



## VISUALISATION OF GENE EXPRESSION PATTERNS IN OVARIAN FOLLICULAR DEVELOPMENT

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As a result of generations of selective breeding, commercial broiler breeders when fed *ad libitum* have a propensity to produce internal ovulations, double-yolked, misshapen or shell-less eggs. This is due to the release of multiple ova at the completion of each ovulatory cycle and results in a significant loss of production. Feed restriction has been shown to control this effect, but with an increasing cost to welfare. The aim of this project is to determine the genetic basis of the regulation of ovarian follicle selection and its failure in broiler breeders, and how this dysfunction might be addressed to limit the impact on welfare for successive generations. A new approach to the analysis of data obtained from a micro-array study augments more traditional statistical data analysis with new visualisation software. The software, BioLayout Express 3D, which is currently under development at the Roslin Institute, is specifically designed to identify patterns and relationships within gene expression data gathered in a high throughput manner, such as with micro-array technology. Four patterns of ovarian gene expression have been identified as being of interest in data from a microarray study carried out using a 20k oligo array and DNA from the anterior stroma, 5-6 mm, 6-7 mm and F1 follicles of eight feed restricted broiler breeders and eight restricted birds fed *ad libitum* for two weeks prior to killing at 31 weeks. Pairs of birds from each feeding regime were competitively hybridised to a cDNA microarray. Comparisons of *ad libitum* and restricted birds failed to provide strong evidence for gene differences, and the most significant results could not be validated by qPCR. Gene intensities from both the feed restricted and *ad libitum* groups for each tissue were therefore analysed using the new approach to identify potential gene candidates that may control selection of follicles into the rapidly growing hierarchy. Over 1,200 of 17,000 microarray probes were shown to have expression profiles of potential interest within the ovarian tissues sampled and 925 of these represented known genes. Growth hormone receptor, for example, was shown to be most highly expressed in 5-6 mm follicles and was gradually down-regulated as follicles develop, along with other genes with known anti-apoptotic activity. The results generated by this new approach have been correlated with those of the original analysis focusing on differential expression between feeding regimes. Through this process 13 genes have been identified as displaying significant differential expression both between stages of follicular development and between feed restricted and *ad libitum* feeding. One of these genes, YAP1, is known to possess an SH3 binding domain and is therefore potentially capable of protein-protein interaction and complex assembly within Kinase cascade signalling pathways such as those involving Tyrosine, PI3 and SRC Kinases. As well as signal transduction, YAP1 also shows transcription factor activity. TBC1D13 and GRP, involved in cell growth and proliferation respectively, were also shown to be differentially expressed both between stages of follicular development and between feed restricted and *ad libitum* feeding. These and other genes which show expression profiles of interest will be further examined by RT-PCR to assess their potential role in follicle recruitment.