EXPRESSION LEVEL AND GENE STRUCTURE IN *ARABODIPSIS THALIANA* AND *ORYZA SATIVA*

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The relationships between gene structure and expression profiles were investigated in the dicot *Arabidopsis thaliana* and the monocot *Oryza sativa* genomes. Gene structure was described in terms of introns/exons number and average length, and SSR content (e.g. number, type and length).

Expression levels and profiles were retrieved from published microarray datasets in their raw format and re-elaborated by the use of available and *ad hoc* developed bioinformatic tools. Genes were first classified in HK (housekeeping) and NHK (non-housekeeping) depending on their tissue expression profile. Within such categorization, the differences between highly and low expressed genes were further investigated.

The results are presented contrasting the coding (CDS) *versus* non-transcribed regions (5'-UTR and 3'-UTR), and the whole mRNA *versus* the corresponding introns.