

A complete genome for a commercial duck

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Biology has been revolutionized by the availability of whole genome sequences, along with all the associated approaches including genome-wide association studies, various -omics methodologies and now precise genome editing^[1–6]. The study of domesticated animal food species has already benefitted from these basic technologies (for a few examples out of many^[7–14]), and it is anticipated that there will be enormous advances arising from deep understanding and precise intervention. However, these improvements depend on the availability of a complete high-quality genomes.

Domestic ducks are an important staple food source in many Asian countries, and a source of fine food in other parts of the world. However, there has been concern about their role as reservoirs for influenza virus due to their apparent tolerance to many strains of avian influenza and thus their potential contribution to zoonotic infections^[15,16]. While relatively resilient to avian influenza compared to poultry, such as chickens, there are also serious infections by the viruses responsible for duck hepatitis B, duck enteritis (duck plague) and duck egg drop syndrome (Tembusu), as well as by bacteria such as *Salmonella*, *Campylobacter* and *Pasteurella*^[15–21].

A significant milestone has been reached with the publication of a complete genome sequence of a domestic duck (Pekin duck, an indigenous breed in China) along with a careful analysis of the major histocompatibility complex (MHC) by Jiaxiang HU and colleagues from the team of Yinhua HUANG at the China Agricultural University in Beijing^[22]. This genome sequence was generated and assembled by the latest technologies to the chromosome level, and appears to be the

most complete duck genome sequence to date. Although there is much to be learned from the rest of the genome, the authors focused their analyses on the MHC, one of the key immune regions in the genomes of all jawed vertebrates, from sharks to humans.

Almost everything known about the MHC comes from research in humans and biomedical models like mice, but among non-mammalian vertebrates, the most detailed and wide-ranging work has been done with chickens^[23–25]. While the basic pathways are very similar, there are stark differences between the MHC of typical mammals and chickens. For example, the human MHC is at least 4 Mb long with hundreds of genes, including multigene families encoding the highly polymorphic class I and class II MHC molecules, which are central in disease resistance and vaccine responses. In contrast, the MHC of chickens is compact and simple (less than 0.1 Mb), with only a few genes devoted mostly to antigen presentation and immune responses, and only single dominantly-expressed class I and class II molecules, leading to strong genetic associations with resistance to infectious pathogens and responses to vaccines. Such compact simple MHC organizations have been found in ratite birds (ostriches and other flightless birds, thought to be the first lineage of extant birds), and are thought to be ancestral^[26]

Unexpectedly, the MHC of the domestic duck is a relatively large genomic region (at least 1.35 Mb in those regions with genes comparable to the chicken MHC), mostly due to big expansions of key immune and regulatory genes, such as those

encoding class II, DM2, butyrophilin, NK receptor and NK ligand molecules^[22]. There are several other notable differences compared to chickens, and altogether these analyses of the duck MHC will provide the basis for understanding the immune response to and developing vaccines for influenza and

various other pathogens that infect ducks. Also, the rest of the genome will provide a valuable information about immune responses, physiology, and behavior of domestic ducks, which will transform understanding of and the ability to improve domestic ducks as a livestock species.

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Compliance with ethics guidelines

Jim Kaufman declare that there has no conflicts of interest or financial conflicts to disclose. This article does not contain any studies with human or animal subjects performed by the author.

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