

# Full Genome Sequences of All Nine *Chlamydia psittaci* Genotype Reference Strains

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***Chlamydia psittaci* primarily infects birds, but zoonotic transmission occurs in people in close contact with infected birds. The clinical outcome ranges from inapparent disease to pneumonia. Here we report the genome sequences of all 9 *Chlamydia psittaci* genotype reference strains.**

*Chlamydia psittaci* is a Gram-negative, obligate intracellular bacterium causing respiratory disease in birds but also in mammals. Sequencing of the *C. psittaci* major outer membrane protein (*ompA*) gene identified 9 genotypes (A to F, E/B, M56, and WC) (4). Strains with genotypes A to F are isolated from birds, and genotypes WC and M56 represent mammalian isolates (1, 7, 8). The genotypes cluster with host species (5). Genotypes A and B are associated with psittacine birds (cockatoos, parrots, parakeets, and lorries) and pigeons, respectively. Genotype C has been isolated from ducks and geese, whereas genotype D was found mainly in turkeys. The host range of genotype E is more diverse, since it has been isolated from pigeons, ratites, ducks, turkeys, and occasionally humans. Genotype F was isolated from psittacine birds and turkeys. Genotype E/B has been isolated mainly from ducks (4). Genotypes WC and M56 represent isolates from epizootics in cattle and muskrats, respectively (2, 6).

Here we report the genome sequences of all *C. psittaci* genotype reference strains (84/55, genotype A; CP3, genotype B; GR9, genotype C; NJ1, genotype D; MN, genotype E; VS225, genotype F; WS/RT/E30, genotype E/B; M56, genotype M56; WC, genotype WC). Table 1 is a summary of the features of the genomes. Comparative genomics analysis of these genomes will give us insight into the differences in pathogenicity, host tropism, and tissue specificity. Sequencing was performed using shotgun 454 Titanium (Roche) pyrosequencing according to the manufacturer's recommendations. *De novo* and reference mapping assemblies

were performed with the software program Newbler (version 2.3; 454 Life Sciences, Branford, CT). If necessary, subsequent gap closure was done by conventional Sanger sequencing. Genome annotation was performed using the IGS prokaryotic annotation pipeline (3).

**Nucleotide sequence accession numbers.** The genome sequences and plasmids of *C. psittaci* 84/55, CP3, GR9, NJ1, MN, VS225, WS/RT/E30, M56, and WC have been deposited at GenBank under the following accession numbers: CP003790 and CP003812; CP003797 and CP003813; CP003791; CP003798 and CP003816; CP003792 and CP003815; CP003793 and CP003817; CP003794 and CP003819; CP003795 and CP003814; and CP003796 and CP003818, respectively.

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TABLE 1 Features of the genome sequences

Genotype	Strain	Host	Length (bp)	No. of putative coding sequences	% GC	Plasmid <sup>b</sup>	Reference
A	84/55	<i>Amazona</i> sp.	1,172,064	1,124	39	Y	9
B	CP3	<i>Columba livia</i> <sup>a</sup>	1,168,150	1,121	39	Y	8
C	GR9	<i>Anas platyrhynchos</i>	1,147,152	1,045	39.1	N	7
D	NJ1	<i>Meleagris gallapavo</i>	1,161,434	1,049	39	Y	8
E	MN	<i>Homo sapiens</i>	1,168,490	1,040	39	Y	4
F	VS225	Parakeet	1,157,385	1,113	39	Y	2
E/B	WS/RT/E30	<i>Anas platyrhynchos</i>	1,140,789	1,048	39	Y	4
M56	M56	<i>Ondatra zibethicus</i>	1,161,385	1,046	38.7	Y	6
WC	WC	<i>Bos taurus</i>	1,172,265	1,050	39.1	Y	2

<sup>a</sup> Isolated from an urban pigeon.

<sup>b</sup> Y, yes; N, no.

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