



Plant & Animal Genomes XVIII Conference

January 9-13, 2010
Town & Country Convention Center
San Diego, CA

P234 : General Comparative

Some Data On Allele Diversity At Orthologous Candidate Genes In GCP Crops

[Dominique This](#)¹, [Brigitte Courtois](#)¹, [Romain Philippe](#)¹, [Pierre Mournet](#)¹, [Claire Billot](#)¹, [Jean-Christophe Glaszmann](#)¹, [Roland Schafleitner](#)², [Reinhardt Simon](#)², [Percy Rojas](#)², [Merideth Bonierbale](#)², [Rajeev Varshney](#)³, [C. Tom Hash](#)³, [Hari Upadhyaya](#)³, [Spurthi Nayak](#)³, [Dominique Brunel](#)⁴, [Redouane El Malki](#)⁴, [Marie Christine Le Paslier](#)⁴, [Kenneth McNally](#)⁵, [Michael Baum](#)⁶, [Wafaa Choumane](#)⁶, [Maria Von Korff](#)⁶, [Matthew Blair](#)⁷, [Martin Fregene](#)⁷

¹ CIRAD - UMR DAP 1098, CIRAD TA A-96/03, Av. Agropolis, 34398 Montpellier cedex 5, France

² CIP P.O. Box 1558 La Molina, Lima 12, Lima, Peru

³ ICRISAT Patancheru, Andhra Pradesh 502 324, India

⁴ INRA, UR 1279 Etude du Polymorphisme des Génomes Végétaux, CEA Institut de Génomique/ Centre National de Génotypage, 2, rue Gaston Crémieux, CP5724, Evry F-91057, France

⁵ IRRI DAPO Box 7777 Manila 1301, Philippines

⁶ ICARDA P.O. Box 5466 Aleppo, Syrian Arab Republic

⁷ CIAT km 17 Recta Cali-Palmira, AA6713, Cali, Colombia

The ADOC project (GCP 2006-02) aimed to characterize allelic diversity at orthologous loci of candidate genes for drought tolerance in seven GCP crops (rice, barley, sorghum, bean, chickpea, cassava and potato), working on reference collections of around 300 accessions for each crop. Six gene families (ERECTA, DREB, SS, SPS, ASR and VIN) were selected as the initial subset of target genes. Except the DREB gene family, for which a specific focus has been given to DREB2A, and the SPS gene family in cereals, for which only the Os01g69030 orthology group was studied, they represent a set of relatively small gene families acting at different levels of the drought stress response (transcriptional regulation, carbohydrate metabolism...) for which a comparative analysis of gene families was undertaken. Obtaining complete gene families was easier in whole sequenced genomes like rice and sorghum. Polyploidy and heterozygosity induced difficulties in analyzing data for cassava and potato; However sequences for a few genes were obtained and analyzed for SNP diversity across all species. Population structure influenced partially haplotype patterns. A large range of haplotype diversity was found and the degrees of this differed between species. Different patterns and range of sequence diversity were found within gene families and between species for orthologous genes. For a few genes, computation of a sequence-based neutrality test suggested selection events acting at the species and/or subgroup level.

Return to the [Intl-PAG](#) home page.

For further assistance, e-mail help18@intl-pag.org