



Draft Genome Sequences of *Flavobacterium coviae* Strains LSU-066-04 and LV-359-01

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TABLE 1 Virulence factors predicted to be produced by *F. coviae* LSU-066-04 and *F. coviae* LV-359-01 based on previous studies; percent similarities are to *F. coviae* AL-02-36^T

Gene	Reference	Strain(s) used	<i>Flavobacterium</i> species	LSU-066-04 percent similarity; E value; query cover	LV-359-01 percent similarity; E value; query cover
<i>porV</i>	13, 14	C#2 and MS-FC-4	<i>F. coviae</i> and <i>F. columnare</i>	99.29%; 0.0; 100%	99.29%; 0.0; 100%
<i>gldN</i>	13, 14	C#2, IA-S-4, and MS-FC-4	<i>F. coviae</i> , <i>F. columnare</i> , and <i>F. columnare</i>	98.67%; 0.0; 100%	98.67%; 0.0; 100%
<i>gldK</i>	13	C#2 and IA-S-4	<i>F. coviae</i> and <i>F. columnare</i>	99.78%; 0.0; 100%	100.00%; 0.0; 100%
<i>gldL</i>	13	C#2 and IA-S-4	<i>F. coviae</i> and <i>F. columnare</i>	100.00%; 4e-116; 100%	100.00%; 4e-116; 100%
<i>gldM</i>	13	C#2 and IA-S-4	<i>F. coviae</i> and <i>F. columnare</i>	99.50%; 0.0; 100%	99.50%; 0.0; 100%
<i>sprA</i>	13	C#2 and IA-S-4	<i>F. coviae</i> and <i>F. columnare</i>	99.36%; 0.0; 100%	99.84%; 0.0; 100%
<i>sprE</i>	13	C#2 and IA-S-4	<i>F. coviae</i> and <i>F. columnare</i>	97.44%; 0.0; 100%	97.18%; 0.0; 100%
<i>sprT</i>	13	C#2 and IA-S-4	<i>F. coviae</i> and <i>F. columnare</i>	99.15%; 6e-163; 100%	99.15%; 6e-163; 100%
<i>nirS</i>	15	94-801	<i>F. coviae</i>	100.00%; 0.0; 100%	100.00%; 0.0; 100%
<i>cylA</i>	15	MS-FC-4	<i>F. columnare</i>	100.00%; 0.0; 100%	100.00%; 0.0; 100%
C6N29_11540	14	MS-FC-4	<i>F. columnare</i>	100.00%; 0.0; 100%	100.00%; 0.0; 100%
C6N29_11545	14	MS-FC-4	<i>F. columnare</i>	99.44%; 0.0; 100%	99.37%; 0.0; 100%

To predict the presence of virulence factors in *F. coviae* LSU-066-04 and *F. coviae* LV-359-01, a tBLASTx analysis of each genome was conducted with previously described virulence factors associated with columnaris disease. Interestingly, both *F. coviae* isolates were predicted to carry all of the genes previously determined to have a role in columnaris disease, with high percent similarities to each gene (Table 1). These predicted virulence factors included genes associated with T9SS, denitrification, and anaerobic growth. It is likely that there are many other virulence factors expressed by these *F. coviae* strains, but their functional roles in virulence have not yet been determined. The genome sequences for these two virulent strains LSU-066-04 and LV-359-01 will provide a resource to explore the specific factors that contribute to *F. coviae* virulence and contrast this with virulence factors expressed by the other *Flavobacterium* spp. that cause columnaris disease.

Data availability. This Whole Genome Shotgun project for both LSU-066-04 and LV-359-01 has been deposited at GenBank under the accession numbers [JALDSR0000000000](#) and [JALDSS0000000000](#), respectively. The versions described in this paper are versions [JALDSR0100000000](#) and [JALDSS0100000000](#), respectively. LSU-066-04 is under the BioSample accession number [SAMN26856626](#), and LV-359-01 is under the BioSample accession number [SAMN26856627](#). Both strains are under BioProject accession number [PRJNA818358](#) with the SRA accession numbers [SRX15461022](#) and [SRX1461023](#).

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