

Draft Genome Sequences of Two Virulent Serotypes of Avian *Pasteurella multocida*

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Here we report the draft genome sequences of two virulent avian strains of *Pasteurella multocida*. Comparative analyses of these genomes were done with the published genome sequence of avirulent *P. multocida* strain Pm70.

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Pasteurella multocida is the etiologic agent of fowl cholera, a highly contagious and severe disease of poultry causing significant mortality and morbidity throughout the world (1). All types of poultry are susceptible to fowl cholera. In peracute/acute disease, death is caused by septicemia and endotoxic shock (2, 3). Serotypes A:1, A:3, and A:3,4 are most commonly associated with fowl cholera in the United States (4). The whole genome of the Pm70 strain of *P. multocida* was sequenced and annotated in 2001 (5). The Pm70 strain was isolated in 1970 from the oviduct of a chicken in Texas. This strain belongs to serotype F:3 and not A:3 as reported earlier (6) and is not virulent in chickens (7). Therefore, we sought to sequence the genomes of two virulent strains, namely *P. multocida* strains X73 (serotype A:1) and P1059 (serotype A:3). Both strains are highly virulent in turkeys, chickens, and other poultry species (8).

The genome sequencing of *P. multocida* strains P1059 and X73 was achieved via 454 pyrosequencing of a shotgun library. The sequences were assembled *de novo* with Newbler V2.6 (454 Life Sciences), and Pm70 was used as a reference strain for scaffolding; the resulting assembly generated 2.30 Mbp (40.21% GC, 24 contigs, 18 contigs >500 bp, N_{50} 256,544) and 2.26 Mbp (40.30% GC, 39 contigs, 28 contigs >500 bp, N_{50} 137,372) genomes for P1059 and X73, respectively. Genome annotation and whole genome comparisons were performed against the Pm70 strain using the RAST server (9). P1059 contained 2,144 predicted coding regions, a gene density of 88.8%, an average coding size of 961 bp, 50 tRNAs, and 4 rRNA operons. X73 contained 2,085 predicted coding regions, a gene density of 88.3%, an average coding size of 964 bp, 51 tRNAs, and 4 rRNA operons. Comparing all three strains, there were 158, 126, and 81 unique genes for strains P1059, X73, and Pm70, respectively. Multigenome comparative analysis identified the presence of a filamentous hemagglutinin *pfhB1* gene, which was highly conserved in all three strains. The *pfhB2* gene was identical in X73 and P1059 strains but shared only 90% sequence identity with the Pm70 strain. A novel gene, here named *pfhB3*, was present in both X73 and P1059 but absent from Pm70. A fourth novel gene, herein named *pfhB4*, was unique to the P1059

strain. The *plpE* gene coding for a cross-protection factor antigen was present in all three strains and highly conserved (10). We identified the presence of a chondroitin synthase gene (*fcbD*) in Pm70 and the hyaluronan synthase gene (*hyaD*) in both P1059 and X73 (11, 12). Whereas the *pcgDABC* gene cluster involved in the decoration of phosphocholine to the outer core of the lipopolysaccharide (LPS) was present only in X73, the *pm1138* gene encoding a glycosyltransferase was present in all Pm70, X73, and P1059 strains (13–15).

Nucleotide sequence accession numbers. The draft genome sequences of *Pasteurella multocida* subsp. *gallicida* P1059 and X73 have been deposited at DDBJ/EMBL/GenBank under the accession numbers [AMBQ01000000](https://www.ncbi.nlm.nih.gov/nuccore/AMBQ01000000) and [AMBP01000000](https://www.ncbi.nlm.nih.gov/nuccore/AMBP01000000).

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