Systems Biology of the Grapevine

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During recent years, an increasing amount of genomics data has been released within the grapevine community, including a significant share from our laboratories (1, 2, 4, 5, 6). The next critical challenge is to annotate the recently released grapevine genome and adapt existing interpretive tools of model species to the specificities of the grapevine genome. Having grapevine specific tools will increase the power and speed of genomic and systems biology data analysis. Our goal is to develop and validate a database of the molecular networks occurring in the grapevine. This tool will allow the visualization of the changes of the transcriptome, proteome and metabolome within molecular networks (for example, metabolic or signal pathways), during a given experiment.

Material and methods
Gene features were assigned to an EC number or an orthology number, which is used by the KEGG: Kyoto Encyclopedia of Genomes and Genes (www.genome.ad.jp/kegg) for regrouping orthologous genes. Assignment was made by blasting genes against various databases (GeneBank, UniProt, Swiss-Prot, KEGG, the Arabidopsis and the rice genomes) and manually curating the annotation. The initial approach for the construction of metabolic pathways was to download xml files from the KEGG website and to convert them into systems biology markup language format (SBML). Genes and mRNA were then placed onto respective pathways with the Cell Designer software (www.celldesigner.org). For processes not present in KEGG, pathways were built using biochemical literature.

Results and discussion
The gene sequences from the French-Italian Public Consortium for Grapevine Genome Characterization (6), EST data assembled at the Dana Farber Cancer Institute (http://compbio.dfci.harvard.edu) and non-vinifera sequences have been matched for determining unique sequences, leading to 39,423 unique potential genes and proteins. Amongst them, 7,265 genes have been assigned to 107 pathways, including: 86 metabolic pathways, 3 transporter pathways, 9 genetic information processing pathways, and 9 signal pathways focused mainly on phytohormone signaling.

A beta version of the molecular networks based on manual annotation of genome and EST sequences, existing Arabidopsis thaliana pathways and biochemical literature will be displayed online through the METNET database (http://metnet.vrac.iastate.edu/). This database allows expert users to curate the pathways through an internet portal. In addition, the pathways can be exported in xml format and subsequently used in Cytoscape (http://www.cytoscape.org/) for quantitative pathway analysis and identification of co-regulation networks of genes.

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