The Plant Resistance Gene Database (PRGdb): a Wikibased system for the annotation of R-genes.

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Abstract.

The Plant Resistance Genes database (PRGdb; http://prgdb.org) is a comprehensive resource on resistance genes (R-genes), a major class of genes in plant genomes that conveys disease resistance against pathogens. Initiated in 2009, the database has grown more than 6 fold to include annotation derived from recent plant genome sequencing projects such as tomato, potato or melon.

As an example, release 2.0 hosts useful biological information on a set of 112 known and 104,310 putative R-genes present in 233 plant species and conferring resistance to 122 different pathogens. Available classification is made up from a custom pipeline called Disease Resistance Analysis and Gene Orthology (DRAGO), based on reference R-gene curated sequence data and developed to search for plant resistance genes in public datasets such as Unigene, Genbank and the Phytozome project.

As part of this effort, the hosting website has been completely redesigned with the implementation of Semantic MediaWiki technologies, which makes the repository freely accessible and more easily editable by the scientific community.

Among other features, the new website includes the possibility to browse the database according to different annotation criteria (such as host protein domains targeted by virulence factors). At the same time, the system offers the possibility of displaying as an additional section all the analyses performed over a specific putative R-gene (for instance, the BLAST reports against the reference R-genes dataset) and allows visitors to perform inquiries of their own sequences against existing database entries (including those contributed by other users). Moreover, in order to promote interest groups, users can decide to populate their profiles with their preferred bibliography.

In the end, the final purpose is to encourage plant biologist experts to join this annotation effort and share their knowledge on resistance-gene biology with the rest of the scientific community.



References

- Sanseverino, W., Roma, G., De Simone, M., Faino, L., Melito, S., Stupka, E., Frusciante, L. and Ercolano, M.R. (2010) PRGdb: a bioinformatics platform for plant resistance gene analysis. Nucleic Acids Res, 38, D814-821
- Sanseverino, W., Hermoso, A., D'Alessandro, R., Vlasova, A., Andolfo G., Frusciante, L., Lowy, E., Roma, G. and Ercolano, M.R.: PRGdb 2.0: towards a community-based database model for the analysis of R-genes in plants. In press.