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HOUSEKEEPING GENE SELECTION *VIA* LARGE-SCALE, "IN SILICO" ANALYSIS OF THE PLANT TRANSCRIPTOME

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Quantitative analysis of gene expression using techniques like RT-Real-time PCR has proven to be a powerful tool for functional genomics. However, to be really informative, RT-PCR results are usually referred to an endogenous control and traditionally housekeeping genes have been employed for such normalization. Actually, since the utilization of single housekeepers can't assure a not-biased result, new normalization methods employing multiple housekeeping genes and normalizing using their mean expression have been recently proposed. Moreover, because there isn't a gold standard gene suitable for every experimental condition, it is also necessary to validate the expression stability of every putative control gene on the specific requirements of the planned experiment. As a consequence, finding a good set of reference genes is for sure a non trivial problem requiring quite a lot of lab-based experimental testing.

Herein we suggest an agile approach, based on *in silico* analysis of plant transcriptome, for the rapid identification of a starter set of candidate reference genes and, in order to assess their value as internal controls, we provide, as an example, an application of this procedure to the analysis of tissue modulation of gene expression in barley.