Antigenic and genetic analyses of foot-and-mouth disea selection of candidate vaccine strain reveals emergence responsible for most recent outbreaks in India

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Citation Report

#	Article	IF	CITATIONS
1	Consistent change in the B–C loop of VP2 observed in foot-and-mouth disease virus from persistently infected cattle: Implications for association with persistence. Virus Research, 2007, 125, 114-118.	2.2	22
2	Molecular epidemiology of foot-and-mouth disease virus types A and O isolated in Argentina during the 2000–2002 epizootic. Veterinary Microbiology, 2007, 124, 1-15.	1.9	24
3	Genotype differentiating RT-PCR and sandwich ELISA: Handy tools in epidemiological investigation of foot and mouth disease. Journal of Virological Methods, 2007, 143, 117-121.	2.1	11
4	Amplification and characterization of bull semen infected naturally with foot-and-mouth disease virus type Asia1 by RT-PCR. Virologica Sinica, 2008, 23, 378-382.	3.0	2
5	Assessment of suitability of two serotype A candidate vaccine strains for inclusion in FMD vaccine in India. Veterinary Microbiology, 2008, 131, 65-72.	1.9	16
6	Comparative analysis of the large fragment of the 5′ untranslated region (LF-5′ UTR) of serotype A foot-and-mouth disease virus field isolates from India. Virus Genes, 2009, 39, 81-89.	1.6	5
7	Genetic analysis of foot-and-mouth disease virus serotype A of Indian origin and detection of positive selection and recombination in leader protease- and capsid-coding regions. Journal of Biosciences, 2009, 34, 85-101.	1.1	14
8	Genetic characterization of type A foot-and-mouth disease virus 3A region in context of the reemergence of VP359-deletion lineage in India. Infection, Genetics and Evolution, 2009, 9, 483-492.	2.3	7
9	Analysis of the leader proteinase (Lpro) region of type A foot-and-mouth disease virus with due emphasis on phylogeny and evolution of the emerging VP359-deletion lineage from India. Virus Research, 2009, 141, 34-46.	2.2	8
10	Molecular characterization of serotype A foot-and-mouth disease viruses circulating in Vietnam in 2009. Veterinary Microbiology, 2010, 144, 58-66.	1.9	23
11	Phylogenetic analysis of Indian serotype Asia1 foot-and-mouth-disease virus isolates revealed emergence and reemergence of different genetic lineages. Veterinary Microbiology, 2010, 144, 198-202.	1.9	14
12	Phylogenetic structure of serotype A foot-and-mouth disease virus: global diversity and the Indian perspective. Journal of General Virology, 2011, 92, 873-879.	2.9	41
13	The Pathogenesis of Foot-and-Mouth Disease I: Viral Pathways in Cattle. Transboundary and Emerging Diseases, 2011, 58, 291-304.	3.0	169
14	Molecular characterization of a 13-amino acid deletion in VP1 (1D) protein and novel amino acid substitutions in 3D polymerase protein of foot and mouth disease virus subtype A/Iran87. Journal of Veterinary Science, 2011, 12, 363.	1.3	4
15	Multiplex PCR for rapid detection of serotype A foot-and-mouth disease virus variants with amino acid deletion at position 59 of the capsid protein VP3. Journal of Virological Methods, 2011, 171, 287-291.	2.1	6
16	Comparative complete genome analysis of Indian type A foot-and-mouth disease virus field isolates. Virus Genes, 2011, 43, 224-233.	1.6	10
17	Predicting antigenic sites on the foot-and-mouth disease virus capsid of the South African Territories types using virus neutralization data. Journal of General Virology, 2011, 92, 2297-2309.	2.9	40
18	Emergence of antigenic variants with in serotype A foot and mouth disease virus in India and evaluation of a new vaccine candidate panel. Veterinary Microbiology, 2012, 158, 405-409.	1.9	16

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19	Status of Foot-and-mouth Disease in India. Transboundary and Emerging Diseases, 2013, 60, 197-203.	3.0	63	
20	Comparison of Test Methodologies for Foot-and-Mouth Disease Virus Serotype A Vaccine Matching. Vaccine Journal, 2014, 21, 674-683.	3.1	20	
21	Complete Genome Sequence of a Serotype A Foot-and-Mouth Disease Virus from an Outbreak in Saudi Arabia during 2015. Genome Announcements, 2016, 4, .	0.8	8	
22	Evolution of foot-and-mouth disease virus serotype A capsid coding (P1) region on a timescale of three decades in an endemic context. Infection, Genetics and Evolution, 2016, 41, 36-46.	2.3	11	
23	Dynamics of widespread footâ€andâ€mouth disease virus serotypes A, O and Asiaâ€1 in southern Asia: A Bayesian phylogenetic perspective. Transboundary and Emerging Diseases, 2018, 65, 696-710.	3.0	16	
24	Foot-and-Mouth Disease in the Middle East Caused by an A/ASIA/G-VII Virus Lineage, 2015–2016. Emerging Infectious Diseases, 2018, 24, 1073-1078.	4.3	26	
25	Phylogenetic and evolutionary analysis of foot-and-mouth disease virus A/ASIA/Sea-97 lineage. Virus Genes, 2021, 57, 443-447.	1.6	4	
26	Phylogenetic analysis of 3C protease (3Cpro) coding region of Foot-and-mouth disease virus type A. Acta Virologica, 2009, 53, 175-183.	0.8	1	
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28	A Vaccine Based on the A/ASIA/G-VII Lineage of Foot-and-Mouth Disease Virus Offers Low Levels of Protection against Circulating Viruses from the A/ASIA/Iran-05 lineage. Viruses, 2022, 14, 97.	3.3	8	
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