

7 Conclusions

- 1) cDNA array was prepared and used to assay transcript abundances of 376 selected *Arabidopsis* transcripts following various treatments with MMS.
 - a) LoTrEC, clustering algorithm based on local trends of expression profiles, was designed and applied to the data. It succeeded to discover functionally relevant clusters of expression profiles.
 - b) Transcriptional responses to various MMS treatment regimes were investigated. While high MMS concentration seemed only to induce nonspecific stress reaction, the low and combined MMS resulted in a set of more specific expression changes.
 - c) Expression levels of five transcripts were estimated by qRT-PCR. Trends of most of the profiles were confirmed.

- 2) Expression of 3 genes related to drought stress and/or response to cytokinin were measured by qRT-PCR in wild type and *ZOG1* transgenic plants. Transcript levels of all the genes were altered by water deficit.
 - a) Although there are no significant macroscopic differences between wild type and *ZOG1* transgenic plants, the mRNA abundances appeared to be influenced by the genotype.
 - b) Leaf position (age) significantly influenced the expression of *cig1* and *ZOG1* driven by *SAG12* promoter.
 - c) RT primed with oligo-dT appeared more efficient than random hexanucleotide-primed reaction for 3 out of 5 mRNAs (*ZOG1*, *Tac9* and *NtERD10B*). The other two genes (*cig1* and *CRK1*) showed marginally more efficiency in random-primed RT.