

NEWS AND COMMENTARY

Genomics

The chicken genome sequence

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Heredity (2005) 94, 567–568. doi:10.1038/sj.hdy.6800665

Published online 13 April 2005

Yet another organism has recently had its genome sequenced – the chicken genome is described and analysed in International Chicken Gene Sequence Consortium (2004), and two accompanying papers in the same issue (International Chicken Polymorphism Map Consortium, 2004; Wallis, 2004) are also devoted to chicken genomics. Chicken breeders will of course be enthusiastic, but the phylogenetic relationship between birds and other sequenced animals also makes this genome particularly interesting for biologists interested in evolution. Moreover, although not as famous as mice or rats, chickens are important research models for human disease and animal behaviour, and scientists in this area now have an important new tool at their disposal. The chicken genome also showed some intriguing features, which might keep scientists busy revising our understanding of genome function for some time into the future (Figure 1).

Ever since the release of the human genome, new species have been sequenced at regular intervals. Sequenced species include representatives of mammals, fish, invertebrates such as *Caenorhabditis elegans* and insects, and single-celled organisms. So, is the chicken only 'yet another genome'? No, this is indeed a special one, and the new results have several important and novel implications. Most notably, it is the first sequenced bird genome. The significance of this may not be obvious to the casual reader, but this will allow new detail in understanding human evolution. Earlier genomes sequenced are either considered to be too evolutionarily remote from man – such as *C. elegans* and Fugu – or too close – mammals such as mice and rats – to offer proper understanding of genome development. A bird is just on the right phylogenetic distance – the common ancestor of birds and mammals dating about 300 million years back – for getting to grips with evolutionary histories of genome structure and function, such as evolution of karyotypes, relation between expressed and non-expressed parts of the genome or gene conservation.

The chicken is also the first sequenced agricultural species, which will benefit researchers involved in breeding and animal production. The chicken is by far the most common domesticated animal and the most important production animal in the world. The total chicken population is about 30 billion, with breeds specialised for either egg production or rapid growth and meat production. The genome sequence will allow researchers to search for links between specific DNA regions and, for example, growth and egg production, allowing more targeted and efficient breeding programs. Animal welfare is also an important scientific concern in modern farming, and side-effects of traditional breeding for increased production may be one of the largest challenges to animal health now and in future (Rauw *et al.*, 1998). One example of how genomic methods can help welfare research is the recent discovery of a gene that affects the risk of becoming victim of feather-pecking, a detrimental behaviour disorder in egg-laying chickens (Keeling *et al.*, 2004).

As Darwin realised, domestication provides one of the most beautiful and potent models for studying evolution. Although domestication of chickens started less than 10 000 years ago, the

amount of within-species phenotypic variation created during that time is stunning. The same is true for all other domesticated animals, and the chicken is an important model species in this aspect. The genome sequence will now allow scientists to identify genes and regulatory regions involved in domestication. One of the accompanying papers in International Chicken Polymorphism Map Consortium (2004) approaches this by comparing genetic variation within and between chicken breeds and their ancestor, the red junglefowl of south-east Asia. Surprisingly, the variation within highly specialised domestic breeds is similar to that between jungle fowl and domestic birds, indicating that domestic chickens are not significantly more inbred than their wild relatives. Analyses such as these will help cast new light on the process of animal domestication, perhaps one of the most significant achievements in human history.

Yet, one important application of this genome must be mentioned: chickens are widely used as models of human diseases, including muscular dystrophy, immunological diseases and thyroid insufficiency. With the genome available, it will be possible to find and investigate candidate genes affecting such traits, in the benefit of human medicine.

What is special about this particular genome, which is actually the sequence of a red junglefowl? First of all, it is compact: packaged in six large and 33 tiny chromosomes, the DNA contains only about one-third of the number of bases compared to humans, while



Figure 1 The chicken genome sequence is based on the red junglefowl (left), ancestor of all modern chicken breeds. It will provide tools for researchers interested in animal production and welfare, domestication, evolution, and human diseases.

harbouring about the same number of genes. There is a low amount of repetitive sequences compared to mammalian genomes, which facilitates sequencing and the search for genes. There is also a high degree of conserved synteny to humans, more so than in the mouse genome, for example. Although gene orders are often rearranged, this synteny means that a particular segment of a chicken chromosome with specific genes will often have a corresponding region with the same genes somewhere in the human genome. The recombination rate is considerably higher than in mammalian genomes, which facilitates gene mapping. All these traits

make the chicken genome very attractive as a tool for the different sort of research outlined above.

A particularly exciting, but still poorly understood, feature of this genome is that about 7% of its sequence is well conserved between humans and chickens. Many of the conserved sequence stretches are found far away from coding regions. This is surprising, since substitution rate is generally believed to be higher in non-coding regions – but the high degree of conservation indicates that the opposite may be true for some regions. Hence, it is quite possible that the conserved non-coding regions have some essential

function in the genome, yet to be understood, but shared by birds and mammals. The chicken genome may therefore be an important tool for future elucidation of genomic mechanisms that are still unknown.

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International Chicken Gene Sequence Consortium (2004). *Nature* **432**: 695–716.

International Chicken Polymorphism Map Consortium (2004). *Nature* **432**: 717–722.

Keeling LJ *et al* (2004). *Nature* **431**: 645–646.

Rauw WM *et al* (1998). *Livestock Prod Sci* **56**: 15–33.

Wallis JW *et al* (2004). *Nature* **432**: 761–763.