

Genome Sequence of *Pasteurella multocida* subsp. *gallicida* Anand1_poultry

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We report the finished and annotated genome sequence of *Pasteurella multocida gallicida* strain Anand1_poultry, which was isolated from the liver of a diseased adult female chicken. The strain causes a disease called “fowl cholera,” which is a contagious disease in birds. We compared it with the published genome sequence of *Pasteurella multocida* Pm70.

Pasteurella multocida, a Gram-negative, nonmotile rod that may exhibit pleomorphism after repeated subculture, is well known as an etiological agent in causation of fowl cholera in a range of avian species, including chickens, turkeys, and waterfowl (listed in increasing order of susceptibility). It usually occurs as a septicemia of sudden onset with high morbidity and mortality, but chronic and asymptomatic infections also occur. It has been seen worldwide and was one of the first infectious diseases to be recognized, by Louis Pasteur (3, 5). In freshly isolated cultures or in tissues, the bacteria have a bipolar appearance when stained with Leishman's strain. Although *Pasteurella multocida* may infect a wide variety of animals, strains isolated from nonavian hosts generally do not produce fowl cholera. Strains that cause fowl cholera represent a number of immunotypes, which complicates widespread prevention by using bacterins. Chronically infected birds are considered to be a major source of infection. Dissemination of infection within a flock is primarily by excretions from the mouth, nose, and conjunctiva of diseased birds that contaminate their environment. The genome sequence of *Pasteurella multocida* subsp. *gallicida* strain Anand1_poultry was achieved by a shotgun sequencing strategy (4) using 454 pyrosequencing. The sequences were assembled with the Newbler assembler (454 Life Sciences). The GS reference mapper was used to create contigs (with *Pasteurella multocida* Pm70 used as a reference genome [6]), and the resulting contigs were subjected to the NCBI Prokaryotic Genome Annotation Pipeline (<http://www.ncbi.nlm.nih.gov/genomes/static/Pipeline.html>). The data generated from the genomic library contained 96,816 reads, and the assembly generated a 2,017,480-bp-long single chromosome with a G+C content of 40.23%.

The genome annotation and comparative analysis of the genome were done with the published genome of strain Pm70 using the RAST server (1). The genomic sequence of *P. multocida* subsp. *gallicida* Anand1_poultry was a little smaller than that of *P. multocida* Pm70 (2.25 Mb). It contained 2,285 predicted coding regions, 5 rRNA operons and 48 tRNAs. The number of coding sequence (CDS) regions was slightly higher than that in *P. multocida* Pm70 (i.e., 2,014). SEED subsystem analysis revealed var-

ious genes involved in (i) metabolic pathways of cofactors, vitamins, prosthetic groups, and pigments, (ii) cell wall and capsule, (iii) virulence, disease, and defense, (iv) potassium metabolism, (v) phages and prophages, (vi) transposable elements, membrane transport, and iron acquisition and metabolism, (vii) RNA and protein metabolism, (viii) cell division and the cell cycle, regulation, and cell signaling, (ix) nitrogen metabolism, (x) stress response, (xi) metabolism of aromatic compounds, amino acids, and derivatives, and (xii) sulfur, phosphorus, and carbohydrate metabolism. The organism revealed the presence of genes for (i) ribosomally synthesized antibacterial peptides (i.e., colicin V and the bacteriocin production cluster) and (ii) resistance to antibiotics and toxic compounds, including lysozyme inhibitors and cobalt-zinc-cadmium resistance, copper homeostasis, copper tolerance, fluoroquinolone resistance, and the presence of β -lactamase and multidrug resistance efflux pumps. Metabolic reconstruction subsystems were assembled to create a metabolic reaction network for *P. multocida* subsp. *gallicida* Anand1_poultry and *P. multocida* Pm70. The study revealed the presence of β -lactamase enzyme and a multidrug resistance efflux pump, suggestive of routine outbreaks under tropical Indian conditions with failure of effective treatments. As well as systems for iron acquisition and metabolism, there is a hemin transport system, which may be responsible for the high pathogenicity of the Indian poultry isolate compared to Pm70 (2, 7).

Nucleotide sequence accession numbers. The complete sequence of the *Pasteurella multocida* subsp. *gallicida* Anand1_poultry genome can be accessed under GenBank accession no. AFRR01000001 to AFRR01000489.

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