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PERFORMANCE ASSESSMENT OF DIFFERENT MICROARRAY GRAPE DESIGNS

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Vitis vinifera, ROC, sensitivity ,specificity, significantly differentially expressed genes

The recent development of transcriptomic approaches based on Next Generation Sequencing is gaining popularity as they provide a genome-wide, precise, quantitative measure of gene expression. However microarray still are a valuable tool for differential gene expression studies as they are cheap, easy to manage and to analyze. In this work we have assessed the performances of two microarray platforms (Combimatrix and Nimblegen) and two strategies of probe design (single or multiple probes per transcript) in gene expression analysis across two *Vitis vinifera* berry developmental stages. The same samples were analyzed by RNASeq analysis using an Illumina GAIIx sequencer. In order to assess sensitivity and specificity of the four microarray designs in detecting significantly differentially expressed genes, assuming RNASeq data as reference, Receive Operating Characteristic (ROC) analysis has been performed. Such analysis showed that, disregarding the microarray platform used, array designs with multiple probes per transcripts allow to detect an higher number of differentially expressed genes and exhibit a better agreement with RNASeq data. Moreover the analysis performed showed that sensitivity of the four microarray designs in regard to RNASeq data augment with the increase of expression levels detected by the Next Generation Sequencing (NGS) approach. This data suggest that most of the differences in detecting differential expression between the two approaches is due to the lower sensitivity of microarray for low expressed genes. In order to validate the results and explain discrepancies among the approaches, a set of genes whose expression is in agreement or disagreement among microarray and RNASeq, has been tested by qPCR analysis.