

Using the chicken genome sequence: bioinformatics tools and prospects for poultry breeding

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The recent sequencing and draft assembly of the chicken genome (Hillier et al., 2004) is an exciting development for all interested in avian biology. It is an invaluable information resource that complements the growing list of tools now available in avian genomics (see www.ark-genomics.org). To fully exploit these resources in poultry research and animal breeding is a challenge. The data is freely available through a number of genome browsers world-wide. However to extract the full benefit of these resources requires much effort and learning new skills in bioinformatics. This paper provides an overview of online genomic resources for the chicken including the genome browsers at Ensembl, NCBI and UCSC. How to access the key objects in the genome, including genes, proteins, genetic variation and genetic regulation are explained. This is a rapidly developing field, with a huge array of open access software freely available over the internet. Finally, the prospects for poultry breeding are discussed in terms of the increased integration of biological and genome data and their future applications.

Hillier, L.W., Miller, W., Birney, E., Warren, W., Hardison, R.C., Ponting, C.P., Bork, P., Burt, D.W., Groenen, M.A., et al. (2004). Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature* 432: 695-716.

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