

# FAO World Reference Laboratory for Foot-and-Mouth Disease (WRLFMD)

## Genotyping Report

Report Date for this Batch: 6 May 2015

FMDV type Asia 1

Country: Pakistan

Period: 2014-2015

No. of samples: 6

BATCH: WRLFMD/2015/00002



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# FAO World Reference Laboratory for FMD Genotyping Report

IAH-P-EP-MEG-FOR-005-3

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Serotype: ASIA1	Report date: 06/05/2015
WRLFMD Ref No: PAK/26/2014	Reported by: N.J. Knowles
Batch No: WRLFMD/2015/00002	Checked by: K. Bachanek-Bankowska
Sender Ref: PK19	
Location: Karachi, Sindh, Pakistan	Topotype: ASIA
Date collected: 18/01/2014	Genotype/strain: Sindh-08
Date received by WRLFMD: 24/02/2015	Sequence filename: PAK14-26.SEQ
Date received for sequencing: 19/03/2015	Date sequence last updated: 24/03/2015
Species: Cattle	No. of Nt determined: 633
Material used: BTy1 06/03/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 633
RT-PCR primers: As1-1C530F/EUR-2B52R	Total no. of comparisons: 566
As1-1C613F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 71 days
	Sequencing time: 48 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	Asia1/PAK/39/2014	PAK14-39	633	633	0	100.00	0.00	ASIA	Sindh-08
2	Asia1/PAK/35/2014	PAK14-35	633	628	0	99.21	0.79	ASIA	Sindh-08
3	Asia1/PAK/37/2014	PAK14-37	633	627	0	99.05	0.95	ASIA	Sindh-08
4	Asia1/PAK/46/2014	PAK14-46	633	625	0	98.74	1.26	ASIA	Sindh-08
5	Asia1/PAK/22/2012	PAK12-22	633	619	0	97.79	2.21	ASIA	Sindh-08
6	Asia1/PAK/27/2012	PAK12-27	633	619	0	97.79	2.21	ASIA	Sindh-08
7	Asia1/PAK/57/2012	PAK12-57	633	619	0	97.79	2.21	ASIA	Sindh-08
8	Asia1/PAK/35/2012	PAK12-35	633	618	0	97.63	2.37	ASIA	Sindh-08
9	Asia1/PAK/10/2012	PAK12-10	633	616	0	97.31	2.69	ASIA	Sindh-08
10	Asia1/AFG/66/2011	AFG11-66	633	614	0	97.00	3.00	ASIA	Sindh-08
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	Asia1/PAK/8/2008	PAK08-08	633	602	0	95.10	4.90	ASIA	Sindh-08
2	Asia1/AFG/1/2001 (DQ121109)	AFG01-01	633	577	0	91.15	8.85	ASIA	Group I
3	Asia1/IND/762/2003* (DQ101240)	IND03-AB	633	543	0	85.78	14.22	ASIA	Group III
4	Asia1/Shamir/ISR/89	ISR89--A	633	539	0	85.15	14.85	ASIA	Unnamed
5	Asia1/IND/14/95* (AF390678)	IND95-AA	633	538	0	84.99	15.01	ASIA	Unnamed
6	Asia1/IND/18/80 (DQ121116)	IND80-18	633	537	0	84.83	15.17	ASIA	Group V
7	Asia1/YNBS/CHA/58 (AY390432)	CHA58-AA	633	535	0	84.52	15.48	ASIA	Unnamed
8	Asia1/IND/63/72* (AY304994)	IND72C63	630	532	0	84.44	15.56	ASIA	Unnamed
9	Asia1/IRN/10/2004 (DQ121119)	IRN04-10	633	533	0	84.20	15.80	ASIA	Group VIb
10	Asia1/HKN/19/74	HKN74-19	633	532	0	84.04	15.96	ASIA	Unnamed

nt, nucleotides

\*, not a WRLFMD reference number

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# FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: ASIA1	Report date: 06/05/2015
WRLFMD Ref No: PAK/35/2014	Reported by: N.J. Knowles
Batch No: WRLFMD/2015/00002	Checked by: K. Bachanek-Bankowska
Sender Ref: PK05	
Location: Rahim Yar Khan, Punjab, Pakistan	Topotype: ASIA
Date collected: 08/11/2014	Genotype/strain: Sindh-08
Date received by WRLFMD: 24/02/2015	Sequence filename: PAK14-35.SEQ
Date received for sequencing: 19/03/2015	Date sequence last updated: 24/03/2015
Species: Water Buffalo	No. of Nt determined: 633
Material used: BTy1 11/03/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 633
RT-PCR primers: As1-1C530F/EUR-2B52R	Total no. of comparisons: 566
As1-1C613F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 71 days
	Sequencing time: 48 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	Asia1/PAK/37/2014	PAK14-37	633	632	0	99.84	0.16	ASIA	Sindh-08
2	Asia1/PAK/46/2014	PAK14-46	633	630	0	99.53	0.47	ASIA	Sindh-08
3	Asia1/PAK/26/2014	PAK14-26	633	628	0	99.21	0.79	ASIA	Sindh-08
4	Asia1/PAK/39/2014	PAK14-39	633	628	0	99.21	0.79	ASIA	Sindh-08
5	Asia1/PAK/22/2012	PAK12-22	633	620	0	97.95	2.05	ASIA	Sindh-08
6	Asia1/PAK/27/2012	PAK12-27	633	620	0	97.95	2.05	ASIA	Sindh-08
7	Asia1/PAK/57/2012	PAK12-57	633	620	0	97.95	2.05	ASIA	Sindh-08
8	Asia1/PAK/35/2012	PAK12-35	633	619	0	97.79	2.21	ASIA	Sindh-08
9	Asia1/BAR/3/2011	BAR11-03	633	617	0	97.47	2.53	ASIA	Sindh-08
10	Asia1/BAR/4/2011	BAR11-04	633	617	0	97.47	2.53	ASIA	Sindh-08
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	Asia1/PAK/8/2008	PAK08-08	633	603	0	95.26	4.74	ASIA	Sindh-08
2	Asia1/AFG/1/2001 (DQ121109)	AFG01-01	633	576	0	91.00	9.00	ASIA	Group I
3	Asia1/IND/762/2003* (DQ101240)	IND03-AB	633	540	0	85.31	14.69	ASIA	Group III
4	Asia1/IND/18/80 (DQ121116)	IND80-18	633	536	0	84.68	15.32	ASIA	Group V
5	Asia1/Shamir/ISR/89	ISR89--A	633	536	0	84.68	15.32	ASIA	Unnamed
6	Asia1/YNBS/CHA/58 (AY390432)	CHA58-AA	633	536	0	84.68	15.32	ASIA	Unnamed
7	Asia1/IND/63/72* (AY304994)	IND72C63	630	533	0	84.60	15.40	ASIA	Unnamed
8	Asia1/IND/14/95* (AF390678)	IND95-AA	633	535	0	84.52	15.48	ASIA	Unnamed
9	Asia1/HKN/19/74	HKN74-19	633	530	0	83.73	16.27	ASIA	Unnamed
10	Asia1/IRN/10/2004 (DQ121119)	IRN04-10	633	530	0	83.73	16.27	ASIA	Group VIb

nt, nucleotides

\*, not a WRLFMD reference number

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# FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: ASIA1	Report date: 06/05/2015
WRLFMD Ref No: PAK/37/2014	Reported by: N.J. Knowles
Batch No: WRLFMD/2015/00002	Checked by: K. Bachanek-Bankowska
Sender Ref: PK31	
Location: Karachi, Sindh, Pakistan	Topotype: ASIA
Date collected: 17/11/2014	Genotype/strain: Sindh-08
Date received by WRLFMD: 24/02/2015	Sequence filename: PAK14-37.SEQ
Date received for sequencing: 19/03/2015	Date sequence last updated: 24/03/2015
Species: Cattle	No. of Nt determined: 633
Material used: BTy2 07/03/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 633
RT-PCR primers: As1-1C530F/EUR-2B52R	Total no. of comparisons: 566
As1-1C613F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 71 days
	Sequencing time: 48 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	Asia1/PAK/35/2014	PAK14-35	633	632	0	99.84	0.16	ASIA	Sindh-08
2	Asia1/PAK/46/2014	PAK14-46	633	629	0	99.37	0.63	ASIA	Sindh-08
3	Asia1/PAK/26/2014	PAK14-26	633	627	0	99.05	0.95	ASIA	Sindh-08
4	Asia1/PAK/39/2014	PAK14-39	633	627	0	99.05	0.95	ASIA	Sindh-08
5	Asia1/PAK/22/2012	PAK12-22	633	619	0	97.79	2.21	ASIA	Sindh-08
6	Asia1/PAK/27/2012	PAK12-27	633	619	0	97.79	2.21	ASIA	Sindh-08
7	Asia1/PAK/57/2012	PAK12-57	633	619	0	97.79	2.21	ASIA	Sindh-08
8	Asia1/PAK/35/2012	PAK12-35	633	618	0	97.63	2.37	ASIA	Sindh-08
9	Asia1/BAR/3/2011	BAR11-03	633	616	0	97.31	2.69	ASIA	Sindh-08
10	Asia1/BAR/4/2011	BAR11-04	633	616	0	97.31	2.69	ASIA	Sindh-08
Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	Asia1/PAK/8/2008	PAK08-08	633	602	0	95.10	4.90	ASIA	Sindh-08
2	Asia1/AFG/1/2001 (DQ121109)	AFG01-01	633	575	0	90.84	9.16	ASIA	Group I
3	Asia1/IND/762/2003* (DQ101240)	IND03-AB	633	539	0	85.15	14.85	ASIA	Group III
4	Asia1/IND/63/72* (AY304994)	IND72C63	630	534	0	84.76	15.24	ASIA	Unnamed
5	Asia1/IND/18/80 (DQ121116)	IND80-18	633	535	0	84.52	15.48	ASIA	Group V
6	Asia1/Shamir/ISR/89	ISR89--A	633	535	0	84.52	15.48	ASIA	Unnamed
7	Asia1/YNBS/CHA/58 (AY390432)	CHA58-AA	633	535	0	84.52	15.48	ASIA	Unnamed
8	Asia1/IND/14/95* (AF390678)	IND95-AA	633	534	0	84.36	15.64	ASIA	Unnamed
9	Asia1/HKN/19/74	HKN74-19	633	529	0	83.57	16.43	ASIA	Unnamed
10	Asia1/IRN/10/2004 (DQ121119)	IRN04-10	633	529	0	83.57	16.43	ASIA	Group VIb

nt, nucleotides

\*, not a WRLFMD reference number

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Serotype: ASIA1 WRLFMD Ref No: PAK/39/2014 Batch No: WRLFMD/2015/00002 Sender Ref: PK21 Location: Karachi, Sindh, Pakistan Date collected: 02/12/2014 Date received by WRLFMD: 24/02/2015 Date received for sequencing: 17/04/2015 Species: Cattle Material used: BTy1 11/03/2015 & BTy2 17/03/2015 Region sequenced: VP1 RT-PCR primers: As1-1C530F/EUR-2B52R As1-1C613F/EUR-2B52R	Report date: 06/05/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska  Topotype: ASIA Genotype/strain: Sindh-08 Sequence filename: PAK14-39.SEQ Date sequence last updated: 22/04/2015 No. of Nt determined: 633 No. of ambiguities: 0 Gene length: 633 Total no. of comparisons: 566 Min. no. of nt for comparison: 600 Total turn-around time: 71 days Sequencing time: 19 days
Comments:	

<b>Most Closely Related Viruses</b>									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	Asia1/PAK/26/2014	PAK14-26	633	633	0	100.00	0.00	ASIA	Sindh-08
2	Asia1/PAK/35/2014	PAK14-35	633	628	0	99.21	0.79	ASIA	Sindh-08
3	Asia1/PAK/37/2014	PAK14-37	633	627	0	99.05	0.95	ASIA	Sindh-08
4	Asia1/PAK/46/2014	PAK14-46	633	625	0	98.74	1.26	ASIA	Sindh-08
5	Asia1/PAK/22/2012	PAK12-22	633	619	0	97.79	2.21	ASIA	Sindh-08
6	Asia1/PAK/27/2012	PAK12-27	633	619	0	97.79	2.21	ASIA	Sindh-08
7	Asia1/PAK/57/2012	PAK12-57	633	619	0	97.79	2.21	ASIA	Sindh-08
8	Asia1/PAK/35/2012	PAK12-35	633	618	0	97.63	2.37	ASIA	Sindh-08
9	Asia1/PAK/10/2012	PAK12-10	633	616	0	97.31	2.69	ASIA	Sindh-08
10	Asia1/AFG/66/2011	AFG11-66	633	614	0	97.00	3.00	ASIA	Sindh-08
<b>Most Closely Related Reference Viruses</b>									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	Asia1/PAK/8/2008	PAK08-08	633	602	0	95.10	4.90	ASIA	Sindh-08
2	Asia1/AFG/1/2001 (DQ121109)	AFG01-01	633	577	0	91.15	8.85	ASIA	Group I
3	Asia1/IND/762/2003* (DQ101240)	IND03-AB	633	543	0	85.78	14.22	ASIA	Group III
4	Asia1/Shamir/ISR/89	ISR89--A	633	539	0	85.15	14.85	ASIA	Unnamed
5	Asia1/IND/14/95* (AF390678)	IND95-AA	633	538	0	84.99	15.01	ASIA	Unnamed
6	Asia1/IND/18/80 (DQ121116)	IND80-18	633	537	0	84.83	15.17	ASIA	Group V
7	Asia1/YNBS/CHA/58 (AY390432)	CHA58-AA	633	535	0	84.52	15.48	ASIA	Unnamed
8	Asia1/IND/63/72* (AY304994)	IND72C63	630	532	0	84.44	15.56	ASIA	Unnamed
9	Asia1/IRN/10/2004 (DQ121119)	IRN04-10	633	533	0	84.20	15.80	ASIA	Group VIb
10	Asia1/HKN/19/74	HKN74-19	633	532	0	84.04	15.96	ASIA	Unnamed

nt, nucleotides

\*, not a WRLFMD reference number

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# FAO World Reference Laboratory for FMD Genotyping Report

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Serotype: ASIA1	Report date: 06/05/2015
WRLFMD Ref No: PAK/46/2014	Reported by: N.J. Knowles
Batch No: WRLFMD/2015/00002	Checked by: K. Bachanek-Bankowska
Sender Ref: PK22	
Location: Swabi, Khyber Pakhtunkhwa, Pakistan	Topotype: ASIA
Date collected: 30/12/2014	Genotype/strain: Sindh-08
Date received by WRLFMD: 24/02/2015	Sequence filename: PAK14-46.SEQ
Date received for sequencing: 13/04/2015	Date sequence last updated: 16/04/2015
Species: Water Buffalo	No. of Nt determined: 633
Material used: BTy1 13/03/2015	No. of ambiguities: 0
Region sequenced: VP1	Gene length: 633
RT-PCR primers: As1-1C530F/EUR-2B52R	Total no. of comparisons: 566
As1-1C613F/EUR-2B52R	Min. no. of nt for comparison: 600
	Total turn-around time: 71 days
	Sequencing time: 23 days
<b>Comments:</b>	

<b>Most Closely Related Viruses</b>									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	Asia1/PAK/35/2014	PAK14-35	633	630	0	99.53	0.47	ASIA	Sindh-08
2	Asia1/PAK/37/2014	PAK14-37	633	629	0	99.37	0.63	ASIA	Sindh-08
3	Asia1/PAK/26/2014	PAK14-26	633	625	0	98.74	1.26	ASIA	Sindh-08
4	Asia1/PAK/39/2014	PAK14-39	633	625	0	98.74	1.26	ASIA	Sindh-08
5	Asia1/PAK/22/2012	PAK12-22	633	617	0	97.47	2.53	ASIA	Sindh-08
6	Asia1/PAK/27/2012	PAK12-27	633	617	0	97.47	2.53	ASIA	Sindh-08
7	Asia1/PAK/57/2012	PAK12-57	633	617	0	97.47	2.53	ASIA	Sindh-08
8	Asia1/PAK/35/2012	PAK12-35	633	616	0	97.31	2.69	ASIA	Sindh-08
9	Asia1/BAR/3/2011	BAR11-03	633	614	0	97.00	3.00	ASIA	Sindh-08
10	Asia1/BAR/4/2011	BAR11-04	633	614	0	97.00	3.00	ASIA	Sindh-08
<b>Most Closely Related Reference Viruses</b>									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	Asia1/PAK/8/2008	PAK08-08	633	600	0	94.79	5.21	ASIA	Sindh-08
2	Asia1/AFG/1/2001 (DQ121109)	AFG01-01	633	575	0	90.84	9.16	ASIA	Group I
3	Asia1/IND/762/2003* (DQ101240)	IND03-AB	633	537	0	84.83	15.17	ASIA	Group III
4	Asia1/IND/63/72* (AY304994)	IND72C63	630	533	0	84.60	15.40	ASIA	Unnamed
5	Asia1/IND/18/80 (DQ121116)	IND80-18	633	535	0	84.52	15.48	ASIA	Group V
6	Asia1/Shamir/ISR/89	ISR89--A	633	535	0	84.52	15.48	ASIA	Unnamed
7	Asia1/YNBS/CHA/58 (AY390432)	CHA58-AA	633	533	0	84.20	15.80	ASIA	Unnamed
8	Asia1/IND/14/95* (AF390678)	IND95-AA	633	532	0	84.04	15.96	ASIA	Unnamed
9	Asia1/HKN/19/74	HKN74-19	633	527	0	83.25	16.75	ASIA	Unnamed
10	Asia1/IRN/10/2004 (DQ121119)	IRN04-10	633	527	0	83.25	16.75	ASIA	Group VIb

nt, nucleotides

\*, not a WRLFMD reference number

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Serotype: ASIA1 WRLFMD Ref No: PAK/1/2015 Batch No: WRLFMD/2015/00002 Sender Ref: PK15 Location: Islamabad, Islamabad Capital Territory, Pakistan Date collected: 09/01/2015 Date received by WRLFMD: 24/02/2015 Date received for sequencing: 13/04/2015 Species: Water Buffalo Material used: BTy1 13/03/2015 Region sequenced: VP1 RT-PCR primers: As1-1C530F/EUR-2B52R As1-1C613F/EUR-2B52R	Report date: 06/05/2015 Reported by: N.J. Knowles Checked by: K. Bachanek-Bankowska  Topotype: ASIA Genotype/strain: Sindh-08 Sequence filename: PAK15-01.SEQ Date sequence last updated: 16/04/2015 No. of Nt determined: 633 No. of ambiguities: 0 Gene length: 633 Total no. of comparisons: 566 Min. no. of nt for comparison: 600 Total turn-around time: 71 days Sequencing time: 23 days
Comments:	

Most Closely Related Viruses									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	Asia1/PAK/19/2014	PAK14-19	633	620	0	97.95	2.05	ASIA	Sindh-08
2	Asia1/PAK/20/2014	PAK14-20	633	619	0	97.79	2.21	ASIA	Sindh-08
3	Asia1/IRN/49/2011	IRN11-49	633	603	0	95.26	4.74	ASIA	Sindh-08
4	Asia1/IRN/7/2012	IRN12-07	633	603	0	95.26	4.74	ASIA	Sindh-08
5	Asia1/IRN/9/2012	IRN12-09	633	603	0	95.26	4.74	ASIA	Sindh-08
6	Asia1/PAK/106/2010	PAK10106	633	603	0	95.26	4.74	ASIA	Sindh-08
7	Asia1/PAK/108/2010	PAK10108	633	603	0	95.26	4.74	ASIA	Sindh-08
8	Asia1/PAK/11/2011	PAK11-11	633	603	0	95.26	4.74	ASIA	Sindh-08
9	Asia1/PAK/110/2010	PAK10110	633	603	0	95.26	4.74	ASIA	Sindh-08
10	Asia1/PAK/111/2010	PAK10111	633	603	0	95.26	4.74	ASIA	Sindh-08

  

Most Closely Related Reference Viruses									
(see <a href="http://www.wrlfmd.org/fmd_genotyping/prototypes.htm">http://www.wrlfmd.org/fmd_genotyping/prototypes.htm</a> )									
Pos.	Virus name	Filename	No. nt comp.	No. nt match.	No. of ambig.	% Id.	% Diff.	Topotype	Strain
1	Asia1/PAK/8/2008	PAK08-08	633	591	0	93.36	6.64	ASIA	Sindh-08
2	Asia1/AFG/1/2001 (DQ121109)	AFG01-01	633	569	0	89.89	10.11	ASIA	Group I
3	Asia1/IND/762/2003* (DQ101240)	IND03-AB	633	537	0	84.83	15.17	ASIA	Group III
4	Asia1/IND/63/72* (AY304994)	IND72C63	630	529	0	83.97	16.03	ASIA	Unnamed
5	Asia1/IND/18/80 (DQ121116)	IND80-18	633	528	0	83.41	16.59	ASIA	Group V
6	Asia1/IND/14/95* (AF390678)	IND95-AA	633	527	0	83.25	16.75	ASIA	Unnamed
7	Asia1/Shamir/ISR/89	ISR89--A	633	525	0	82.94	17.06	ASIA	Unnamed
8	Asia1/HKN/19/74	HKN74-19	633	524	0	82.78	17.22	ASIA	Unnamed
9	Asia1/YNBS/CHA/58 (AY390432)	CHA58-AA	633	523	0	82.62	17.38	ASIA	Unnamed
10	Asia1/IRN/10/2004 (DQ121119)	IRN04-10	633	522	0	82.46	17.54	ASIA	Group VIb

nt, nucleotides

\*, not a WRLFMD reference number

Assembled with Report Generator v4.3

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# Report on FMDV Asia 1 in Pakistan in 2014-2015

Batch: WRLFMD/2015/00002

◆ indicates viruses in this batch

Software: MEGA 6.06

Analysis

----- Phylogeny Reconstruction

Scope ----- All Selected Taxa

Statistical Method ----- Neighbor-joining

Phylogeny Test

Test of Phylogeny ----- Bootstrap method

No. of Bootstrap Replications ----- 1000

Substitution Model

Substitutions Type ----- Nucleotide

Model/Method ----- Kimura 2-parameter model

Substitutions to Include ----- d: Transitions + Transversions

Rates and Patterns

Rates among Sites ----- Uniform rates

Pattern among Lineages ----- Same (Homogeneous)

Data Subset to Use

Gaps/Missing Data Treatment ----- Pairwise deletion

Codons Included ----- 1st+2nd+3rd+Non-Coding

No. of Sites : 633

No Of Bootstrap Reps = 1000

Only bootstrap values of 70% and above are shown

\*, not a WRLFMD Ref. No.

N.J. Knowles, J. Wadsworth & K. Bachanek-Bankowska,  
06 May 2015

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