Invited Talk

Integrative analysis of transcriptome and metabolome data

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Abstract

Biological systems have to react to environmental and/or developmental changes by adjusting their biochemical/cellular machinery on numerous levels. In many cases small molecules play a crucial role as signal molecules transmitting changes in state to receptor molecules which subsequently translate this into changes on various levels of the realization of genomic information.
We here start out from the hypothesis that in most biological systems there are many more small molecules which also serve a signalling function than generally acknowledged. This hypothesis is based on three simple arguments, which present limitations in classical approaches to detect signalling molecules:

- In order to identify a signalling molecule one has to be able to monitor the response of the system under study towards this signal
- In order to identify a signalling molecule one has to be able to detect and quantify this molecule
- A third important point to consider is the fact that in many cases test for signalling molecules were performed by externally applying the putative signal molecule to the system. It is obvious that further problem linked to uptake and mobility of the compound arise during this approach.

We therefore set out to design an experiment where we tried to largely overcome these three limitations.
As to the response of the system we decided to use the transcriptional response as a read-out.

As to the second and third limitation, we decided to rather monitor endogenous changes of small molecules. To this end we applied metabolomics techniques for analysing the state of a system which at least in an ideal world should allow the quantification and identification of all small molecules present in the biological system.
We here present a first set of data resulting from a large experiment where the response of a plant system (leaves of *Arabidopsis thaliana*) as a function of numerous environmental conditions applied has been followed in parallel on both analytic levels described above, i.e. RNA expression and metabolite profiles.

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