Transcriptomic Analysis of the Chicken Interferome

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Chicken, which is almost universally-acceptable, will shortly become the most consumed meat in the developed and developing world. Viruses of chickens, whether enzootic (e.g. Newcastle, Mareks or infectious bursal disease viruses or infectious bronchitis virus) or zoonotic (especially avian influenza viruses such as H5N1 and H7N9), pose major threats to the supply of this globally important source of protein. Understanding the nature of the chicken innate responses will help us better understand these viruses, their evolution and their pathogenesis, and may help us develop more effective methods of controlling them. Although first discovered in chicken cells, details of the chicken interferon response are only just being elucidated, because chicken interferon was only cloned in 1994 and the chicken genome sequence was only reported in 2004. It is noteworthy that the identity of interferon-stimulated genes is far better described in mammals. Although there are increasing numbers of reports of chicken responses to virus infection, most of the regulated genes described are involved in the cell cycle, metabolic pathways and cellular structures required for virus replication. We have conducted a study aimed at describing the complement of potential anti-viral genes, identifying those induced by recombinant type I interferon in a common research and vaccine production substrate, namely primary chick embryo fibroblasts. The results are robust because 155 of the 193 genes induced were detected by at least two of the three transcriptomic technologies employed: Illumina RNA-seq, the Affymetrix 32K GeneChip Chicken Genome Array and the Chicken Gene 1.0 ST Array.