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Gene expression measurements with microarray technology in bacteria: transcriptome analysis of the symbiotic bacteria, *Buchnera aphidicola*, in nutritional stress conditions of its aphid host *Acyrthosiphon pisum*.

Charles H.[1,4], Calevro F.[1,4], Reymond N.[1], Rahbé Y.[1], Laugier, C.[1,4], Bernillon J.[2], Febvay G.[1], Tchounikine A.[3,4], Laforest F.[3,4], Fayard J.M.[1,4]

[1]UMR 203 INRA / INSA de Lyon, Biologie Fonctionnelle, Insectes et Interactions, INSA, Bât. Louis Pasteur, 69621 Villeurbanne Cedex.

[2]DTAMB, Université Claude Bernard Lyon I, Bât. G. Mendel, 69 622 Villeurbanne Cedex.

[3]UMR CNRS 5205 LIRIS, Laboratoire d'InfoRmatique en Images et Systèmes d'information, 69621 Villeurbanne Cedex.

[4]Biologie des Systèmes et Modélisation Cellulaire (http://bsmc.insa-lyon.fr/)

« High flow » technology, such as sequencing, SAGE and microarray, have revolutionized modern biology. Although molecular biologists have long been used to managing qualitative single gene data, or data limited to a very small number of genes, nowadays they have to handle huge amounts of heterogeneous data requiring tool development for storage, visualization, analysis and modeling results.

In 2001, the UMR BF2I started a research activity on transcriptome analysis with microarray technology applied on the intracellular symbiotic bacteria *Buchnera aphidicola* associated with the aphid *Acyrthosiphon pisum*. The aim of this study was to analyze molecular and physiologic interactions taking place between bacteria and their host, especially in regard to the amino acid nutritional complementation that *Buchnera* furnishes to the aphid. Numerous developments had to be achieved to go from experimental design to functional analyses.

Building the microarray was the first step of the process. Probe sequence optimization, determination of the number of probe repeats and of positive and negative controls have been major constraints in this work. Software dedicated to oligonucleotide probe sequence optimization was developed by N. Reymond in BF2I (http://pbil.univ-lyon1.fr/roso/).

Acquiring data requires a number of different successive steps: biological sample preparation, experimental design, target RNA labeling, slide spotting, hybridization reaction, washing and scanning. Each of these steps may bring specific biases that should be discarded by appropriate normalization methods. Hence, quality process is essential for microarray technology. An information system for the storage, visualization and data exchange (http://sitrans.insa-lyon.fr/) was created for this purpose.

Expression level estimations and microarray quality analysis were performed using the GenePix software. Statistical analyses (nested and mixed anova models) were performed by using R libraries of the Bioconductor project (http://www.bioconductor.org/). Selected genes were grouped on Venn's diagram in regard to their significance for principal effects or interaction terms and a functional analysis was performed using projection on Gene Ontology trees (http://www.geneontology.org/).