377 - IDENTIFICATION OF GENES INVOLVED IN CATTLE-TICK RESPONSE MECHANISM BY DIFFERENTIALL CO-EXPRESSION

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In microarray data, gene co-regulation is marked by strong correlations with expression levels (1). Genes with similar expression patterns across a set of samples are hypothesized to have functional relationship and may be involved in the same biological network. On the other hand, differential co-expression is defined as a change in the correlation relationships among genes. According to (2), we could consider differential co-expression as potentially revealing rewiring of gene networks, reflecting dynamic changes in the regulatory relationships between genes which can then be read out at the level of transcription. Because of the potential importance of network rewiring, differential co-expression could be useful for uncovering molecular mechanisms between two contrasting samples such as normal and disease tissue. By comparing microarray data sets of cattle before and after artificial infestation, we used a differential co-expression based analysis in searching for candidate genes to be involved in a mechanism of bovine response to tick *Rhipicephalus microplus*. Microarray data were processed using the *affy*, a BioConductor package. The background was corrected by RMA and normalization was made by quantile method. Summarization was performed using the medianpolish algorithm and filtering was done by using an intensity filter. Co-expression was calculated separately in BI (before artificial infestation) and AI (after artificial infestation) data sets, using as a guide the transcription factor (*CREM – cAMP responsive element modulator*) known to be involved in bovine-tick resistance (3). For co-expressed genes identification, an N-dimensional vector was created for each *chip* present gene, and co-expression was calculated using Pearson correlation coefficient (≥ 0.85). The results revealed different transcripts co-expressed with *CREM* between BI and AI groups. Despite that most of the co-expressed genes in both groups were unknown, we were able to identify candidate genes to be involved in immune response in both, BI and AI groups. Efforts are being made to understand infestation response mechanisms, based on the expression of these two sets of genes which are potential targets of *CREM*. The known function of some genes among the candidates would be used to assign roles for novel target co-expressed genes. This could be accomplished by computational means using promoter sequence analysis. We believe that this approach is very useful to identify functional changes that accompanying co-expression changes revealed by microarray data. Also, novel genes can be identified which may be new targets for use in drug development to improve the resistance of cattle against ticks.

(1) Eisen et al. (1998) , PNAS, 95(25): 14863-14868. **(2)** Gillis, J; Pavlids, P (2009), BMC Bioinformatics, 10:306.

378 - MORPHOLOGICAL ANALYSIS OF THREE CALLUS OF OIL PALM *(ELAEIS GUINEENSIS)*

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The biological characteristics of oil palm trees make it difficult to generate clones of elite species. One possibility to propagate elite species of palm trees is through the induction of somatic embryogenesis from callus derived from different tissues. In this study, *Elaeis guineensis* explants were inoculated in tissue