REFERENCE GENES SELECTION FOR GENE EXPRESSION STUDIES IN BARLEY AND GRAPE

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Advanced gene expression analysis methods, such as microarray and real-time RT PCR, require efficient normalization approaches to be really informative. Normalization means to adjust expression data for effects arising from the lab technology applied rather than from real biological differences among samples. Inhibitory factors in the tissues, loading errors, integrity of the RNA are just some of the parameters to be taken into account during the quantification process. Therefore, expression results are now normalized against a set of reference genes that should be expressed in an unchanging fashion regardless of experimental conditions. However, in plants, there are just few examples of studies specifically concerned with housekeeping gene expression analysis and very often they are focused on validation of a list of literature based reference genes in the experimental condition of interest.

In our work, an EST based approach has been developed to identify novel candidate housekeeping genes in two plants of great economic concern, like barley (Faccioli et al, 2007) and grape, for which EST databases are publicly available. A set of reference genes has been identified for both species, their expression stabilities have been measured in different experimental conditions through RT qPCR analyses and the results obtained have been evaluated with dedicated bioinformatics tools.

Reference