

PLANT FUNCTIONAL GENOMICS CENTRE: CURRENT STATUS AND FUTURE PLANS

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The Plant Functional Genomics Centre, located at the University of Verona, is a structure devoted to the development of cutting edge technologies for the study of functional genomics. After one year and half of activity the Centre is acquiring a leading position in the genome wide transcriptomics analysis. As a member of French-Italian Consortium for the structural and functional characterization of the grape genome, the Centre is carrying on the development of the microarray reference platform for *Vitis vinifera* transcriptome analysis. Moreover, many collaborations have been already established at national and international level for the study of transcriptome in plants, animals and prokaryotic organisms.

The Centre is based on Combimatrix microarray platform which is characterized by an electricity driven *in situ* synthesis technology of 35-40mer oligonucleotides which allows an extreme flexibility in custom chip design. Different versions of the chip are available with 90.000, 12.000 or 4 x 2000 spots for different applications. This innovative technology allows the reuse of the chip up to 4-5 times, with a significant reduction of the analysis costs. We have established a reliable protocol from sample labeling to data analysis both for transcriptome analysis and for the analysis and validation of miRNAs. To assess the reproducibility of the system we performed Pearson correlation plots of data obtained by several hybridizations of the same array with the same sample. A good reproducibility of inter- and intra-chip data ($R^2=0.97-0.99$) have been obtained up to 4-5 hybridizations.

Furthermore, in the next few months new higher density technologies will be acquired and setup such as a NimbleGen platform (2.1 millions of features). This will allow the analysis of even more complex transcriptomes and to setup genome-wide tiling arrays, comparative genome sequencing assays, and the performing of exon trapping experiments for deep sequencing of specific genome regions.