BIOLOGY TEXTS

Short Written Texts (Journals)

Siegel, P.B., Dodgson, J.B. and Andersson, L. ***'Progress from Chicken Genetics to the Chicken Genome'.*** *Poultry Science* 85(12):2050-2060 (2006). *Extracts from pp. 2051, 2052, 2057 & 2058.*

Earlier, we wrote of the long, publicly supported research foundation that enhanced the sophistication of chicken genetics and breeding. One example is the chicken gene mapping reviewed later in this paper, as well as development of experimental lines and mutant stocks (http://animalscience.ucdavis.edu/AvianResources/). At present, chicken breeders estimate genotypes for quantitative traits from information on phenotypes. Although we can now map and assay the genotype with great precision, the path to the phenotype can be distant and complex, with interacting networks of pleiotropic genes facilitating dynamic genotypic and phenotypic plasticity. The map, which remains a work in progress, means an exciting future for studies that combine quantitative and molecular techniques.

There are concerns that intense selection for egg production or meat production may exhaust genetic variation for these traits. This concern for plateaus is not new, and proactive papers on genetic reasons for such plateaus for egg production are in the literature (Dickerson, 1955; Clayton, 1972). Although these early concerns of plateaus in egg production became moot with procedures for identifying leucosis shedders from breeding populations (Spencer et al., 1979), physiological and genetic limits should not be lightly regarded. Today, human intervention is necessary to control feed intake of meat stocks. Skeletal and metabolic issues exist for meat and egg stocks. Yet, genetic variation exists for the primary economic traits. Why? Small molecular changes in genes may introduce variability in populations (Hill, 2005) as well as selection-induced genetic variation (Eitan and Soller, 2004; Carlborg et al., 2006). In the case of the latter, the hypothesis is that as selection proceeds to change the genetic background, new sets of genes come into play as sources of variation.

Applications in the Breeding Industry

The industry is already using MAS, to some extent, in their breeding programs. This can be used to increase the frequency of favorable alleles or to eliminate unfavorable alleles. For instance, breeders can now use a DNA test for dominant white if they would like to ensure that their line breeds true for color. An emerging opportunity is to use genomic selection as a method to predict the total genetic value of an animal based on data from genome-wide dense marker maps (Meuwissen et al., 2001). This is becoming feasible due to the huge collection of SNP available in the chicken and the reduced cost of high-throughput SNP typing. With this approach, breeders can estimate the effect of QTL haplotypes without any need to understand the underlying molecular nature of the QTL. They may also be able to estimate modes of action and possibly interactions for each haplotype and use this to improve their breeding program.

In a long-term perspective, the ability to improve the genetic constitution of chicken lines by transgenic technology may eventually become the most important practical application of molecular genetics. Not only is such technology critical to the use of the chicken as a model organism (Dodgson, 2003), it may be essential to verify candidate QTL alleles and to sort out the interactions between QTL and the genetic background. Furthermore, the wealth of knowledge in biology that is currently accumulating, not only from research on chickens but with all organisms, will lead to new opportunities to genetically modify chickens in ways that are of value to agriculture. Most important, the benefits obtainable must be sufficient to outweigh consumer resistance, as they have been, in at least some countries, for crop plants. It appears that disease resistance provides an excellent example of an area in which this technology can have great benefit. For instance, if we could learn more about the biology of influenza infection in birds, it may be possible to genetically engineer chickens to be highly resistant to this disease, a very important achievement that should reduce a major animal welfare problem and a risk to human health.

Notes:

MAS = Marker assisted selection. Where morphological genetic or biochemical markers are used for indirect selection of deteminants of traits such as growth or disease resisitance.

QTL = quantitative Trait Locus. A section of DNA that correlates with phenotype variation.

Haplotype = A set of DNA variation that tends to be inherited together.

© Siegel, P.B., Dodgson, J.B. and Andersson, L. 'Progress from Chicken Genetics to the Chicken Genome'. *Poultry Science* 85(12) (2006). Reproduced with permission of Oxford University Press.