WP4 To integrate all information produced by the other WPs, identifying the most relevant connection hubs and demonstrating their role in the targeted biological pathways
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RESULTS

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PERSPECTIVES

'The data from the project (exression and Y2H) will be inserted into the OrygenesDB. Mutants in the genes corresponding to the starting nodes have been produced and will be evaluated for all traits targeted by the project. One expectation is to dis-connect the regulation of drought and disease resistance.'