

## Electronic Supplementary Material

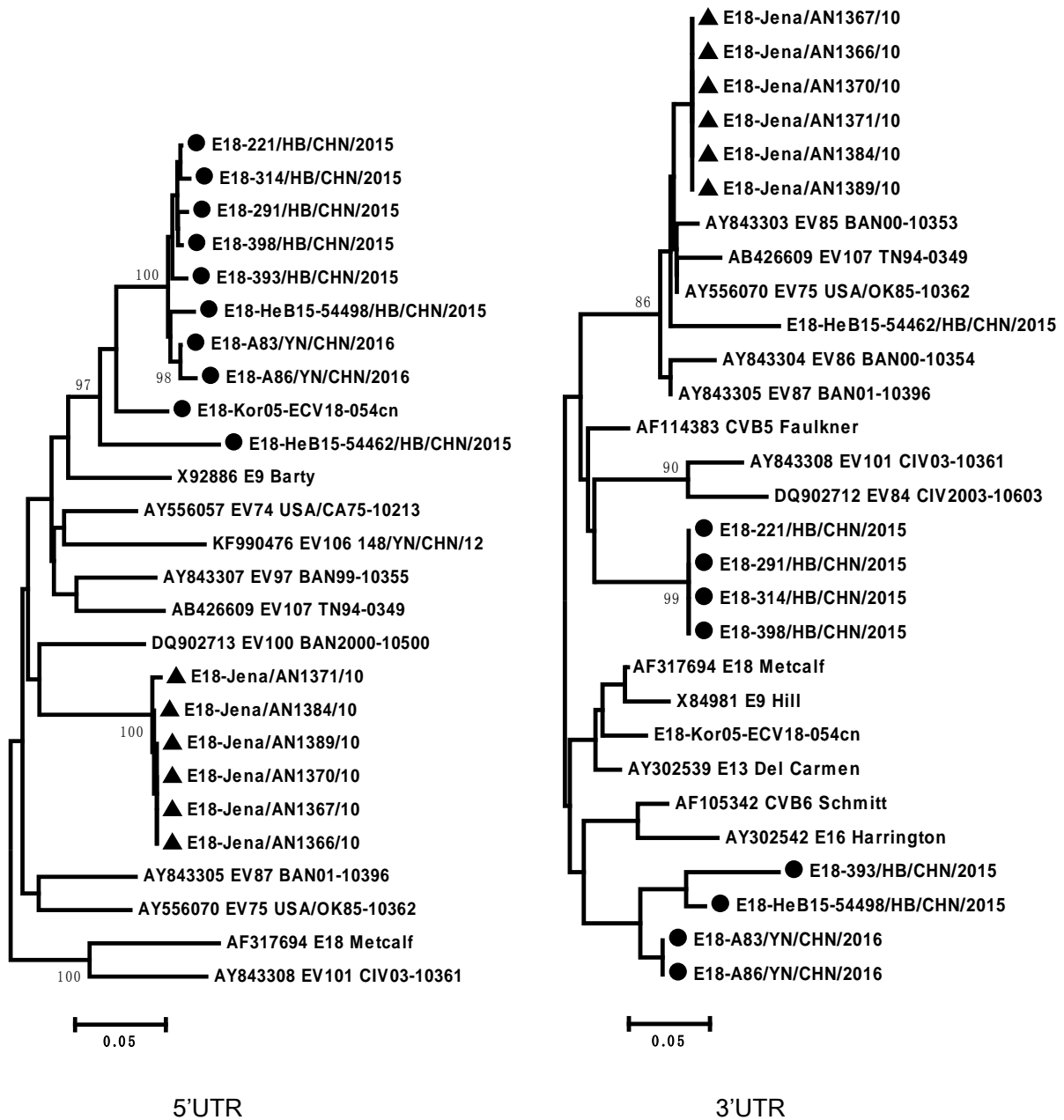
### Molecular Epidemiology of Echovirus 18 Circulating in Mainland China from 2015 to 2016

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**Figure S1.** Phylogenetic trees showing the relationships between the E18 isolates and EV-B prototypes. These were constructed by the different genomic regions of 17 complete E18 genomic sequences and other EV-B prototype sequences. The neighbour-joining trees were reconstructed based on the 5' UTR and 3' UTR regions, respectively. Triangles indicated the subgenotype C1. Filled circle indicated the subgenotype C2. Squares indicated the E18 prototype Metcalf strain. The percentage of bootstrap (percentage of 1000 pseudoreplicate datasets) replicates supporting the trees are indicated at the nodes.

**Table S1.** List of nucleotide sequences of primer for amplification of the whole genome sequences of E18

Primer	Nucleotide position (nt)	Primer sequence (5'–3')	Orientation	Reference
0001S48a		GGGGACAAGTTTGTACAAAAAAGCAGGCT TAAAACAGCTCTGGGGTT	Forward	[1]
E18-3A	944–963	TCACTATACCCGCATTCCTC	Reverse	This study
E18-4S	861–880	GCATCAAACAGGCAAGAGT	Forward	This study
E18-4A	2044–2061	TTTCACACTCCCGACCA	Reverse	This study
E18-5S	1788–1807	CAATCGCCATCTGCTATGCC	Forward	This study
E18-5A	2798–2818	CTTGCTCTAATTGCGTCCCTT	Reverse	This study
E18-VP1-S	2270–2289	GCAGCAAGACCCGTACACCA	Forward	This study
E18-VP1-A	3662–3681	ATCCCCTCACCGCCCATAGT	Reverse	This study
E18-6S	2726–2745	GGAGATGGCACAGTTAAGAA	Forward	This study
E18-6A	3733–3752	AATCCCTGACTCCCTGTTCC	Reverse	This study
E18-7S	3604–3623	TACTAGCAGCAGGGTTTTCC	Forward	This study
E18-7A	4577–4596	ACATCCTTTCCATCCGGGTT	Reverse	This study
E18-8S	4457–4574	GAAGTCAGTTGCCACGAA	Forward	This study
E18-8A	5538–5456	CCTATCGTAAATACCCAGC	Reverse	This study
E18-9S	5324–5343	GATGCCCAACCAAAAGCCTA	Forward	This study
E18-9A	6389–6409	GCCACCTTTTCTGCTGATCTAA	Reverse	This study
E18-10S	6277–6296	ACCCGTATGTAGCACTAGGT	Forward	This study
E18-10A	7235–7255	ACGCAGGCAAAGTTAAACAGC	Reverse	This study
E18-11S	6688–6707	AGTTGGGATACTCTCATAAG	Forward	This study
7500Aa		GGGGACCACTTTGTACAAGAAAGCTGGG(T) 24	Reverse	[1]

1. Yang CF, Naguib T, Yang SJ, Nasr E, Jorba J, Ahmed N, et al. Circulation of endemic type 2 vaccine-derived poliovirus in Egypt from 1983 to 1993. *J Virol.* 2003;77(15):8366–77. Epub 2003/07/15. PubMed PMID: 12857906; PubMed Central PMCID: PMC165252.

**Table S2.** List of the 84 complete VP1 encoding sequences and 11 complete genome sequences of E18 downloaded from GenBank.

Isolates	GenBank Accession Number	The place of isolation	The year of isolation	Sequences
HBPS201501	KU216191	China	2015	VP1
HBPS201506	KU216196	China	2015	VP1
HBPS201510	KU216200	China	2015	VP1
HBPS201512	KU216202	China	2015	VP1
SJZ-211	KY303780	China	2015	VP1
SJZ-255	KY303815	China	2015	VP1
SJZ-221	KY303805	China	2015	VP1
SJZ-262	KY303804	China	2015	VP1
SJZ-291	KY303813	China	2015	VP1
SJZ-299	KY303827	China	2015	VP1
SJZ-306	KY303810	China	2015	VP1
SJZ-314	KY303825	China	2015	VP1
SJZ-309	KY303818	China	2015	VP1
SJZ-321	KY303794	China	2015	VP1
SJZ-319	KY303799	China	2015	VP1
SJZ-351	KY303776	China	2015	VP1
SJZ-289	KY303823	China	2015	VP1
SJZ-360	KY303826	China	2015	VP1
SJZ-375	KY303821	China	2015	VP1
SJZ-422	KY303811	China	2015	VP1
SJZ-433	KY303789	China	2015	VP1
SJZ-392	KY303820	China	2015	VP1
SJZ-398	KY303781	China	2015	VP1
SJZ-393	KY303784	China	2015	VP1

SJZ-405	KY303779	China	2015	VP1
SJZ-418	KY303792	China	2015	VP1
399-CSF/ECHO18/RUS/Omsk/2013	KU133628	Russia	2013	VP1
CF018014/CSF_3.64_FRA12	HG793724	France	2012	VP1
CF214038/PL_CF214020/CSF_5.27	HG793725	France	2012	VP1
CF284048/PL_CF284010/CSF_4.24	HG793726	France	2012	VP1
CF293061/CSF_4.68_FRA12	HG793727	France	2012	VP1
284-CSF/ECHO18/RUS/Omsk/2012	KU133587	Russia	2012	VP1
330-CSF/ECHO18/RUS/Omsk/2012	KU133609	Russia	2012	VP1
383-CSF/ECHO18/RUS/Omsk/2013	KU133621	Russia	2012	VP1
Mahdia/M3/CSF_5.42_TUN_2012	LN713457	Tunisia	2012	VP1
ChZJ-1/ZJ/CHN	KF311743	China	2011	VP1
CF217037/CSF_4.16_FRA11	HG793719	France	2011	VP1
CF298011/CSF_5.11_FRA11	HG793720	France	2011	VP1
CF332118/CSF_4.76_FRA11	HG793722	France	2011	VP1
CF339116/CSF_4.65_FRA11	HG793723	France	2011	VP1
EV_NL_120	KU561038	Netherlands	2011	VP1
EV_NL_130	KU561039	Netherlands	2011	VP1
CF247028/CSF_3.47_FRA10	HG793718	France	2010	VP1
E-18/PMKD0134/THA/2010	KU574621	Thailand	2010	VP1
N-242	JN203849	India	2007	VP1
N-291	JN203850	India	2007	VP1
N-766	JN203851	India	2007	VP1
N-904B	JN203852	India	2007	VP1
247016-06	AM711068	France	2006	VP1
303018-06	AM711073	France	2006	VP1
CF272084-06	AM711101	France	2006	VP1

CF303024-06	AM711105	France	2006	VP1
CF287012-06	AM711103	France	2006	VP1
05430/SD/CHN/2005/E18	GQ329813	China	2005	VP1
TR157051-05	AM236978	France	2005	VP1
CF1400191-05	AM236918	France	2005	VP1
TR129002-05	AM236972	France	2005	VP1
TR178027-05	AM236984	France	2005	VP1
04.356.3127	FJ868349	Australia	2005	VP1
05.318.4308	FJ868307	Australia	2005	VP1
05.073.4094	FJ868350	Australia	2005	VP1
05.165.3625	FJ868306	Australia	2005	VP1
05.206.3218	FJ868351	Australia	2005	VP1
05.207.4410	FJ868353	Australia	2005	VP1
05.220.3740	GU142897	Australia	2005	VP1
04.090.3608	FJ868347	Australia	2004	VP1
E18_CF1442_FRA02	HF948106	France	2002	VP1
01.092.3110	GU142900	Australia	2001	VP1
01.267.3334	GU142901	Australia	2001	VP1
E18_CF506_FRA00	HF948104	France	2000	VP1
E18_CF703_FRA00	HF948105	France	2000	VP1
00.220.3243	GU142898	Australia	2000	VP1
96/15364-23/99	AY208091	Sweden	1999	VP1
99/00010-41/99	AY208092	Sweden	1999	VP1
97.113.0269	GU142902	Australia	1997	VP1
Metcalf	AF081331	United States	1955	VP1
Kor05-ECV18-054cn	HM777023	South Korea	2005	VP1
TR115015-05	AM236597	France	2005	VP1

Jena/ST9524/10	KX139446	Germany	2010	VP1
Jena/AN1362/10	KX139450	Germany	2010	VP1
Jena/AN1384/10	KX139457	Germany	2010	VP1
Jena/VI10517/10	KX139449	Germany	2010	VP1
E18-A83	KY828851	China	2016	VP1
E18-A86	KY828852	China	2016	VP1
Metcalf	AF081331	United States	1955	Genome
Kor05-ECV18-054cn	HM777023	South Korea	2005	Genome
Jena/AN1366/10	KX139453	Germany	2010	Genome
Jena/AN1367/10	KX139454	Germany	2010	Genome
Jena/AN1370/10	KX139455	Germany	2010	Genome
Jena/AN1371/10	KX139456	Germany	2010	Genome
Jena/AN1384/10	KX139457	Germany	2010	Genome
Jena/AN1389/10	KX139458	Germany	2010	Genome
E18-314/HB/CHN/2015	KX767786	China	2015	Genome
E18-A83/YN/CHN/2016	KY828851	China	2016	Genome
E18-A86/YN/CHN/2016	KY828852	China	2016	Genome

**Table S3.** Amino acid changes in *VPI* gene of E18 strains belonged to subgenotypes C1 and C2 comparing with the prototype strain Metcalf.

No.	Amino acid site	Subgenotpe C1 & Metcalf		Subgenotpe C2 & Metcalf	
		Variation.	Frequency (%)	Variation.	Frequency (%)
1	3	N3K	3.6	N3K/D	1.5/ 1.5
2	4			Q4P	1.5
3	6	R6K	96.4	R6K	3.1
4	8	V8G	3.6	V8A	1.5
5	9	A9V	3.6	A9T	3.1
6	10	N10D/ E	92.9/ 3.6	N10D/ S	32.3, 1.5
7	11			T11I	1.5
8	12			Q12R	1.5
9	17			S17T/A	12.3/ 1.5
10	20	T20K/ R	96.4/ 3.6	T20K/ R	96.9/ 3.1
11	21	E21K	3.6		
12	22	I22K	3.6		
13	25	L25I	3.6		
14	34	S34L	3.6		
15	38	P38H	3.6		
16	39			S39R	1.5
17	40	D40E	3.6		
18	42	I42M	10.7	I42L	100
19	44	T44I	3.6	T44S	1.5
20	45	R45K	7.1		
21	47	V47G	3.6		
22	48			V48M	1.5
23	58	I58V	100	I58V	100
24	59	E59K	3.6		
25	67	C67W	3.6		
26	69	F69S	3.6		
27	70	M70I	3.6	M70I	1.5
28	72			Q72H	1.5
29	75	I75L	100	I75L	98.5
30	77	G77E	3.6		



31	79	E79K	3.6		
32	81	S81T	3.6		
33	83	D83N	3.6		
34	84	R84N	100	R84N/ S	98.5/ 1.5
35	86	A86S	10.7		
36	92	I92V	3.6	I92V	93.8
37	93			R93K	1.5
38	104			M104L	26.9 <sup>a</sup>
39	107	Y107D	3.6		
40	114	M114I	3.6		
41	121	C121S	3.6		
42	127	I127Q	100	I127Q	100
43	129	D129E	100	D129E	100
44	136	T136K	3.6		
45	139	I139V	7.1		
46	150	A150P	3.6		
47	155	Y155N	3.6		
48	163	P163Q	3.6		
49	169	E169K	7.1		
50	174	P174A	100	P174A	100
51	187	Y187N	7.1		
52	189	S189L	100	S189L	100
53	202	T202I	3.6	T202A	3.1
54	204	G204S	3.6		
55	211	M211L	3.6		
56	215	Y215F	3.6	Y215F	66.2 <sup>a</sup>
57	216	I216V	3.6	I216V	66.2 <sup>a</sup>
58	217	R217K	7.1	R217T	1.5
59	221	R221K	100	R221K/ N	96.9/ 3.1
60	222	S222N	3.6		
61	233			V233I	1.5
62	240			I240V	1.5
63	254	I254N	3.6		
64	257	R257G	100	R257G/ S/ N	66.2/ 32.3/ 1.5
65	262	V262A/ T/ M	71.4/ 25.0/ 3.6	V262A	3.1

66	266	I266V	100	I266V	93.8
67	269	S269A/ P	96.4/ 3.6	S269A/ V/ T/ P	90.8/ 4.6/ 3.1/ 1.5
68	271	T271K	96.4	T271K	100
69	275	D275E	100		
70	282	S282G	10.7	S282G	4.6
71	285	A285V/ T	21.4/ 10.7	A285V/ T	72.3/ 3.1
72	287	H287R	64.3	H287R/ F	66.2/ 1.5

Notes: <sup>a</sup>All from China.