

Draft Genome of a Brazilian Avian-Pathogenic *Escherichia coli* Strain and *In Silico* Characterization of Virulence-Related Genes

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Avian-pathogenic *Escherichia coli* (APEC) strains cause extraintestinal diseases in avian species. Here, we present the draft genome of an APEC strain (SCI-07) from Brazil that was isolated from skin lesions (gelatinous edema) on the head and periorbital tissues of a laying hen with swollen head syndrome.

Escherichia coli strains that cause diseases in birds are designated avian-pathogenic *E. coli* (APEC) (4). The infection may be present as perihepatitis, airsacculitis, pericarditis, peritonitis, salpingitis, coligranuloma, omphalitis, cellulitis, osteomyelitis/ arthritis, and swollen head syndrome (2), collectively termed colibacillosis. These diseases are responsible for severe economic losses to the multibillion-dollar poultry industry worldwide (3).

Birds presenting swollen head syndrome disease present gelatinous edema on the skin of the head and periorbital tissues and, in some cases, fibrous exudates in the subcutaneous head tissues and in the lachrymal glands. Swollen head syndrome was first described in South America (9) and is considered to be an important avian disease in various countries, including Brazil (1).

The APEC strain SCI-07 was isolated from lesions (gelatinous edema) on the skin of the head and periorbital tissues from a laying hen showing clinical signs of swollen head syndrome. The serotyping as O nontypeable:H31 was carried out in the Institute Adolfo Lutz of São Paulo. The genome sequence was obtained using 454 Life Sciences technology (8), and the assembly was performed with the program GS De Novo Assembler version 2.5.3 with default parameters for bacteria, resulting in 382,008 reads with an average size of 424 bp and coverage of $32 \times$. The resulting contigs were ordered by alignment to the reference genome of E. coli APEC O1 (6), available in the GenBank database under accession number CP000468.1, with PROmer application version 3.0 (7) and mapping "one for one" from the show-tiling option. The total size of the assembly was 4,972,327 bp, with a mean contig size of 199,495, resulting in 68 contigs, with an average G+C content of 50.61%. The NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) was employed for gene annotation (http: //www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html).

Genes used as virulence-associated markers were sought on the SCI-07 genome with the BLAST tool. Strain SCI-07 was characterized as being an APEC strain because it harbored the genes *iucD* (aerobactin), *irp2* (iron-repressible protein), *vat* (vacuolating autotransporter protein), *astA* (enteroaggregative toxin), *iss* (increased serum survival), and *cvi* (colicin V immunity protein) (5). In conclusion, this is the first published draft genome of a Brazilian APEC strain and will be useful to enrich further comparative studies between *Escherichia coli* strains from either avian or human sources.

Nucleotide sequence accession numbers. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/ GenBank under the accession number AJFG00000000. The version described in this paper is the first version, AJFG01000000.

ACKNOWLEDGMENTS

The authors are indebted to Kinue Irino (Adolfo Lutz Institute, São Paulo, Brazil) for serotyping strain SCI-07.

This work was supported by Fapesp (Proc. 2010/51421-8) and CAPES (Proc. 23038.042588/2008-11). CNPq provided a fellowship to Thaís Cabrera Galvão Rojas.

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Received 13 March 2012 Accepted 22 March 2012

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