

# Drastic: A Database Resource for the Analysis of Signal Transduction In Cells

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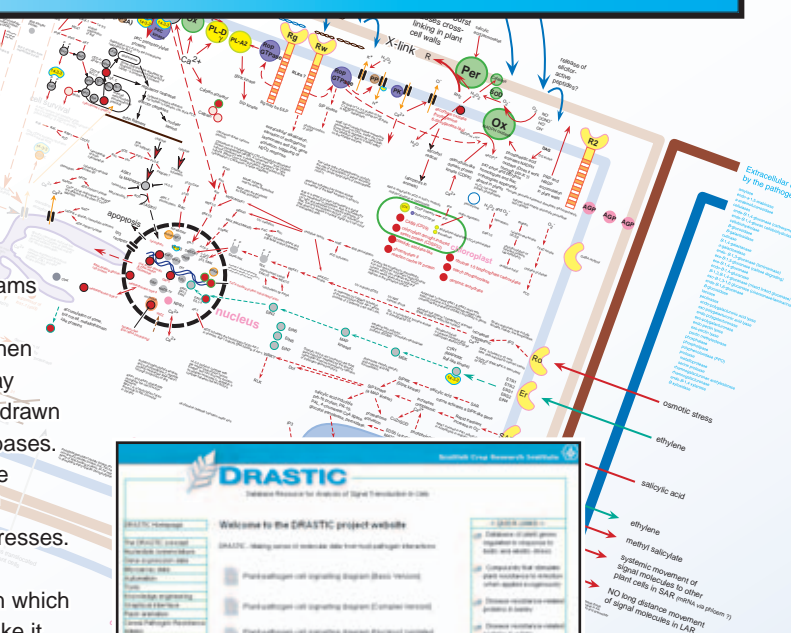
**DRASTIC**  
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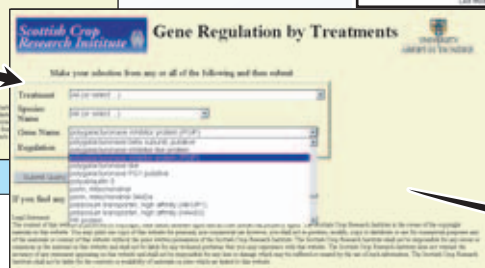
Although there has been an explosion in data acquisition regarding the molecular biology of plant-microbe interactions in recent years our understanding of the implications of that data has not been fully exploited. As a consequence of this data swamp much published information on plant gene expression is ignored or 'lost'.

Whilst we have been able to draw 'static' cell signalling diagrams containing a limited amount of (sometimes speculative) information such diagrams are going to be of limited value when interpreting the large amounts of data derived from microarray experiments. Thus, in future, we expect such diagrams to be drawn dynamically in response to a query and to be driven by databases. To this end we have been acquiring information on plant gene expression data and will use it to drive 'dynamic' diagrams of molecular responses of plants to various biotic and abiotic stresses.

We have therefore set up a web site at [www.drastic.org.uk](http://www.drastic.org.uk) on which we are attempting to summarise some of this data and to make it available through a searchable database.



Result of searching for information on PGIP



## The database

The database currently contains approximately 8,000 entries covering >260 treatments and >52 plant species. Information on these 'stress-responsive' genes is being added regularly to the database by taking information from published papers with, predictably, most information being derived from *Arabidopsis thaliana*.

## Accession numbers

The importance of providing accession numbers rather than primer sequences in papers is demonstrated by the fact that the putative identification of some ESTs has changed markedly over the years.

## Unknown genes

14.17% of entries in the database are described as 'unknown' function. The database is useful for linking together information on ESTs described as genes of unknown function. For example, by converting accession numbers into AGI numbers we have shown that the following ESTs that are down-regulated by chitin (H37231, R90140, T41806), drought (AV823744), ethylene (R90140), low oxygen (At2g10940), or sodium chloride (AV823744), or up-regulated by salicylic acid (R90140, H37231) are all the same gene i.e. At2g10940.

## Data input

We are currently working on a 'submissions page' to permit remote input of gene expression data.

## Gene classification

A Nucleotide Function Code (Lyon et al., 2002) that would provide a unique identifier to genes and which would contain information related to the function of that gene would be of great benefit in 'data mining'. Such a code number would enable true comparisons of gene function to be made across species in a manner analogous to current EC numbers for proteins. We believe that such a concept has currently been rejected as 'too difficult to implement' but for the long term benefit should be reconsidered.

## References

Lyon GD, Newton AC and Marshall B. 2002. The need for a standard nomenclature for gene classification (a Nucleotide Function Code) and an automated data-based tool to assist in understanding the molecular associations in cell signalling in plant-pathogen interactions. *Molecular Plant Pathology*, 3, 103-109.

## Acknowledgements

GL, AN and BM are grateful to SEERAD for funding