ABSTRACT
Weier Bao

Alpha (α) and beta (β) keratins are the major structural proteins found in vertebrate epidermis and the β-keratins are only found in reptiles and birds. With the recent published 48 avian genomes, we searched and studied the molecular evolution of these gene families. We discovered that the expansion and contraction of different α- and β- keratins among the 48 phylogenetically diverse birds supports the importance of their role in the evolution of the feathers and the adaptation of birds to different ecological niches. Using a customized 44K microarray, we also performed transcriptome analysis on different epidermal regions (scutate scale, dorsal feather and wing feather) at important time points (day 8, 17 and 19) during chicken embryonic development. We profiled the differentially expressed α- and β-keratin genes in those comparison groups and demonstrated the important roles of α- and β-keratins in the development of the chicken epidermal appendages.

MicroRNAs have been found to widely regulate many biological processes in animals. Here we also utilized the 44K microarray transcriptome data to profile the miRNA expression during chicken embryonic development. With the application of various bioinformatic tools, based on the differentially expressed miRNA genes and mRNAs, we identified highly possible target genes for epidermal development in the chicken, and provided a rational for future miRNA target validation.

In previous studies, hundreds of genes (i.e., signaling pathway genes, structural genes, cell adhesion genes, etc.) have been associated with the morphogenesis of chicken epidermal structures as complex, interactive networks. A Weighted Gene Co-expression Network Analysis
(WGCNA) using our microarray transcriptome data was performed to construct a co-expression network associated with traits. We identified two modules that were highly correlated with the developmental traits of the chicken scale and feather. The combination of traditional enrichment (KEGG and Gene Ontology) and novel enrichment (MSET and MeSH) analysis further demonstrated the important functional role of epidermal development related genes (EDRGs) and the hub genes to the development of scales and feathers. In the future, the discoveries of trait related modules will contribute to our understanding of the morphogenesis and differentiation of other epidermal appendages.