



## A Resource for Comparative Plant Genomics

Nicholas Provart, PhD  
Associate Professor, Department of Cell & Systems Biology  
Rm 3051, 25 Willcocks St.,  
Toronto, ON. M5S 3B2

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Dear Dr. Provart,

We are writing this letter as PI and co-PI of the Gramene database project ([www.gramene.org](http://www.gramene.org)) to strongly endorse your application to NSERC's Major Resources Support program for the Bio-Array Resource based at the Centre for the Analysis of Genome Evolution and Function. We are excited to collaborate with the BAR for the curation of plant-specific signaling pathways. In the current state "core" Reactome is a web-based, open-source, curated pathway database for many areas of human biology. Entries are provided by biological researchers who are experts in a specific area, and are maintained by the Reactome curatorial staff and cross-referenced to a wide range of standard biological databases, including NCBI Entrez Gene, Ensembl and UniProt databases, the KEGG Compound and ChEBI small molecule databases, PubMed, and GO. The curated human data are used to infer orthologous genes in 20 non-human species including two plant species, *Arabidopsis thaliana* and *Oryza sativa* (rice) based on the gene orthology datasets provided by the Gramene's Compara pipeline. However, to avoid the human centric projections of plant pathways in totality, Gramene project has established collaboration with Dr. Lincoln Stein, the PI on the Reactome database on delivering, managing the plant specific pathways. We are working with them to create a Plant Reactome portal for the Plant Biologists that will host the curated Reactome pathway databases for Rice and Arabidopsis and electronically annotated pathway databases for upcoming new model and reference plants. Rice is being populated from the curated metabolic network provided by Gramene's RiceCyc. The Arabidopsis data is being subsumed from its current home [www.arabidopsisreactome.org](http://www.arabidopsisreactome.org) which is likely due to lack of funds and any new development/maintenance.

While the "core" human Reactome is well-funded through the National Institutes of Health in the US, an ENFIN grant from the European Union, and the European Bioinformatics Institute, currently support for the plant Reactomes is non-existent. We would heartily welcome the BAR's contribution to the curation of these plant Reactomes, specifically in the area of signal transduction for Arabidopsis. This would be a very important contribution for plant biologists in Canada and world-wide, who are struggling to cope with the ever expanding volume of data. Besides Arabidopsis, continues to harbor the best plant model status that is being studied and has the most mature genomics and signaling pathway network datasets. Reactome provides a convenient and intuitive way of organizing genomic information into a more familiar landscape of biochemical and signaling pathways, which is vital for making sense of these large data sets. It is also capable of providing data for advanced users in various standardized formats like SBML and BioPax formats.



[www.gramene.org](http://www.gramene.org) | [gramene@gramene.org](mailto:gramene@gramene.org)

Collaboration with BAR is very timely and important because this will also leverage us to consolidate not only the curational aspects but to develop analysis tools in conjunction with BAR on creating better interfaces to overlay expression and gene-gene network datasets.

We are pleased to know that unless specified, you will be the primary contact person to work with us on this collaboration. We should note that we can only guarantee this arrangement through the end of our current round of NSF, USA funding on the Gramene database project, which is until 09/30/2011. However, we will be requesting support for plant Reactome infrastructure and curation activities in the next round of renewal funding for our project.

We wish you luck with your project and look forward to build on this collaboration.

Sincerely,



Doreen Ware USDA ARS  
PI, Gramene database project  
Adjunct Assistant Professor  
Cold Spring Harbor Laboratory  
1 Bungtown Rd.  
Cold Spring Harbor, NY 11724

Phone: 516 367-6979  
Fax: 516 367-6851  
Email: ware@cshl.edu



Pankaj Jaiswal  
Co-PI, Gramene database project  
Assistant Professor  
Dept. of Botany and Plant Pathology  
3082 Cordley Hall  
Oregon State University  
Corvallis, OR, 97331-2902, USA

Ph.: +1-541-737-8471  
Fax: +1-541-737-3573  
Email: jaiswalp@science.oregonstate.edu