

P023 Translational state array analysis of *Arabidopsis* cell cultures: effect of growth stage and cellular polyamine levels

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We have used translational state array analysis to evaluate global ribosome loading in *Arabidopsis thaliana* cell cultures. Extracts from log-phase cells (2 days post subculturing) and cells entering stationary phase (7 days post subculturing) were fractionated on sucrose density gradients, and RNA from fractions 1 to 8 ('subpolysomal') and 9 to 20 ('polysomal') were pooled together and used to interrogate Affymetrix whole genome *Arabidopsis* microarrays. Of the 8,638 genes scored as 'present' in all samples, 974 showed a migration from the subpolysomal to polysomal fraction between log-phase and stationary phase, suggesting translational up-regulation, whilst 722 genes appeared to be translationally down-regulated at stationary phase.

The experiment was repeated with cell cultures grown to log- and stationary phase in the presence of added polyamines. In log-phase cells, of the 10,728 genes scored as 'present' in all samples 2 were translationally up-regulated, and 39 were translationally down-regulated in response to polyamines. At stationary phase, 8,039 genes were 'present' in all samples, 220 were translationally up-regulated, and 345 were translationally down-regulated in response to polyamines. Amongst the down-regulated genes, the most abundant functional class (approximately 20%) was protein synthesis.