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Poster presentation

A systems biology approach to modelling tea (*Camellia sinensis*)

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Abstract

Tea manufacture induces a variety of stresses that affect tea quality. We are using microarray data to track transcriptional changes occurring during wounding and withering of the leaves to identify metabolic pathways that could influence tea aroma and flavour. Current transcriptomic approaches include the use of a partial, tea-specific array. In order to monitor a larger number of genes we have performed cross-species analyses using Affymetrix *Arabidopsis* genome arrays [1]. *Arabidopsis* metabolic SBML [2] network data from AraCyc [3], KEGG and Reactome were collated and merged, then subsequently overlaid with the tea expression data. Subnetworks were constructed by connecting the shortest paths between the differentially expressed genes and the downstream aroma-related compounds, therefore identifying the pathways involved in aroma.

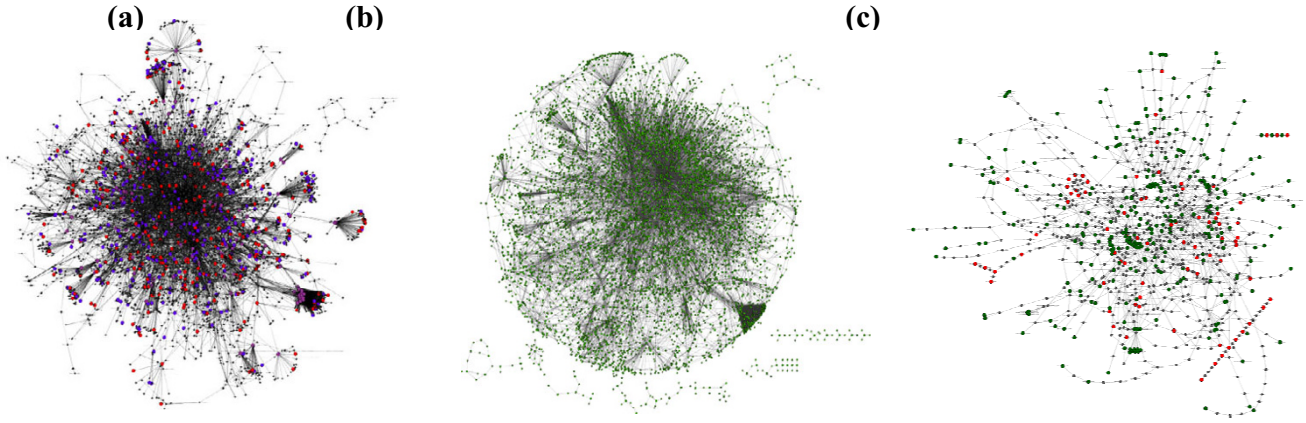

Figure 1

This figure shows Cytoscape [4] layouts of (a) the merged AraCyc, KEGG and Reactome network, (b) the AraCyc metabolic network with gene identifiers, (c) the subgraph extracted based on the tea wounding and withering expression data [identified by green nodes] connected to tea aroma related compounds [identified by red nodes].

Conclusion

We present the initial output of this project and address how cross-species expression data can be used to colour a network and analysed using a variety of subgraph analyses.

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