

Genome Sequences of Avian Pathogenic *Escherichia coli* Strains Isolated from Brazilian Commercial Poultry

Thaís Cabrera Galvão Rojas,^a Renato Pariz Maluta,^a Lucas Pedersen Parizzi,^a Luciano Vieira Koenigkan,^b Jian Yang,^c Jun Yu,^d Gonçalo Amarante Guimarães Pereira,^a Wanderley Dias da Silveira^a

Department of Genetics, Evolution, and Bioagents, Institute of Biology, University of Campinas (UNICAMP), Campinas, São Paulo, Brazil^a; Embrapa Informática Agropecuária, Campinas, São Paulo, Brazil^b; MOH Key Laboratory of Systems Biology of Pathogens, Institute of Pathogen Biology, Chinese Academy of Medical Sciences & Peking Union Medical College, Beijing, China^c; Strathclyde Institutes of Pharmacy and Biomedical Sciences, University of Strathclyde, Glasgow, United Kingdom^d

Avian pathogenic *Escherichia coli* (APEC) infections are responsible for significant losses in the poultry industry worldwide. The disease might present as different local infections or as septicemia. Here, we present the draft genome sequences of three Brazilian APEC strains isolated from different kinds of infections. The availability of these APEC genome sequences is important for gaining a thorough understanding of the genomic features of *E. coli*, particularly those of this pathotype.

Received 19 February 2013 Accepted 21 February 2013 Published 21 March 2013

Citation Rojas TCG, Maluta RP, Parizzi LP, Koenigkan LV, Yang J, Yu J, Pereira GAG, Dias da Silveira W. 2013. Genome sequences of avian pathogenic *Escherichia coli* strains isolated from Brazilian commercial poultry. *Genome Announc*. 1(2):e00110-13. doi:10.1128/genomeA.00110-13.

Copyright © 2013 Rojas et al. This is an open-access article distributed under the terms of the [Creative Commons Attribution 3.0 Unported license](http://creativecommons.org/licenses/by/3.0/).

Address correspondence to Wanderley Dias da Silveira, wds@unicamp.br.

Escherichia coli strains are Gram-negative enterobacteria that are part of the normal intestinal microbiota of mammals and birds. Most *E. coli* strains are commensal, but subsets of these bacteria have acquired the capacity to cause intestinal and extraintestinal diseases in humans and animals (1, 2). *E. coli* strains responsible for bird diseases are collectively named avian pathogenic *E. coli* (APEC), and the infection due to APEC is known as colibacillosis (2, 3).

APEC infections are responsible for significant losses in the poultry industry worldwide due to high mortality, carcass condemnation, decrease of egg production, and other losses in productivity. The disease might present as a local infection, such as perihepatitis, pericarditis, peritonitis, salpingitis, cellulitis, omphalitis, air sacculitis, or swollen head syndrome, or as septicemia (4, 5).

Three APEC strains were sequenced. *E. coli* strain SEPT362 (OR:H10) was isolated from the liver of a laying hen with clinical signs of septicemia. *E. coli* strain S17 (O113:H4) was also isolated from the liver, but from a broiler chick with septicemia. *E. coli* strain O08 (O38:H10) was obtained from the yolk of the abdomen of a diseased 1-day-old chick.

The genomes were sequenced using 454 Life Sciences technology (6). The read assembly was performed with Genome Sequencer (GS) *de novo* Assembler version 2.5.3, and the resulting contigs were ordered with the PROmer application version 3.0 (7) and mapped “one for one” from the show-tiling option, using APEC O1 (available in the GenBank database accession no. CP000468.1) as a reference genome.

The genome assembly of the 3 strains resulted only in draft assemblies with high coverage, which should represent most of the functional annotated genes and allow for comparative studies using these genomes (8). Genome sequencing for the strains O08, S17, and SEPT362 resulted in 301,852, 342,817, and 305,381 reads, with average read sizes of 445, 369, and 345 bp, and coverages of 26×, 25×, and 21×, respectively. The total sizes of the assemblies

were 5,084,722, 4,591,470, and 5,279,952 bp, resulting in 160, 187, and 173 contigs for the strains O08, S17, and SEPT362, respectively.

APEC genome sequences were annotated by the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (PGAAP) (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>). The numbers of annotated genes were 4,908, 4,463, and 5,151 for O08, S17, and SEPT362 strains, respectively.

The availability of several APEC genome sequences (9, 10, 11) permits the comparison of genome contents between APEC and other pathogenic and nonpathogenic *E. coli* strains, which might help us understand the evolutionary processes involved in the shaping of the phenotypes of different pathotypes. A detailed study of these genomes and those of other available *E. coli* strains will be reported soon.

Nucleotide sequence accession numbers. These GenBank Whole Genome Shotgun projects have been deposited at DDBJ/EMBL/GenBank under the accession no. [AOGM000000000](https://www.ncbi.nlm.nih.gov/nuccore/AOGM000000000), [AOGN000000000](https://www.ncbi.nlm.nih.gov/nuccore/AOGN000000000), and [AOGL000000000](https://www.ncbi.nlm.nih.gov/nuccore/AOGL000000000) for the O08, S17, and SEPT362 strains, respectively. The versions described in this paper are the first versions, accession no. [AOGL010000000](https://www.ncbi.nlm.nih.gov/nuccore/AOGL010000000), [AOGL010000000](https://www.ncbi.nlm.nih.gov/nuccore/AOGL010000000), and [AOGL010000000](https://www.ncbi.nlm.nih.gov/nuccore/AOGL010000000) for strains O08, S17, and SEPT362, respectively.

ACKNOWLEDGMENTS

This work was supported by Fapesp (procs. 2010/51421-8 and 2012/04931-6) and CAPES (proc. 23038.042588/2008-11). CNPq provided a fellowship to T.C.G.R., and FAPESP provided a fellowship to R.P.M. (proc. 2012/05073-3).

REFERENCES

1. DebRoy C, Maddox CW. 2001. Identification of virulence attributes of gastrointestinal *Escherichia coli* isolates of veterinary significance. *Anim Health Res. Rev.* 2:129–140.
2. Barnes HJ, Vaillancourt JP, Gross WB. 2003. Colibacillosis, p 631–652.

- In Saif YM, Barnes HJ, Glisson JR, Fadly AM, McDougald LR, Swayne DE (ed), Diseases of poultry, 11th ed. Iowa State University Press, Ames, IA.
3. Dziva F, Stevens MP. 2008. Colibacillosis in poultry: unravelling the molecular basis of virulence of avian pathogenic *Escherichia coli* in their natural hosts. *Avian Pathol.* 37:355–366.
 4. Dho-Moulin M, Fairbrother JM. 1999. Avian pathogenic *Escherichia coli* (APEC). *Vet. Res.* 30:299–316.
 5. Barnes HJ, Nolan LK, Vaillancourt JP. 2008. Colibacillosis, p 691–732. In Saif YM, Fadly AM, Glisson JR, McDougald LR, Nolan LK, Swayne DE (ed), Diseases of poultry, 12th ed. Blackwell Publishing, Ames, IA.
 6. Margulies M, Egholm M, Altman WE, Attiya S, Bader JS, Bemben LA, Berka J, Braverman MS, Chen YJ, Chen Z, Dewell SB, Du L, Fierro JM, Gomes XV, Godwin BC, He W, Helgesen S, Ho CH, Irzyk GP, Jando SC, Alenquer ML, Jarvie TP, Jirage KB, Kim JB, Knight JR, Lanza JR, Leamon JH, Lefkowitz SM, Lei M, Li J, Lohman KL, Lu H, Makhijani VB, McDade KE, McKenna MP, Myers EW, Nickerson E, Nobile JR, Plant R, Puc BP, Ronan MT, Roth GT, Sarkis GJ, Simons JF, Simpson JW, Srinivasan M, Tartaro KR, Tomasz A, Vogt KA, Volkmer GA, Wang SH, Wang Y, Weiner MP, Yu P, Begley RF, Rothberg JM. 2005. Genome sequencing in microfabricated high-density picolitre reactors. *Nature* 437:376–380.
 7. Kurtz S, Phillippy A, Delcher AL, Smoot M, Shumway M, Antonescu C, Salzberg SL. 2004. Versatile and open software for comparing large genomes. *Genome Biol.* 5:R12.
 8. Li J, Jiang J, Leung FC. 2012. 6–10× pyrosequencing is a practical approach for whole prokaryote genome studies. *Gene* 494:57–64.
 9. Johnson TJ, Kariyawasam S, Wannemuehler Y, Mangiamela P, Johnson SJ, Doetkott C, Skyberg JA, Lynne AM, Johnson JR, Nolan LK. 2007. 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.
 10. Rojas TC, Parizzi LP, Tiba MR, Chen L, Pereira GA, Sangal V, Yang J, Yu J, Dias da Silveira W. 2012. Draft genome of a Brazilian avian-pathogenic *Escherichia coli* strain and *in silico* characterization of virulence-related genes. *J. Bacteriol.* 194:3023.
 11. Dziva F, Hauser H, Connor TR, van Diemen PM, Prescott G, Langridge GC, Eckert S, Chaudhuri RR, Ewers C, Mellata M, Mukhopadhyay S, Curtiss R, III, Dougan G, Wieler LH, Thomson NR, Pickard DJ, Stevens MP. 2012. Sequencing and functional annotation of avian pathogenic *Escherichia coli* serogroup O78 strains reveals the evolution of *E. coli* lineages pathogenic for poultry via distinct mechanisms. *Infect. Immun.* 81:838–849.