Year of CfP: 2008

Project No 0803-013 Completed

Project title: Developing a statistical framework to study genotype and environment interactions in association studies

Units managing the project: DIAPC (Diversity and Adaptation of Cultivated Plants) (CIRAD, IRD, INRA, Montpellier SupAgro, UMII), Institute of Genomic Diversity, Cornell University, USA

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Country involved in the project: USA

Sub-thematic axis: IPB-1 (Integrative Plant Biology 1: *Genetics and genomics, plant breeding, ecophysiology*)

Objectives:

During the last five years, new promising methodologies have been developed to identify genes that play a significant role in plant adaptation: 1) methods allowing the identification of the signature of selection events in a high number of markers or genes 2) association detection between phenotypic variation and genetic polymorphism in structured populations, so called association studies.

Association studies offer new opportunities to assess the role of a particular gene on a phenotype. Compared to QTL analyses, which deal with the descent from two known parents, association studies have the advantage to take into consideration a much broader diversity, and to rely on a much more recombined material. The DIAPC laboratory is involved in the development of an association framework in pearl millet (*Pennisetum glaucum* L.) for the study of genetic basis of flowering time differences between varieties. The strategy relies on the observation of flowering time variability on the one hand, and of existing polymorphism on candidate genes on the other hand. Testing for an association between phenotypic and genetic variability requires appropriate statistical models. The current state of the art of the corresponding statistical framework allows taking into account the population structure and the existence of kinship in the population. To date, interaction terms of the model are not considered. However, genotype x environment and/or structure/kinship x environment interactions may exist, and may interfere with our ability to detect genotype-phenotype association. In addition, ignoring these interactions limits our understanding of complex traits expression.

The proposed research will lead to assess the possibility And /or limits to detect genotype x environment interaction in genetically structured populations.

Action carried-out and results obtained:

We developed a statistical model to perform association study taking into account genetic and environment interactions. A mixed linear model which uses population structure and kinship matrix to perform an association between phenotype and genotype was extended to take into account interactions with the environment. To assess the power of this new model, we simulated a thousand datasets showing a given genetic/environment interaction effect. The statistical model was then used to detect genetic/environment effect on these simulated datasets. This analysis helps understand when such interactions can be readily detected (Figure 1). Finally, we used the model on two real datasets (maize and pearl millet) and identified some flowering time gene showing significant interactions with the environment.

Prospects for the future:

The relationship between genotype and phenotype is a central question in biology. Taking into account gene/gene and gene/environment interactions is important to understand this relationship. One of the main challenges in the next years will be to adapt the model to process genome wide genetic data.

Total Agropolis Fondation funding: € 6,240 (travel expenses for a PhD student)

Funding categorie(s): Agropolis Fondation small grants (overseas travel grants for Doctoral and Post-doctoral scientists)

Project duration: 15 January 2009 – 31 December 2009

Keywords: statistics – genotype – environment – association studies