Electronic supplementary materials
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Pathogenicity of an FAdV-4 isolate to chickens and its genomic analysis[*#]

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Table S1 Primers used to amplify the complete genomic sequence of FAdV-4 strain SD1511

Primer	Location (bp)	Upstream primer	Downstream primer	Length (bp)
1	1~1213	CATCATCTTATATAACCGCGTCT	CCTCCTCGGATCGTGTCAT	1213
2	1150~2399	TTGAGCGAATCTTTACACCG	TCCACCATAGTTCCCTCCC	1250
3	2263~3620	GTGGATTGGCGGAATAGGG	TTGGGTTGACGAAGTAAGAGCA	1358
4	3387~4734	GCGTCCTTCTTGATCCTCG	CGTCCACCTGTCCTGCTTC	1351
5	4605~5979	ACTTGTTCGTCTTCGGGTGTC	CCTGTTCCTCCAACTGCCTC	1375
6	5859~7295	GGATGCTACTCTGGCGTTGT	CGACTCCTTTCGCTGGTG	1437
7	7114~8511	GCGAGTCTGAGGGAGAAATG	CCACAACGAGCAGCTAACG	1398
8	8415~9781	GGGGTGTTCGGTGTCGTA	TAGACATCATCACGCTTCACAA	1367
9	9593~10995	GGGCGTTGCTGAGCATTT	CACCTTACCGTCCGATTTCTA	1404
10	10705~12235	ATGAAACGCACAAAGACGG	AGACAAGTCGGGAGACATCG	1530
11	12044~13411	GATGGTATCGCTGTTGGAAGTC	GTCACCGACAGATCCGGATTAC	910
12	13174~14680	TATCGCTGTTGGAAGTCGC	AGAGGAGTCGTCGTGGGTC	1364
13	14383~15859	TCTATACGTGCTTTCGGTGGT	GCTGCGGGTTCAGTTTGA	1507
14	15617~16954	TATCGCTCGGGACAGGTAGT	GCCGTAGTCGTAGAAGGTGC	1477
15	16836~18132	TTGCTCCGCTTGTTCGTG	CGGTAAGTGTCCCTTAATAATGG	1338
16	17974~19310	GCGGAATCAGAGGGTCGGGACT	ATCGGGCACCGTCAGCAAGG	1297
17	18920~20333	AACGCTGCTCCCCTTTTA	GCCCGTAGTCAGGTCTCG	1337
18	20096~21856	ACAGACAGGACGGACCAGC	TGCGAACCTAGACGAAACG	1414
19	21567~23236	GAGATGGTGACGGAGGTG	CCAGTTTCTGTGGTGGTTG	1786

20	12044~13411	CCAACGCCACTACCAACT	GAAAGCGGTGACGAGGAT	1670
21	22906~24375	GTGGACCATCCCGTTCAGT	GCATCGAGCAGTGCGTGT	1470
22	24196~25465	TGTGCGGGTGCTTGTGGT	GCGAGGTAGGAGGCGACTAA	1270
23	25104~26537	CTGGTCGTCTTCTTCTTCGG	CAGAGTCGCTAGAGTGGCTAAA	1434
24	26362~27617	CGGTTACTATTCGGCAGATGG	GATAAGCCTCGATGGTTTCCT	1256
25	27372~28701	CCTTCCATCACGGTTTCG	TGCTCATCTGGTCCTCTTCC	1330
26	28610~29820	GCCCGAAATCTACAATCCC	ACCTCCCATCATGCCTCC	1210
27	29675~30942	CAGACCAACAGCCCTACGC	CGAGCACTTTGAGCACCC	1268
28	30804~32221	GCCACTAAGCAAGCCAACG	CCTGATCCACGAGCAAGGT	1418
29	32117~33234	ACGATGACTGGGAACTGGC	GGACAAATGGACGATCAATAAA	1118
30	33039~34380	CCGCTACACCCTTCTATGCT	CGGTCCCTTCTGTGATTGC	1342
31	34253~35709	CGGAGATTTGCGATTGTGAGT	TGACTCATCATGGGTGTGGC	1456
32	35553~37068	ACACTAACTTCCTCATTGACCCTC	TGTCTGTCTGAACCTGCCTACC	1512
33	36770~37942	ACGATGGCGTGATAGGCGGAGC	ATGAACCGTAGCCCCGCCCTTT	1173
34	37667~38921	ACTACCGAGATCAGCCTGAAGA	CAGACTAAGGGAAAGTTGGAGAA	1225
35	38750~40038	GAAATGCTTCCTCCTTCACG	AAGTTTATAGGGATCTCGGGTTA	1239
36	39930~41132	AACCCGAGATCCCTATAAACTT	TAGTGCCTGTCCATTTGCC	1203
37	40945~42236	TGGCAAATGGACAGGCACT	TTGATTCGGTGGAGGTCGT	1292
38	42047~43398	CCCACTACCGCTACCACCAC	ATCACGCTGACGCTCCTCC	1356
39	42817~43756	AGCATGAATCAACTCGGTGTC	CATCATCTTATATAACCGCGTCT	945

Primers were designed based on the available nucleotide sequence of FAdV-4 strain JSJ13 (GenBank Accession No. KM096544). Primer locations are listed according to the genome sequence of JSJ13.

Table S2 Genome sequence identities (%) among SD1511 and FAdV-4 reference strains

	SD1511	**ON1**	**KR5**	**MX-SHP95**	**B1-7**	**HLJFAd15**	**HB1510**	**JSJ13**	**CH\SXCZ\2015**
SD1511		93.6	93.8	94.6	93.5	100.0	100.0	99.9	100.0
ON1	1.7		98.9	98.5	97.7	93.6	93.6	93.5	93.6
KR5	1.5	0.7		98.4	98.1	93.8	93.8	93.7	93.8
MX-SHP95	1.0	1.2	1.2		97.8	94.6	94.6	94.5	94.6
B1-7	1.8	1.6	1.4	1.8		93.6	93.6	93.5	93.6
HLJFAd15	0.0	1.7	1.5	1.0	1.8		100.0	99.9	100.0
HB1510	0.0	1.7	1.5	1.0	1.8	0.0		99.9	100.0
JSJ13	0.0	1.7	1.5	1.0	1.8	0.0	0.0		99.9
CH\SXCZ\2015	0.0	1.7	1.5	1.0	1.8	0.0	0.0	0.0	

Percent identify

Percent Divergence