



Welcome !

- Education and Training in 'Omics' Sciences
- Demonstration of on-line 'Omics' resources
- Hands on lab of modern Proteomics

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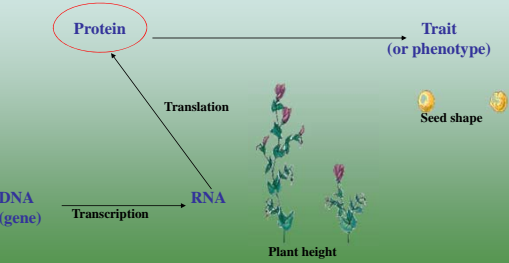
Outline



- What is modern and future biological sciences ?
- Large scale biology – 'Omics': revolution in screening important traits and creation of 'in silico' organisms
- 'Omics' modules – example of proteomics in addressing the differences in control and pathogen infected tomato leaves

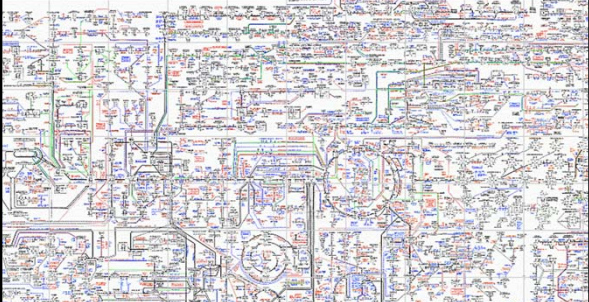
Central Dogma of Molecular Genetics

(The guiding principle that controls trait expression)



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graph LR; DNA["DNA (gene)"] -- Transcription --> RNA["RNA"]; RNA -- Translation --> Protein["Protein"]; Protein --> Trait["Trait (or phenotype)"]; Trait --- PlantHeight["Plant height"]; Trait --- SeedShape["Seed shape"];
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Traits and Phenotypes are Controlled by Molecular Networks




Trying to understand life without knowledge of biochemical network would be like trying to understand Shakespeare without knowledge of English grammar.

Our Problems

- That one gene encodes one protein, which catalyzes one reaction and determines one phenotype is no longer the case.
- Manipulating one gene can cause pleiotropic effects.
- How to capture all molecules and their interactions, dynamics, regulations and turnover ... ?
- How to determine the rate-limiting molecule and step ? How to predict ?

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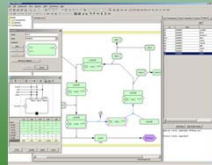
'Omics' and Systems Biology

• "Omics"

- Genomics – the comprehensive study of whole sets of genes & their interactions (DNA microarrays)
- Proteomics - the study of the full set of proteins encoded by a genome
- Metabolomics - the comprehensive study of the small molecules or metabolites
- Bioinformatics - the application of computer & statistical techniques to the management of biological information

Systems Biology-

"An interdisciplinary approach for integrating experimental data with mathematical modeling tools to analyze & predict the behavior of biological systems." (Henson, 2005)



Starvation: Importance of Cassava

Cassava (*Manihot esculenta*) - yucca, manihot, tapioca

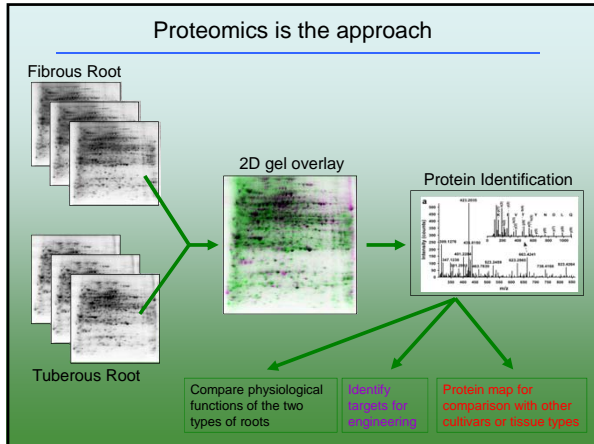
- cultivated in tropics and sub-tropics for its edible storage root
- a major source of dietary energy for more than 700 million people
- source for a variety of food stuffs, animal feed and industrial products
- major component in micro-economies of more than 150 countries

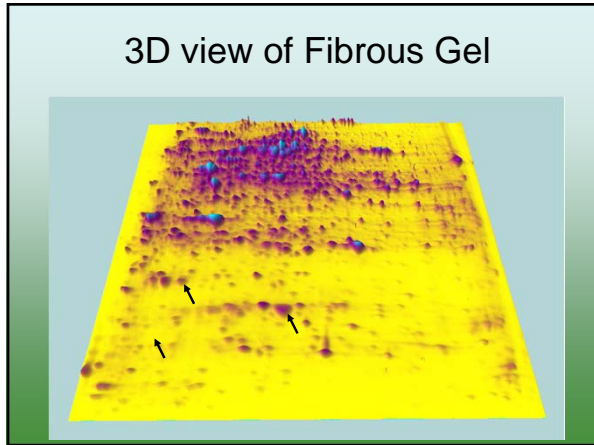


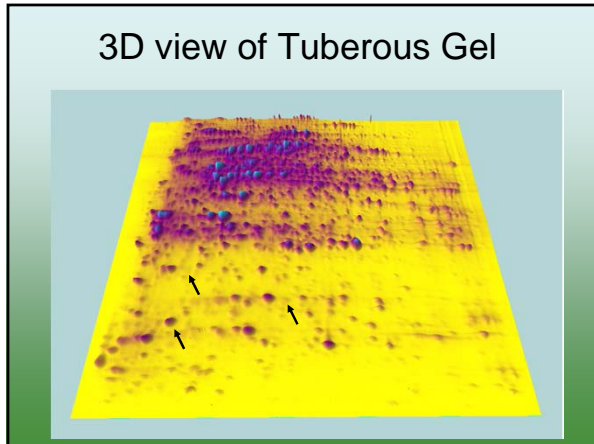
Cassava tuberous roots developed from fibrous roots

- Tuberous roots develop from fibrous roots through massive cell division and differentiation of parenchyma cell of the secondary xylem
- Not all fibrous roots are designated for tuberous root formation



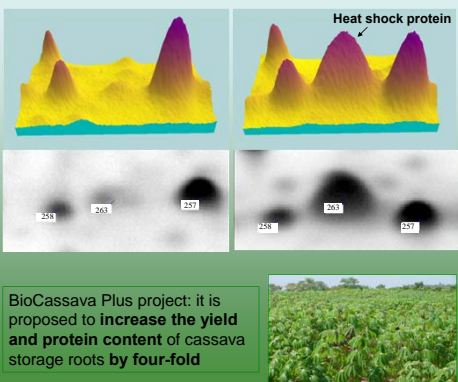








Novel Targets for Biotechnological Application



Heat shock protein

BioCassava Plus project: it is proposed to **increase the yield and protein content of cassava storage roots by four-fold**

The slide features a 2x2 grid of images. The top row shows 3D surface plots of protein abundance, with the right plot labeled "Heat shock protein" and an arrow pointing to a prominent peak. The bottom row shows corresponding 2D mass spectrometry spots, with labels 258, 263, and 257. To the right is a photograph of a cassava field.

The cover of the journal "PROTEOMICS" issue 5'06. The title "PROTEOMICS" is in large white letters on a red background. Below it is the website "www.proteomics-journal.com" and the issue number "5'06". A list of topics includes Technology, Cell Biology, Microbiology, Plant Proteomics, Animal Proteomics, and Clinical Proteomics. The cover features several illustrations: a cassava plant, a 2D mass spec spot array, and a 3D surface plot. The Wiley-VCH logo is at the bottom. A note states: "Cover Illustrations have kindly been provided by Sixue Chen, Proteomics and Mass Spectrometry Facility, Donald Danforth Plant Science Center, St. Louis, MO, USA." The ISSN and issue information are at the very bottom.

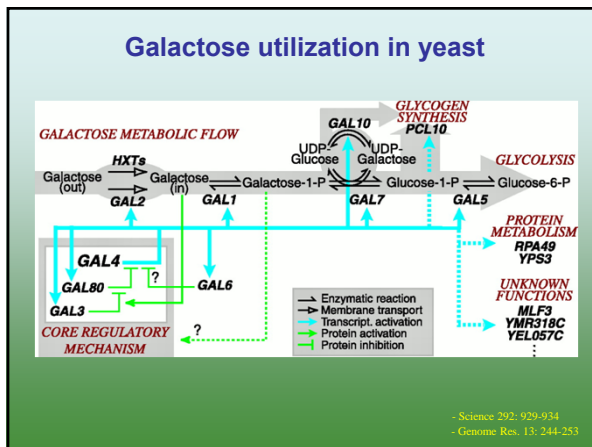
Galactose utilization in yeast

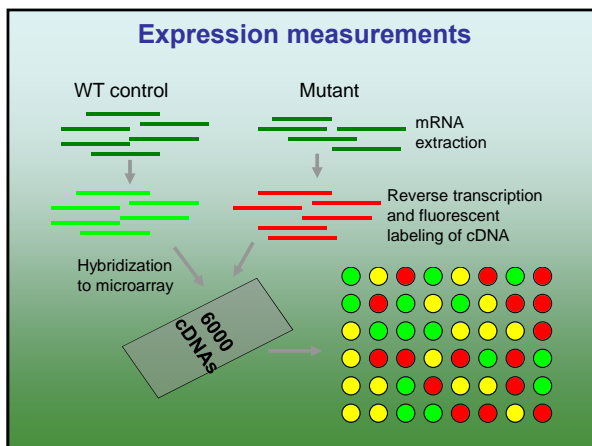
Strategy

- For each gene or condition change (i.e. delete the gene) and measure the global effect on both mRNA and protein levels.
- Integrate mRNA and protein responses with the pathway model and with global network of protein interactions.
- Formulate new hypotheses to explain novel observations and refine models.

- Science 292: 929-934 (galactose utilization)
 Combines literature knowledge, microarray, proteomics, visualization, and network techniques to refine what is known about galactose utilization in yeast.

- Genome Res. 13: 244-253 (Genome scale network reconstruction)

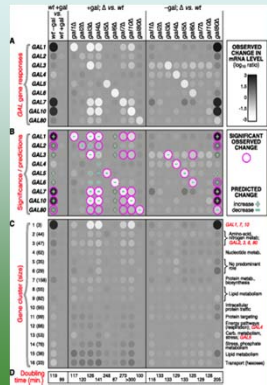




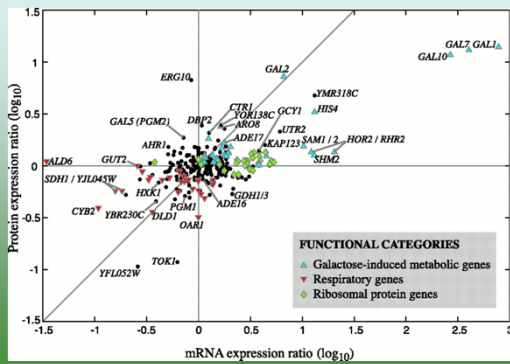
Expression measurements

Microarray:

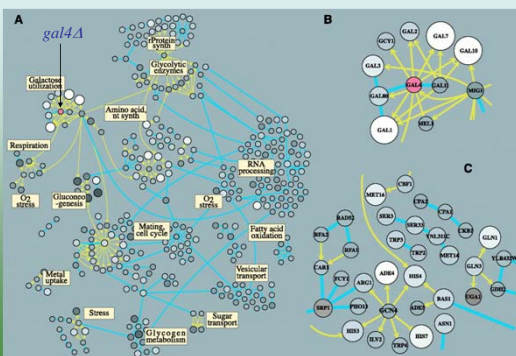
- a perturbed strain vs. wt + gal, 4 replicates
- statistics: maximum-likelihood estimation → 997 significant genes → 16 clusters by self-organizing maps, each cluster contains genes with similar responses over all perturbations.



Expression measurements



Visualizing the data



- Blue line (p-p); Yellow line (p-d); node diameter scales with the magnitude of change

More Systems Biology to follow...



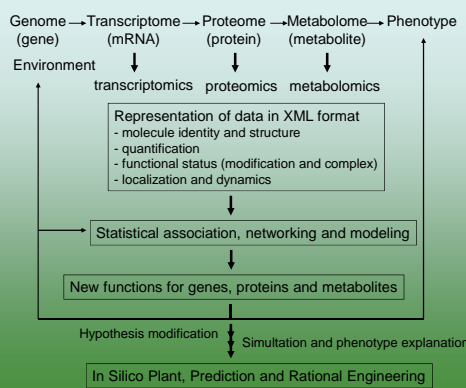
Multiple High-Throughput Analyses Monitor the Response of *E. coli* to Perturbations
 Nobuyoshi Ishii, et al.
 Science 316, 593 (2007)
 DOI: 10.1126/science.1132067

Multiple High-Throughput Analyses Monitor the Response of *E. coli* to Perturbations

Nobuyoshi Ishii,^{1,2,*} Kenji Nakahigashi,^{1,2,*} Tomoya Baba,^{1,2,3} Martin Robert,^{1,2,*} Tomoyoshi Soga,^{1,2,4} Akio Kanai,^{1,2,4} Takashi Hirasawa,^{1,2,*} Miki Naba,² Kenta Hirai,¹ Aminul Hoque,^{1,2} Pei Yee Ho,³ Yuji Kakazu,¹ Kaori Sugawara,¹ Saori Igarashi,¹ Satoshi Harada,¹ Takeshi Masuda,^{1,2} Naoyuki Sugiyama,⁶ Takashi Togashi,¹ Miki Hasegawa,¹ Yuki Takai,³ Katsuyuki Yugi,^{1,2} Kazuharu Arakawa,² Nayuta Iwata,^{1,2} Yoshihiro Toya,^{1,2} Yoichi Nakayama,^{2,4} Takaaki Nishioka,^{1,2,7} Kazuyuki Shimizu,^{1,2,5} Hirotsada Mori,^{1,2,7} Masaru Tomita^{1,2,4†}

Analysis of cellular components at multiple levels of biological information can provide valuable functional insights. We performed multiple high-throughput measurements to study the response of *Escherichia coli* cells to genetic and environmental perturbations. Analysis of metabolic enzyme gene disruptants revealed unexpectedly small changes in messenger RNA and proteins for most disruptants. Overall, metabolite levels were also stable, reflecting the rerouting of fluxes in the metabolic network. In contrast, *E. coli* actively regulated enzyme levels to maintain a stable metabolic state in response to changes in growth rate. *E. coli* thus seems to use complementary strategies that result in a metabolic network robust against perturbations.

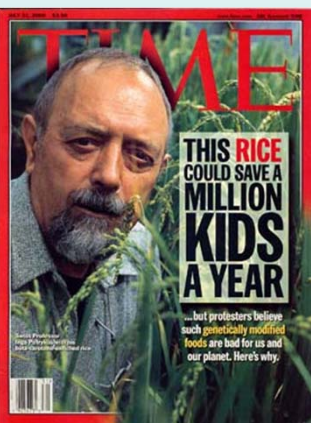
Systems Biology Scheme






"Golden Rice"

Over 120 million children worldwide are deficient in vitamin A. Rice has been engineered to accumulate β-carotene, incorporation of this trait into rice cultivars and widespread distribution could prevent 1 to 2 million deaths each year.

Vitamin A deficiency is a serious problem
 • Causes blindness
 • Influences severity of diarrhea, measles



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Thank you !



