



GENOME WATCH

A poultry existence

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The two poultry pathogens discussed in this month's Genome Watch are closely related to well-characterized organisms that infect humans, so scrutinizing their genomes could reveal factors that determine host-specificity.

Avian influenza has the potential to ravage the poultry industry and be transmitted to humans. Bacterial pathogens of poultry are also economically important. *Bordetella avium* causes non-lethal respiratory disease, which can predispose birds (mainly turkeys) to secondary infections. Infection of the respiratory tract by avian pathogenic *Escherichia coli* (APEC) strains can result in colibacillosis, which can be lethal.

The genome of *B. avium* consists of 3,732,255 base pairs and contains 3,417 coding sequences (CDSs)¹. The genome of the related strain *Bordetella bronchiseptica*, which is responsible for respiratory disease in mammals, was sequenced previously. A comparison of the two could pinpoint those genomic features that are important to host specificity, that is, the infection of either an avian or a mammalian host. These 2 strains share a conserved *Bordetella* backbone of 2,380 orthologous CDSs that constitutes two thirds of the *B. avium* genome. The CDSs that are unique to *B. avium* mainly encode surface-associated proteins that might be important in adhesion and immune-system evasion. The *B. avium* genome

contains CDSs that encode many novel adhesins that are presumably specific for the avian trachea, including several filamentous haemagglutinins. There are potentially novel biosynthetic pathways for both lipopolysaccharide (LPS) and capsular polysaccharide, which would also modify the bacterial-cell surface. There are eleven CDSs that seem to encode fimbriae, which could aid binding of the bacteria to cells of the respiratory tract. The interaction with the host might also be mediated by 2 novel surface proteins, each of which comprises more than 4,000 amino acids, and 7 autotransporters. *Bordetella* species often synthesize toxins; *B. avium* can produce dermonecrotic toxin, which has been shown to be important in causing disease in turkeys, and tracheal cytotoxin.

Most *E. coli* strains are associated with the intestine. Strains that have strayed from this lifestyle are known as ExPEC (extraintestinal pathogenic *E. coli*) and include APEC and UPEC (uropathogenic) strains, of which the UPEC strains are responsible for urinary-tract infections in humans. Multiple *E. coli* genomes have been sequenced, including laboratory strains, those that cause food poisoning and other ExPEC strains. It has been proposed that UPEC originated from APEC, and genome comparisons could help us to understand these evolutionary connections.

Strain APEC 01 has a chromosome of 5,082,025 base pairs, and comprises 4,467 CDSs². It also harbours four plasmids: one involved in virulence; one involved in antibiotic resistance;

and two cryptic plasmids. Comparative analyses revealed that 78% of the CDSs from the APEC 01 chromosome are common to all sequenced *E. coli* strains, which means that these CDSs comprise the minimal *E. coli* backbone. A further 9% of the CDSs are shared among all the sequenced ExPECs, which might indicate their importance to the survival of the bacteria outside the intestine. These genes include those that code for LPS synthesis, fimbriae, virulence-associated pili and iron acquisition. The remaining 13% of CDSs are unique to APEC 01 and are predominantly located on 4 APEC-specific pathogenicity islands (PAIs), which are phage-related and might contain additional virulence factors.

The differences between the avian and mammalian *Bordetella* strains seem to reflect evolution over millions of years through the vertical transfer of genes. The *E. coli* genomes show more evidence of horizontal gene transfer, and many of the differences between strains are restricted to PAIs and plasmids.

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1. Sebahia, M. *et al.* Comparison of the genome sequence of the poultry pathogen *Bordetella avium* with those of *B. bronchiseptica*, *B. pertussis*, and *B. parapertussis* reveals extensive diversity in surface structures associated with host interaction. *J. Bacteriol.* **188**, 6002–6015 (2006).
2. Johnson, T. J. *et al.* The genome sequence of avian pathogenic *Escherichia coli* strain O1:K1:H7 shares strong similarities with human extraintestinal pathogenic *E. coli* genomes. *J. Bacteriol.* **189**, 3228–3236 (2007).

DATABASES

Entrez Genome Project: <http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=genomepj>
APEC 01 | [Bordetella avium](#) | [Bordetella bronchiseptica](#)
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