

Evidence of neutral transcriptome evolution in plants – a cautionary tale for comparative transcriptomics

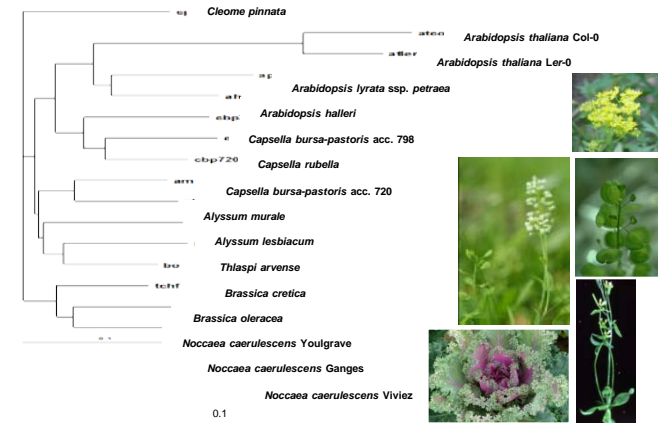


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An organism's transcriptome is highly dynamic and varies markedly in response to environmental perturbations and during development. It has been assumed that transcriptome evolution, *differences in transcription between the transcriptomes of different species*, is dominated by positive adaptive phenotypic selection. An alternative theory states that neutral evolution plays an important role (Khaltovich *et al* 2004 PLoS Biology, 2, 0682-0689). Here we show that neutral evolution plays a role in transcriptome evolution among 14 members of the Brassicaceae.

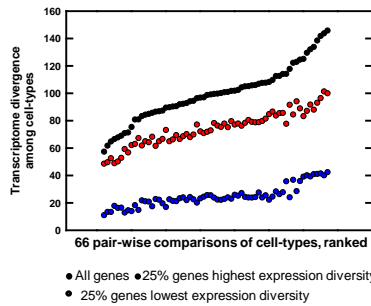
Phylogenetic reconstruction from genomic DNA hybridisations

Genomic DNA was hybridised to the ATH1 array. After probe selection, 18,494 probes sets were retained and used in the RNA analysis; these hybridisations can also be used to reconstruct the Brassicaceae phylogeny in a very simple and accurate manner



Transcriptome divergence among tissues

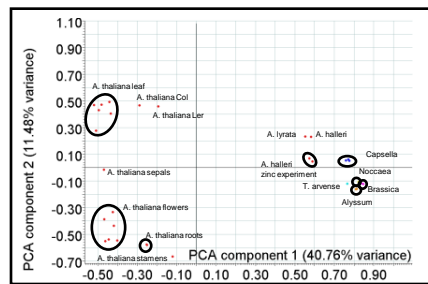
Neutral evolution should also apply at the tissue level. Data from 12 zones of the Arabidopsis root (Benfey & colleagues) using 66 pair-wise comparisons



- Genes with high expression diversity among samples diverged at a faster rate between tissues

Transcriptome divergence between tissues

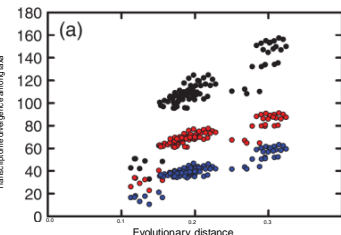
Additional transcript data for leaf and flowers, including sepals and petals, analysed from *Arabidopsis thaliana* (AtGenExpress; Schmid *et al.* 2005, *Nature Genetics*, 37, 501-506). Leaf samples from zinc experiment using *Arabidopsis halleri* (Filatov *et al.* 2006, *Molecular Ecology*, 15, 3045-3059)



- PCA 1 separates taxa
- The *Arabidopsis thaliana* leaf is more generally similar to same species root than leaves from other species.

Transcriptome divergence between taxa

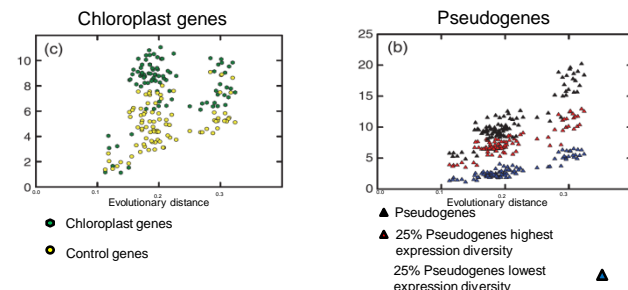
Triplicate samples from non-senescing leaves were hybridised to the ATH1 and filtered based on gDNA hybridisation thresholds. Transcriptome divergence (variance among taxa) and expression diversity (variance among replicates) was calculated.



- Transcriptome divergence correlates with evolutionary distance
- Genes with higher expression diversity have higher divergence among taxa

Chloroplast genes and pseudogenes

Chloroplast genes and pseudogenes show the same pattern, transcriptome divergence correlates with evolutionary distance.



Conclusions

- Neutral transcriptome evolution is evident in plants
- DNA hybridisations can be used to reconstruct phylogeny
- Transcriptome divergence correlates with evolutionary distance and expression diversity
- Expression diversity in root samples correlates with divergence among tissues.
- Principal Component 1 separates taxa but minor Principal components separate samples based on tissue type, environmental effects, and others.



The University of Nottingham