

Supplementary data

Supplementary Table S1 Information on primers for amplifying all regions of 15 CVA14 strains.

Primer	Position (nt)	Primer sequence (5'-3')	Orientation
0001S48		GGGGACAAGTTTGTACAAAAAAGCAGGCTTTAAACAGCTCTGGGGTT	Forward
CVA14-872R	872-891	TTGGTGAAGTTCAGGGTGGA	Reverse
CVA14-636F	617-636	AGCTATTGGATTGGCCATCC	Forward
CVA14-1419R	1419-1438	GGGGGTGTGTGTGTTTCATTA	Reverse
CVA14-815F	798-815	AACACCGTTCGTGATGGG	Forward
CVA14-1640R	1640-1657	CTGAAGATGCATAGGCCA	Reverse
CVA14-1489F	1470-1489	GTGTTGGATGCTGGTATAACC	Forward
CVA14-2407R	2407-2426	GTGTCTCAGCTGGTACAACA	Reverse
CVA14-2135F	2119-2135	GCTTACACTCCACCAGG	Forward
CVA14-2974R	2974-2993	TGCCATTCATAGGTGTTGCG	Reverse
CVA14-2871F	2852-2871	ATAGCTTCCACCCCAGATGG	Forward
CVA14-3721R	3721-3740	ATGCCAACAACACCGTGTTG	Reverse
CVA14-3560F	3541-3560	AAACACTACCCAGTCAGCTT	Forward
CVA14-4470R	4470-4490	CAGGTTCAATACGGTGTTTGC	Reverse
CVA14-4307F	4288-4307	TCTGCTGCTTCACAAGAGGA	Forward
CVA14-4871R	4871-4890	TGAGTCCGTCACCTCAATGT	Reverse
CVA14-4589F	4570-4589	CTGTCGTAAGTTCCAACCAC	Forward

CVA14-5401R	5401-5420	AGGTCGCTAATAGCATCCGG	Reverse
Primer	Position (nt)	Primer sequence (5'-3')	Orientation
CVA14-5070F	5050-5070	GACCACCCAAGTTTAGACCAA	Forward
CVA14-5863R	5863-5882	GACCTGCCTTAGTGGGAAAA	Reverse
CVA14-5742F	5723-5742	ATGCCATCAATGTTTGTGCC	Forward
CVA14-6689R	6689-6711	CTAGCATCATAACCTGAGTAGTC	Reverse
CVA14-6478F	6457-6478	AAAGGGAAATCTCGCCTGATAG	Forward
CVA14-7410R	7410-7429	GTGGATACAAATTTACCCCC	Reverse
CVA14-6911F	6892-6911	TTGTGTCCTTGGTGGAATGC	Forward
7500A		GGGGACCACTTTGTACAAGAAAGCTGGG(T) ₂₄	Reverse

Supplementary Table S3 Nucleotide and amino identity (%) of 15 CVA14 strains compared with the CVA14 prototype strain (AY421769.1/G-14)

Name of strain	5'UTR	P1				P2			P3				3'UTR
		VP4	VP3	VP2	VP1	2A	2B	2C	3A	3B	3C	3D	
CHN_2013_BJ_30	85.3	86.9 (89.7)	83.8 (97.9)	83.3 (97.2)	81.9 (95.9)	81.7 (95.3)	82.4 (100)	84.2 (98.7)	82.5 (98.8)	93.9 (95.4)	85.2 (98.3)	84.6 (96.3)	93.8
CHN_2013_BJ_59	85.9	85.9 (89.7)	84.5 (97.9)	83 (97.2)	82.6 (95.9)	81.5 (95.3)	82.8 (100)	84.1 (98.7)	82.5 (98.8)	90.9 (95.4)	84.8 (98.3)	84.7 (96.1)	93.8
CHN_2009_HE_27	86.9	87.4 (89.7)	84.5 (97.9)	82 (96.8)	82.9 (96.2)	81.3 (95.3)	82.4 (100)	85.2 (98.4)	79.4 (98.8)	92.4 (100)	83 (97.8)	84.7 (97.8)	91.3
CHN_2013_HE_81	86.7	86.9 (91.1)	84.8 (97.5)	82.4 (98.4)	82.9 (96.6)	81.3 (94)	81.4 (98.9)	85.3 (97.8)	79.8 (98.8)	87.8 (100)	83.6 (96.7)	84 (96.7)	93.8
CHN_2019_HA_317	86.6	85 (91.1)	84.9 (97.9)	83.9 (97.6)	82.8 (95.9)	81.1 (94.6)	83.5 (98.9)	85 (98.4)	82.5 (97.6)	87.8 (100)	85.4 (98.3)	84.1 (96.3)	91.3
CHN_2013_HA_07	86.7	86.4 (89.7)	84.8 (97.9)	83.4 (97.6)	82.3 (95.9)	80.8 (94.6)	82.8 (100)	84.4 (98.7)	83.3 (98.8)	93.9 (95.4)	84.6 (98.3)	84 (95.8)	92.5
CHN_2013_HA_08	85.6	86.4 (91.1)	84.9 (97.9)	82.8 (98.4)	82.5 (96.9)	82 (94)	81.1 (98.9)	85.4 (98.1)	79.8 (98.8)	89.3 (100)	83.6 (96.1)	84.3 (96.9)	93.8
CHN_2013_HA_25	86.3	86.4 (89.7)	84.2 (97.9)	83.4 (97.2)	81.8 (95.9)	81.5 (95.3)	82.8 (100)	84.2 (98.7)	82.9 (98.8)	93.9 (95.4)	84.8 (98.3)	84.5 (96.1)	93.8
CHN_2013_HA_90	85.9	86.4 (89.7)	84.5 (97.9)	83.4 (97.6)	82 (95.9)	81.5 (94.6)	82.1 (100)	84.5 (98.4)	83.3 (98.8)	93.9 (95.4)	84.6 (98.3)	84.4 (96.3)	92.5
CHN_2013_LN_05	87	87.4 (91.1)	83.6 (97.5)	83 (96.8)	82.2 (95.9)	82.4 (95.3)	83.1 (100)	84.3 (98.7)	82.9 (98.8)	90.9 (95.4)	85.6 (98.3)	84.5 (96.1)	92.5

CHN_2013_TJ_52	86.1	86.4 (89.7)	84.4 (97.9)	82.9 (97.2)	82.2 (95.9)	80.6 (94.6)	82.1 (100)	84.4 (98.7)	82.1 (98.8)	93.9 (95.4)	85.4 (98.3)	84.1 (96.3)	93.8
Name of strain	5'UTR	P1				P2			P3				3'UTR
		VP4	VP3	VP2	VP1	2A	2B	2C	3A	3B	3C	3D	
CHN_2014_YN_41	86.5	87.9 (89.7)	84.2 (97.9)	83.2 (97.2)	81.9 (95.6)	81.1 (94.6)	83.1 (97.9)	84.3 (98.7)	82.9 (98.8)	95.4 (95.4)	84.8 (98.9)	84.1 (96.3)	91.3
CHN_2015_SN_61	89.9	89.4 (89.8)	84.5 (97.9)	84.1 (97.2)	82.2 (95.9)	84.6 (96)	85.1 (100)	83.7 (97.8)	83.3 (97.6)	84.8 (90.9)	84.1 (97.2)	83.9 (95.6)	92.5
CHN_2013_SC_30	85	86.9 (91.1)	84.4 (97.9)	83 (97.2)	82.6 (95.9)	81.1 (95.3)	82.8 (100)	83.9 (98.4)	82.9 (98.8)	92.4 (95.4)	85.7 (98.3)	84.7 (96.3)	92.5
CHN_2013_SC_36	86.8	86.9 (91.1)	84.5 (97.9)	82.6 (97.2)	82.5 (95.9)	81.5 (95.3)	82.8 (98.9)	84.1 (98.7)	82.9 (98.8)	93.9 (100)	85.4 (98.3)	84.4 (96.3)	92.5