

Draft Genome Sequences for 10 Isolates of the Swine Pathogen *Haemophilus parasuis*

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***Haemophilus parasuis* colonizes the upper respiratory tract of swine and can cause a severe systemic disease known as Glässer's disease. We report here the draft genome sequences of 10 isolates from geographically diverse locations representing the full virulence spectrum of the microorganism, which will aid in understanding the pathobiology of *H. parasuis*.**

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Haemophilus parasuis is a Gram-negative microorganism that colonizes the upper respiratory tract of pigs, where it can cause a severe systemic infection known as Glässer's disease. This disease is characterized by fibrinous polyserositis (inflammation of the serous membranes), arthritis, and meningitis. At least 15 serovars of *H. parasuis* have been recognized, and untypeable strains are also common (1). *H. parasuis* is an important pathogen in all major swine-raising countries throughout the world, especially in age-segregated production systems, where it is responsible for significant economical losses due to mortality and lost production.

Until relatively recently, no genomic sequence data for *H. parasuis* have been available. The initial release of the draft sequence of *H. parasuis* 29755 in GenBank (accession no. ABKM000000000), done by Roche/454 pyrosequencing (2), was followed by the complete genome sequence of *H. parasuis* SH0165 (3); these sequences have been valuable resources to researchers of this pathogen (4–6). However, these initial genome sequences provide a limited reference, as they both represent virulent serovar 5 strains. The additional draft sequences of the strains presented here, including a second genomic sequence of strain 29755, in-

clude multiple serovars and virulence phenotypes that will likely lead to the discovery of virulence mechanisms, as well as improved vaccines for disease prevention.

Based on sequences obtained using Illumina GAIIX whole-genome shotgun sequencing, we announce the availability of draft sequences for the following 10 *H. parasuis* strains and their serovars: 29755 (serovar 5), Nagasaki (serovar 5), SW114 (serovar 3), MN-H (serovar 13), 12939 (serovar unknown), 84-15995 (serovar 15), H465 (serovar 11), D74 (serovar 9), 174 (serovar 7), and SW140 (serovar 2). Strains Nagasaki, SW114, 84-15995, H465, D74, 174, and SW140 are serovar reference strains (1). Sequencing libraries were prepared from genomic DNA using an Illumina paired-end DNA sample preparation kit according to the manufacturer's instructions, with a modification to the gel extraction incubation temperature (7). Each library was run on a single sequencing lane for 2 × 75 (strains SW114, 12939, 84-15995, H465, and D74) or 2 × 100 (strains Nagasaki, MN-H, 29755, 174, and SW140) cycles. *De novo* paired-end assembly was performed using the NextGENe assembler version 2.00 (Softgenetics). A total of 15,227,504 to 36,219,053 reads per strain were assembled and produced sequences for which the estimated coverage exceeded 100-

TABLE 1 Genome features and accession no. of the sequenced strains

Strain	Accession no.	No. of contigs	Avg. contig length (bp)	N ₅₀ (bp)	Genome size (Mb)	No. of proteins
29755	ABKM000000000	96	15,760	52,793	1.51	2,127
Nagasaki	APBT000000000	78	27,930	69,670	2.18	2,308
SW114	APBU000000000	98	19,781	83,504	1.94	1,947
MN-H	APBV000000000	82	21,476	68,488	1.76	1,859
12939	APBW000000000	76	25,697	48,588	1.95	1,974
84-15995	APBX000000000	73	28,641	59,326	2.09	2,206
H465	APBY000000000	94	15,941	46,667	1.50	1,540
D74	APBZ000000000	68	32,787	147,970	2.23	2,218
174	APCA000000000	63	21,743	48,645	1.37	1,433
SW140	APCB000000000	77	18,356	84,269	1.41	1,484

fold for each strain. NextGENe ContigMerge was used to assemble contigs. The average G+C percentages of the drafts range from 39.6% to 39.9%. The genome sequences were annotated using the Institute for Genome Sciences (IGS) Annotation Engine (8). The features of the *H. parasuis* draft genomes are summarized in [Table 1](#). Additional characterization of these *H. parasuis* strains is forthcoming.

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/EMBL/GenBank under the accession no. shown in [Table 1](#).

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