Why Do We Need to Conserve What We Have? A Post-Genome Sequencing Perspective on Existing Chicken Strains1,2

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ABSTRACT The recent publication of the chicken genome sequence along with the extensive single nucleotide polymorphism and physical map open exciting avenues for defining gene function and for understanding the genotypic basis of phenotypic variation in the chicken. The number of genes identified on the sequence map is growing rapidly. Genetically uniform lines and crosses derived from them will allow identification of gene function and gene interactions that contribute to traits such as immunity, disease resistance, growth, production, and behavior. Selected, inbred, and congenic lines will continue to be essential in defining the genetics of many traits. Although dwindling under budgetary pressures, a number of well characterized lines and genetic strains remain. If preserved, these can be used to address questions regarding newly mapped candidate genes defining their importance in a variety of problems in basic, biomedical, and applied avian biology. If lost, years of breeding and selection will be required to replace them.

Key words: disease resistance, gene mapping and function, recombinant congenic line, conservation of genetically defined strain

INTRODUCTION

One has only to look back into recent history to see the contributions made by research using defined chicken strains. Understanding of the etiology of common viral diseases, availability of highly informative consensus linkage maps, and recognition of the unique features of chicken major histocompatibility complex (MHC) genetics in immune function are but a few examples of achievements gained through the use of genetically defined strains. Genetically defined strains include fully pedigreed populations, closed populations, inbred lines, recombinant inbred lines, and a number of phenotypic mutants. Despite their value and the need for continued maintenance of these strains, their numbers have dwindled in the United States largely because of budgetary constraints and further cuts are pending. Few, if any, new lines are being produced despite the opportunities provided by the genome sequence.

Immediate “gap-filling” efforts are needed to preserve the remaining poultry resources. Long-term, sustainable solutions are needed, such as an internationally supported plan for maintaining avian genetic stocks, so that the chicken can continue to be exploited as a means of understanding health and disease. A few of the many achievements provided by these stocks are highlighted in the following paragraphs, as are some future opportunities.

DEFINED INBRED STRAINS CLARIFYING THE BASIS OF AVIAN DISEASE

The systematic breeding of genetically defined, disease-free, inbred lines of chickens performed at the USDA ARS Avian Disease and Oncology Laboratory (ADOL) has been and continues to be essential in understanding host factors and viral agents in the etiology of diseases in the avian leukosis complex (Stone, 1975; Bacon et al., 2000). Using the ADOL genetic lines, it was possible to resolve the once-considered single disease called “avian leukosis complex” into lymphoid leukosis, myeloid leukosis, reticuloendotheliosis, and Marek’s disease (MD). Furthermore, cells cultured from the defined inbred lines were used to define the heritability of cell infectivity among different forms of leukosis/sarcoma viruses. The receptors for different leukosis/sarcoma viral subgroups have proven to be diverse cellular elements including members of the low-density lipoprotein receptor family (Tva; Bates...
et al., 1993), members of the tumor necrosis factor family (Tvf; Adkins et al., 2000), and the butyrophilin-like members of the immunoglobulin protein family (Tvc; Elleder et al., 2005). These studies that taught us the capacity of retroviruses to evolve new ways to gain entry were all made using defined genetic strains. Congenic and semi-congenic lines are now helping to define the genetic basis of resistance to ALV-J, a new avian retrovirus causing severe economic losses in broiler breeders (Mays et al., 2005).

THE CONTEMPORARY CONSENSUS LINKAGE MAPS

A robust consensus linkage map is essential for quantitative trait locus mapping and for completing the assembly of the chicken genome sequence. Mapping efforts have used crosses between a variety of defined genetic lines, often inbred lines (Groenen et al., 2000). Crosses between additional defined stains are now being used to complete the map (Jacobsson et al., 2004; Aerts et al., 2005).

DEFINED LINES AND STRAINS IN THE DISSECTION OF CHICKEN MHC FUNCTION IN MD

Defined lines, lines carrying recombinant haplotypes, and congenic lines carrying recombinant haplotypes are allowing the genetics of MD resistance to be dissected. The classical progeny testing and selection experiments of Cole vividly demonstrated the heritability of susceptibility and resistance to MD (Cole, 1968). Soon it became apparent that haplotypes of the polymorphic major histocompatibility B complex segregated in concert with resistance (Briles et al., 1977).

To further investigate the genetic basis for this fascinating association between the MHC and MD, Briles and coworkers (1983) followed the inheritance of MHC alloantigens within crosses of fully pedigreed lines to isolate recombinant MHC haplotypes that might differ in their influence on tumor formation following infection with the MD herpesvirus. Using a recombinant haplotype formed by meiotic recombination between B21 and B19, MHC B haplotypes associated respectively with resistance and susceptibility to MD, Briles et al. (1983) were able to show that “a gene, or genes, within or closely linked to the B-F region [MHC1] of the B complex appears to be responsible for the observed resistance to Marek’s disease.”

Briles and Briles (1980) continued this quest for the gene or genes by isolating additional recombinant haplotypes including series of “duplicate” double recombinants. Briefly, these were derived from an initial crossing-over event within the MHC B region between haplotypes B23 and B24. Briles and Briles (1977) used BR1, the first of these recombinants, to derive 6 additional new recombinant haplotypes. Two of these, BR2 and BR4, were the result of crossing-over events providing new combinations of genes from BR1 and B2 haplotypes. By serological typing, BR2 and BR4 are identical. Schat et al. (1994) assumed that the crossover breakpoints would likely be unique in each new haplotype and that BR2 and BR4 might differ in their contribution to MD resistance. Initial trials with semicongenic lines carrying BR2 and BR4 provided evidence that the BR2 haplotype was associated with greater disease resistance to MD caused by the very virulent strain RB1B (Schat et al., 1994). Recent replication of this disease trial using now fully congenic BR2 and BR4 lines developed by Robert L. Taylor Jr. (University of New Hampshire) provided evidence of a highly significant association of higher resistance with the BR2 haplotype (R. L. Taylor Jr. and P. S. Wakenell, University of California, Davis; and M. M. Miller, unpublished data). Interestingly, the position of the BR2 and BR4 crossover breakpoints identify BGl as the candidate gene responsible for the difference in resistance to MD tumor formation in these 2 lines (R. M. Goto, Y. Wang, and M. M. Miller, Beckman Research Institute of the City of Hope, unpublished data). Thus, genetically defined lines bearing recombinant haplotypes are providing the means of dissecting MHC function in the chicken.

In the absence of methods for routinely producing transgenic chickens, defined lines, especially those carrying recombinant haplotypes, are perhaps the most powerful means at hand by which gene function in complex traits can be identified. The series of 6C7 recombinant congenic strains developed by Larry Bacon (ADOL) represents valuable genetic material for defining genes that influence various traits that differ between the parental lines (Bacon et al., 2000; Yonash et al., 2002; Dennis et al., 2004). It has taken years of careful breeding, testing, and selection to obtain recombinant congenic lines. These are vital components of avian genetic research in the postgenomic era.

REFERENCES


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