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2010 : January 2010 - New Hot Papers : Yukihisa Shimada Talks About the AtGenExpress Consortium

NEW HOT PAPERS - 2010

January 2010

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Yukihisa Shimada talks with *ScienceWatch.com* and answers a few questions about this month's New Hot Paper in the field of Plant & Animal Science.

Article Title: The AtGenExpress hormone and chemical treatment data set: experimental design, data evaluation, model data analysis and data access
Authors: Goda, H., *et al.*
Journal: PLANT J, Volume: 55, Issue: 3, Page: 526-542, Year: AUG 2008
* RIKEN, Plant Sci Ctr, Kanagawa 2300045, Japan.
* RIKEN, Plant Sci Ctr, Kanagawa 2300045, Japan.
* Nagoya Univ, Sch Agr, Mol Microbiol Lab, Chikusa Ku, Nagoya, Aichi 4648601, Japan.
(addresses have been truncated.)

Why do you think your paper is highly cited?

SW:

As part of an international research effort, the AtGenExpress consortium was organized to make an important contribution to the scientific community by the accumulation of large-scale transcriptome datasets. This data has been available without charge for public access since 2004.

Together with the other contributions of the AtGenExpress project, our dataset composes a large-scale transcriptome database. This data constitutes one of the earliest infrastructures made freely available for public access for conducting systems biology in multicellular organisms across a very large scale.

Does it describe a new discovery, methodology, or synthesis of knowledge?

SW:

One purpose of this study was to establish a comprehensive database in order to facilitate gene-expression pattern searches. However, another and more ambitious motivation was to analyze genome-wide co-expression in *Arabidopsis,* so that the functions of unknown genes can be predicted based on similarities between their expression patterns and those of known genes.

Until quite recently, in the eukaryotes, the only and most reliable approach to predict the functions of unknown genes was to conduct an analysis of the amino acid sequence of the encoded protein, such as homology analysis or motif analysis of the amino acid sequence.

On the one hand, in the prokaryote genome, functionally related genes form an operon structure, in order to maintain coordinated expression of the genes in the operon. Since the genes included in the identical operon participate in the same biological functions, operon structure is an important clue used to identify the gene's function, especially when there is no clue from the amino acid sequence alone.

In general, since no general rule has been yet found between a gene's function and their chromosomal positions in the eukaryotes, it is impossible to predict a gene's function from the positional relation of the gene in the genome.

"Our data and model studies will be useful in many of the aspects of biological studies, such as gene hunting, systems biology, and hormone studies"

Would you summarize the significance of your paper in layman's terms?

SW:

We analyzed global gene expression in *Arabidopsis* in response to various hormones—auxin, cytokinin, gibberellin, brassinosteroid, abscisic acid, jasmonate, and ethylene—and in related experiments as part of the AtGenExpress project. This was reported for the first time in plants. Hormone-inducible genes were identified from the hormone-response data.

We also analyzed relationships among the expression profiles of hormone response and those included in the AtGenExpress stress response, using a correlation coefficient. This approach was useful in monitoring the hormonal status of stress-related samples.

Genome-wide transcriptional gene-to-gene correlations were also analyzed, and the result indicated that our dataset is useful when used to find clusters of co-expressed genes, and also to predict the functions of unknown genes. The dataset presented here will be a versatile resource for future hormone studies and constitutes a reference of genome-wide gene expression in *Arabidopsis*.

How did you become involved in this research, and were there any problems along the way?

I began my transcriptome studies of plant hormone actions at RIKEN. This work has been supported by a RIKEN Plant Science Center (PSC) project. Many collaborators have also supported this project, and their contributions were of great value. I would therefore like to take a moment to express my profound appreciation for their efforts.

Where do you see your research leading in the future?

Our data and model studies will be useful in many of the aspects of biological studies, such as gene hunting, systems biology, and hormone studies.

Do you foresee any social or political implications for your research?

We are currently developing a system to help us to discover a drug that regulates hormone actions based primarily on our genomics data. This study may assist in the development of a novel agricultural technology.

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