

Altered gene co-expression profile in extreme feather-pecking behaviour

G.C.G. Abreu, R. Labouriau, A.J. Buitenhuis

Department of Genetics and Biotechnology, Faculty of Agricultural Sciences, Aarhus University – Denmark
Blichers Allé 20, P.O. BOX 50 - DK-8830 Tjele

Background

Feather pecking (FP) is a behaviour observed in laying hens with direct impact on the animal's welfare and production. FP is defined as pecking and pulling out the feathers of another animal in the group. To learn more about the underlying genetics of FP behaviour we have studied the gene expression profile in the brain of extreme severe feather pecking laying hens.

Gene transcription profiles of 36 animals selected for high-feather pecking were determined. Among the 14,077 genes investigated, 456 were significantly differentially transcribed.

Objective

To characterize the relative position in the co-expression network of the differentially expressed genes in the extreme high-feather pecking animals.

Methods

We used the framework of graphical gaussian models to determine the network structure of 1,529 genes (the 456 differentially expressed – DEG, and 1,073 other genes with higher variance – NDEG), where each gene is represented as a vertex and two genes are connected by an edge if they carry information about each other. The search was restricted to decomposable models, and the edges were selected according to the minimum BIC (Bayesian Information Criteria).

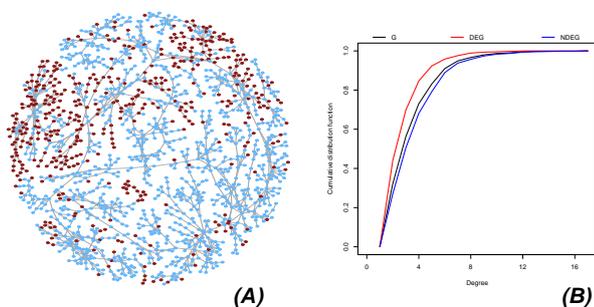


Figure 1: (A) The network found. The red dots represent the 456 differentially expressed genes (DEG), and the blue the non-differentially expressed genes (NDEG); (B) Cumulative distribution function of the degree (number of edges a vertex has), for the whole network (G), the DEG, and the NDEG.

Results

1. The network has 2,129 edges (out of 1,168,156 possible edges, Figure 1A).
2. The network presents a single connected component, including all the differentially expressed genes (DEG).
3. Mean degree: 2.8 (Figure 1B).
4. The DEG are not homogeneously distributed along the network, as indicated by the homogeneity test ($p < 0.0001$). Table 1.
5. The NDEG present a higher centrality than the DEG ($p < 0.0001$).
6. There are genes clusters with predominance of DEG occurring in central positions in the network (Figure 2).

Table 1: Distributions of the type of edges.

Edge connection	Observed	Expected under uniformity
DEG – DEG	315 (14.80%)	189 (8.99%)
DEG – NDEG	365 (17.14%)	892 (41.90%)
NDEG – NDEG	1,449 (68.06%)	1,048 (49.11%)

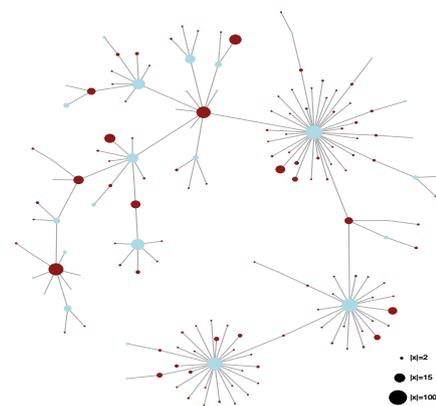


Figure 2: Cluster tree, representing the connection of the clusters in the network (DEG in red, and NDEG in blue).

Conclusions

We present evidences that some of the differentially expressed genes in extreme high-pecking animals occupy a central position in the co-expression network, suggesting that in these animals basic processes influencing severe feather pecking are altered.