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Editorial

Livestock Issue

The relationship between humans and agricultural livestock species has developed during the past 10 millennia and has profoundly shaped the evolution of human societies. As well as a growing dependence on livestock as a source of nutrition, livestock are beginning to contribute to our understanding of the genetic factors underlying human disease. Domestic animals have emerged as valuable models for dissecting the molecular genetic basis of complex traits [1, 2] as the genomes of livestock and other domesticates have been shaped by artificial selection for thousands of years. During this time, humans have produced many unique phenotypes through intense selection for agricultural production and specific traits relating to behaviour, physiology and disease tolerance. This has led to distinct phenotypic characteristics that clearly demarcate breeds and differentiate livestock from their wild ancestors and related species.

Recent rapid advances in genomics technologies have provided platforms from which livestock scientists may understand the genetic variation responsible for such phenotypic adaptation and variation. For example, draft genome sequences are now available for chicken (*Gallus gallus*) [3], horse (*Equus caballus*) [4], cow (*Bos taurus*) [5], pig (*Sus scrofa*) and sheep (*Ovis aries*) (www.genome.iastate.edu). The variation in phenotype is attributed to structural variation that produces variation in gene expression, which has clear phenotypic consequences. Functional genomics studies at the pan-genomic level have revolutionised biological research and have enabled a greater understanding of genetic regulatory networks and molecular interactions in many biological realms.

Dedicated functional genomics tools for livestock species have emerged in the past decade, initially for cattle [6] and chicken [7]. Livestock genomics can now utilise platform-based tools such as SNP arrays and gene expression microarrays as well as next-generation sequencing technologies to deepen our understanding of the molecular control of cellular function.

In this issue, Bellone *et al.* describe the fine-mapping of a candidate gene locus in the horse associated with a coat colour phenotype (Leopard complex) that segregates with the disease. Congenital stationary night blindness in the horse closely resembles a human form of the disease, the causative mutation for which has not been identified. Employing a combined structural and functional approach they provide an example of the opportunity to further our understanding of disease mechanisms.

Other potential models of human inherited diseases are also described in this issue. The pig has long been considered a useful model for biomedical research. Bendixen *et al.* describe the value of using closely related mammalian species as models for human disease as the biology more closely resembles human biology than traditional model species for genetics such as *Drosophila* and zebrafish. As our understanding of genomics advances to an applied level, it will become more pertinent to utilise such species. In this context, Bendixen *et al.* review the available resources for pig genomics and the development of transgenic models for human disease.

Animal health is itself a fundamental responsibility of humans stemming from the intimate relationship that exists between us and livestock. Kabara *et al.* and Mienaltowski *et al.* describe the application of genomics technologies to understanding disease phenotypes using *in vitro* systems. RNA derived from disease-infected macrophages (Kabara *et al.*) and various stage and state cartilage tissue (Mienaltowski *et al.*) were evaluated for differential expression of genes using species- and system-specific cDNA microarray platforms that were developed in their own laboratories. Although both studies will impact animal health, they also represent the opportunities for translation to human health in understanding disease mechanisms and the development of novel therapeutics.

The principal purpose of domestic livestock is to ensure food security. Wimmers *et al.* discuss genomics-based approaches aimed towards understanding key genetic contributors to economically important traits in pigs and the application of this information for trait improvement. Their review focuses on the overlap between structural genomics and functional genomics at the pan-genomic level. Continuing this theme, Picard *et al.* contribute a review of proteomics-based approaches to understanding meat quality in cattle, pigs and domestic avian species.

There are, therefore, a number of key focus points for livestock genomics: the improvement of global food security; improvement of economic well-being of agriculturalists; improvement of animal health; and translation to human health and medicine. Animal functional genomics, therefore, not only encompasses agricultural production, but also represents a clear opportunity to better our understanding of human disease by studying species that share our environment and have recent evolutionary histories profoundly influenced by humans.

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