



A Resource for Comparative Plant Genomics

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Dear Henning,

We are writing this letter as PI and co-PI of the Gramene database project (www.gramene.org) to strongly endorse your application to BBSRC's BBR program for the Aractome resource integrating and further curating Arabidopsis pathway data from the current Arabidopsis Reactome and Arabidopsis protein interaction datasets in IntAct and BioGRID. We are excited to collaborate with the Aractome 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, the Gramene project has established collaboration with Dr. Lincoln Stein, the PI on the Reactome database, on 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. We hope the Arabidopsis data is being subsumed from its current home www.arabidopsisreactome.org in the context of your Aractome proposal.

While the "core" human Reactome is funded through the National Institutes of Health in the US, the ENFIN grant from the European Union, and the European Bioinformatics Institute, currently support for the plant Reactomes is non-existent. We would heartily welcome Aractome's contribution to the curation of plant Reactomes, specifically in the area of signal transduction for Arabidopsis. This would be a very important contribution for plant biologists in the UK and world-wide, who are struggling to cope with the ever expanding



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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. The combination with existing Arabidopsis interaction datasets based on existing software approaches is an elegant and resource-efficient method to extend the scope of Arabidopsis pathway data, and also a promising method to support further pathway curation.

As you are aware Gramene already has a long standing collaboration working with EBI on making use of the Ensembl infrastructure for hosting plant genomes. We see the collaboration with Aractome as timely and a natural extension of our ongoing collaborations with EBI to support plant genome resources for the community. Working collaboratively with Aractome will allow us to consolidate not only the curational aspects but to support active development of plant specific views for the international plant community.

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,



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