

Oral Communication Abstract – 6.01

TELL ME WHO YOUR FRIENDS ARE AND I'LL TELL WHAT GENE YOU ARE

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Metabolic control analysis has several interesting implications for (plant) biotechnologists, the main one being that the parallel activation of enzyme activities is the best strategy to modulate metabolic fluxes. We explored publicly available expression data from microarray measurements (Affimetrix) of *Arabidopsis thaliana* to highlight the parallel activation of transcripts. We analysed mainly genes coding for enzymes or signal transduction players and shall provide one example each (Menges et al. (2008) *New Phytologist* 179: 643–662 and Beekwilder et al. (2008) *PLoS ONE*. 3:e2068).

I demonstrate that correlation analysis can be a powerful tool for gene function discovery, at least in several specific cases. The method's limitations and the reasons for failing in providing predictions for many other genes are discussed. Apart from trivial causes (mRNA does not equal protein and protein does not equal activity), the limited spatial resolution of the collected samples and the limited temporal resolution of the statistical analysis are presumably the main reasons for the low success rate. This leaves, however ample room for improvement.

Finally, a plea for a different perspective of control in metabolic pathways is put forward (Morandini P. (2009) *Rethinking Metabolic Control*, *Plant Science*, 176:441-45).