Perspectives in Chicken Genetics and Genomics

Susan J. Lamont
Iowa State University, sjlamont@iastate.edu

Follow this and additional works at: https://lib.dr.iastate.edu/ans_pubs

Part of the Agriculture Commons, Genetics and Genomics Commons, and the Poultry or Avian Science Commons

The complete bibliographic information for this item can be found at https://lib.dr.iastate.edu/ans_pubs/604. For information on how to cite this item, please visit http://lib.dr.iastate.edu/howtocite.html.
Perspectives in Chicken Genetics and Genomics

Abstract
Poultry science has entered a new era with the completion of a century of investigative studies in chicken genetics, sequencing of the chicken genome, application of genomic tools into systems biology studies, and rapid advances in the development of the statistical theory for application of molecular genetic information in commercial breeding programs. This perspectives paper sets the context for the accompanying series of reviews on chicken genetics and genomics, introduces important issues in the field of poultry molecular genetics, and briefly describes the topics of each of the reviews.

Keywords
genetics, genomics, chicken, sequence, model organism

Disciplines
Agriculture | Animal Sciences | Genetics and Genomics | Poultry or Avian Science

Comments

Creative Commons License
This work is licensed under a Creative Commons Attribution-Noncommercial-No Derivative Works 4.0 License.
ABSTRACT  Poultry science has entered a new era with the completion of a century of investigative studies in chicken genetics, sequencing of the chicken genome, application of genomic tools into systems biology studies, and rapid advances in the development of the statistical theory for application of molecular genetic information in commercial breeding programs. This perspectives paper sets the context for the accompanying series of reviews on chicken genetics and genomics, introduces important issues in the field of poultry molecular genetics, and briefly describes the topics of each of the reviews.

Key words: genetics, genomics, chicken, sequence, model organism

A NEW ERA IN CHICKEN GENETICS

Unprecedented opportunities now exist to understand the complex molecular genetic control of biological traits in the chicken. Long recognized as a valuable animal model for fundamental scientific investigation, the chicken is again reemerging in importance as a model organism (Stern, 2005). Studies of developmental biology, physiology, immunology, oncology, and virology have traditionally capitalized on the amenable nature of the chicken to genetic studies, and these investigations will now be greatly enhanced by the availability of the chicken genome sequence (International Chicken Genome Sequencing Consortium, 2004). The study of genetics is no longer an isolated field but, rather, genetics and genomics are now integral components of investigations in almost all disciplines of poultry science. The application of molecular genetics-based technologies can be viewed as an essential unifying feature of contemporary investigations in most disciplines. This series of reviews on chicken genetics and genomics covers the path from genetics to genomics and introduces the reader to research strategies and methods, as well as reviewing results of published studies, in assessment of structural and functional variation in the chicken genome.

Many issues remain to be addressed before the full promise of molecular genetics can be realized. Because of economic pressures at public institutions, many scientifically valuable research lines of poultry are being terminated at just the time that these populations could serve as key resources for defining the genetics that controls their unique traits. The tools of molecular genetics can generate datasets of unprecedented size for animal agriculture, such as those resulting from studies of genomic sequence and sequence polymorphisms and from large-scale gene expression analyses using microarrays. Thus, development of new statistical theory and methodology and, especially, bioinformatics tools to address these genomic data analysis challenges is essential (Tuggle et al., 2006). Development of standard ontology for poultry traits is also needed, because the mammal-based ontologies fall short on traits such as feather length and eggshell strength! Keys to maximize success of research in the genomic era will be to effectively form research teams with expertise in multiple disciplines and to integrate the results of various complementary technologies in addressing systems-based research problems.

OVERVIEW OF THE REVIEW SERIES

The review papers in this series on chicken genetics and genomics are published at a pivotal point in the progress of poultry science. The first paper (Siegel et al., 2006) traces a century of advances in chicken genetics, spanning from the crucial role of the chicken in demonstrating Mendel’s principles in the animal kingdom, through the emergence of molecular genetics, and up to the current genomics era. From that paper, readers will gain insight into the role of genetics in the development of today’s poultry industry, the foundation of public research that resulted in the chicken being the first farm animal with a completely sequenced genome, the merits of the chicken as a model organism, and how research in chicken genetics and genomics is advancing our understanding of biology. The second paper (Soller et al., 2006) details the research strategies that can be used to analyze structural variation in the chicken genome, with application to assess biodiversity and to determine associations...
of structural variation with biological performance. Readers will find the information in that paper useful in designing and analyzing future experiments of their own, as well as interpreting studies published by others. The third paper (Abasht et al., 2006) reviews studies identifying QTL in chickens and discusses the major biological genetic lessons that emerge from these studies. It is timely to summarize results in this quickly moving field, because the scale of experiments is now undergoing a major shift. Most studies to date have used 150 to 300 markers for genomic scans, generally limiting the usefulness of such studies to experimental populations with high levels of linkage disequilibrium. Current studies include designs with 10-fold to 50-fold more markers, enabled by availability of information on sequence polymorphisms in the chicken genome (International Chicken Polymorphism Map Consortium, 2004) and decreasing costs of high-throughput genotyping. The high marker density will make the results much more amenable to use and apply in commercial breeding populations toward the goal of incorporating total genetic value through genome-wide marker analysis (Meuwissen et al., 2001).

Three papers in the series appear in the current issue. A fourth paper, to be published in the future, will review functional genomics of the chicken, including gene expression and transgenic technologies and the results of application of these techniques in studies of several physiological systems. Also of interest to readers of this review series will be the proceedings papers to be published in 2007, based upon presentations delivered at the Ancillary Scientists Symposium on functional genomics held during the 2006 Poultry Science Association annual meeting.

REFERENCES