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► To cite this version:

Timothy Giles, Scott Hulme, Paul Barrow, Nathalie Le Floc'H, Anne-Marie Chaussé, et al.. Identification of genes which are associated with production diseases in pigs and chickens. 7. International conference on the assessment of animal welfare at farm and grip level (Walf), Sep 2017, Ede, Netherlands. Wageningen Academic Publishers, 2017, Proceedings of the 7th international conference on the assessment of animal welfare at farm and group level. hal-01595012

HAL Id: hal-01595012

<https://hal.science/hal-01595012>

Submitted on 2 Jun 2020

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Identification of genes which are associated with production diseases in pigs and chickens

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Production disease in pigs and chickens is caused by a variety of different pathogens, mainly enteric and respiratory, which may result in significant economic losses. Other factors such as stress, poor husbandry and nutrition can also contribute to an animal's susceptibility to disease. Molecular biomarkers of production disease could be of value by improving diagnosis and risk analysis to determine best practice with an impact on increased economic output and animal welfare. Over 480 chicken tissue samples from countries including Belgium, Spain and the UK, and over 115 pig samples from Belgium, Spain, France and Ireland were available. Samples included lung, intestine, mesenteric and tracheobronchic lymph node, bone, cartilage and sciatic nerve. Two types of software were used to analyse the microarray data; Genespring was used for statistical analysis and visualisation of transcriptomic data and Cytoscape was used to visualise molecular interaction networks between genes. Results indicated that panels of genes may identify a broad spectrum of infectious disease in chickens, whereas combinations of upregulated genes may be used as biomarkers of specific pathogens such as *Escherichia coli* or *Eimeria*. Pigs from two lines (RFI high and low) were kept in dirty environments which had the same bedding and clean environments which had fresh bedding. A greater difference was observed in the number of genes differentially expressed in the RFI high pigs than RFI low pigs. Pathway analysis from both chicken and pig experiments indicated that many networks were affected including those involved in regulating the immune-system. Whilst a large number of studies have been carried out in human medicine, further work is needed to identify molecular biomarkers in veterinary medicine and in particular those associated with production disease in the pig and poultry livestock industry.