

Spatial Mapping of Foot and Mouth Disease Serotypes in Karnataka using Geographical information System (GIS)

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Abstract

Foot and mouth disease (FMD) is an economically important disease affected domestic livestock. There are seven serotypes of the FMD virus reported globally. In India, serotypes O, A, C and Asia 1 are reported. The spatial distribution of different serotypes is not known. In this study, we used Geographical Information System (GIS) for mapping of different serotypes in different years for Karnataka state. We found that serotype O is the main serotype in Karnataka. The serotype distribution maps will be useful for planning FMD surveillance and disease control strategies for the state of Karnataka and can be extended to other states of India.

Key words: Geographical Information System, Spatial distribution, Foot and Mouth Disease, Serotypes of FMD, Surveillance

Foot and mouth disease (FMD), which affects animals cloven footed animals and cause economic losses. There are seven serotypes of the FMD virus (FMDV) namely: O, A, C, SAT 1, SAT 2, SAT 3, and Asia 1 [1]. Clinically, it is difficult to differentiate between FMD and other vesicular diseases such as swine vesicular disease, vesicular stomatitis, vesicular exanthema, and infection with the Seneca Valley virus.

Serotype O is the most widely studied and prevalent Foot and mouth disease (FMD) serotype worldwide [2]. It is the most common and widely distributed serotype, causing frequent outbreaks in India. Serotype O is known to be the most prevalent and widely studied serotype of FMD globally, with frequent outbreaks occurring in India, particularly in Karnataka. Despite its significance, there has been a lack of GIS-based mapping of livestock disease outbreaks in this region [3]. It affects a wide range of host species and has numerous subtypes. GIS provides a powerful tool for visualizing and analyzing spatial data, allowing for the identification of high-risk areas and the planning of intervention strategies. By incorporating serotype distribution data, we aimed to create spatial maps that can be used by disease managers and policymakers to allocate resources effectively and implement timely control measures to prevent and mitigate outbreaks [4]. Spatial mapping of livestock disease outbreaks using Geographical Information System (GIS) is very powerful tool for visualizing of outbreaks and planning for intervention strategies in high-risk areas. The spatial maps are useful for diseases managers, policy makers in allocating resources and timely control of outbreaks and prevention [5]. The use of GIS in mapping of livestock diseases

has not been used in India and in Karnataka. In this study we used serotype distribution data for make spatial maps [6].

By utilizing GIS technology to map the distribution of FMD serotype O outbreaks, we can improve the allocation of resources and the implementation of control measures to reduce the impact of this devastating disease on livestock populations and agricultural economies. Our spatial maps provide valuable information for policymakers, veterinarians, and other stakeholders involved in Foot and mouth disease (FMD) control efforts, facilitating more informed decision-making and more effective disease management practices.

MATERIALS AND METHODS

Serotype data collection

Village-wise serotype data from the year 2012 to 2021 were collected from the Foot and mouth disease (FMD) Regional Centre, IAH & VB, Bengaluru, and Karnataka, India. Village-wise serotype master data was prepared, and the spatial mapping of serotype data was done using the QGIS software (3.28.0). Our study collected data on the distribution of Foot and mouth disease (FMD) serotype O outbreaks in Karnataka, including information on the affected host species and subtype variations. We then employed GIS techniques to overlay this data onto geographic maps, allowing us to visualize the spatial distribution of outbreaks across the region. By identifying hotspots of Foot and mouth disease (FMD) serotype O activity, we can better understand the epidemiology of the disease and prioritize areas for targeted intervention efforts.

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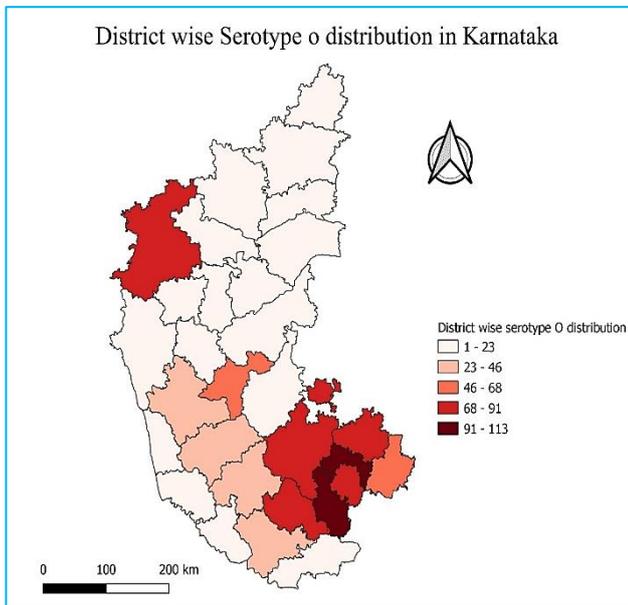


Fig 1 Map of serotype O distribution in Karnataka state

RESULTS AND DISCUSSION

The maximum number of FMD outbreaks (n=448) was observed in 2013. In Karnataka, serotype O is more prevalent compared to all other serotypes. In Karnataka, all 31 districts have reported FMDV serotype O. Bangalore rural district has reported the highest number of outbreaks followed by

Ramanagara, Belgaum, Tumkur, Bangalore Urban, Mandya, Chikkaballapura, Kolar, Davangere, Shivamogga, Chikkamagaluru, Hassan, Mysuru, Gadag, Dakshina Kannada, Koppal, Haveri, Bagalkot, Uttara Kannada, Chitradurga, Raichur, Chamarajanagara, Gulbarga, Dharwad, Udupi, Bidar, Bellary, Bijapur, Kodagu, and Vijayanarag reported very less number of FMD outbreaks.

The map shows the distribution of Serotype O in Karnataka state. Year wise serotypes distribution from 2012 to 2021 map is shown in (Fig 2-6). Serotype O was reported maximum in the year 2013 followed by 2021, 2018 and 2017. In this study, we collated data on serotype distribution in Karnataka state of India. The spatial distribution of serotypes was prepared using GIS (Geographical Information System). Overall, serotype O was predominantly distributed across districts of Karnataka with the year 2013 reporting maximum outbreaks.

In one study, ELISA and multiplex PCR was used to type the serotypes and found that serotype O and Asia 1 were responsible for the outbreaks [7].

It has spread in East Asian countries which include Hong Kong, South Korea, North Korea, Japan, Mongolia, Eastern Russia, Taiwan and China [8-12]. It is also reported from South East Asia countries including Myanmar, Malaysia, Vietnam, and Thailand [13-17], Southern Asian countries such as Iran, Iraq, Afghanistan, and Pakistan [10], [18-19], Western Asian countries such as Turkey, Jordan and Israel [19]. In Indian subcontinent the serotype O was found in India, Sri Lanka, Bhutan, Bangladesh and Nepal [20-29]. Serotype O is reported from Karnataka from many districts [30].

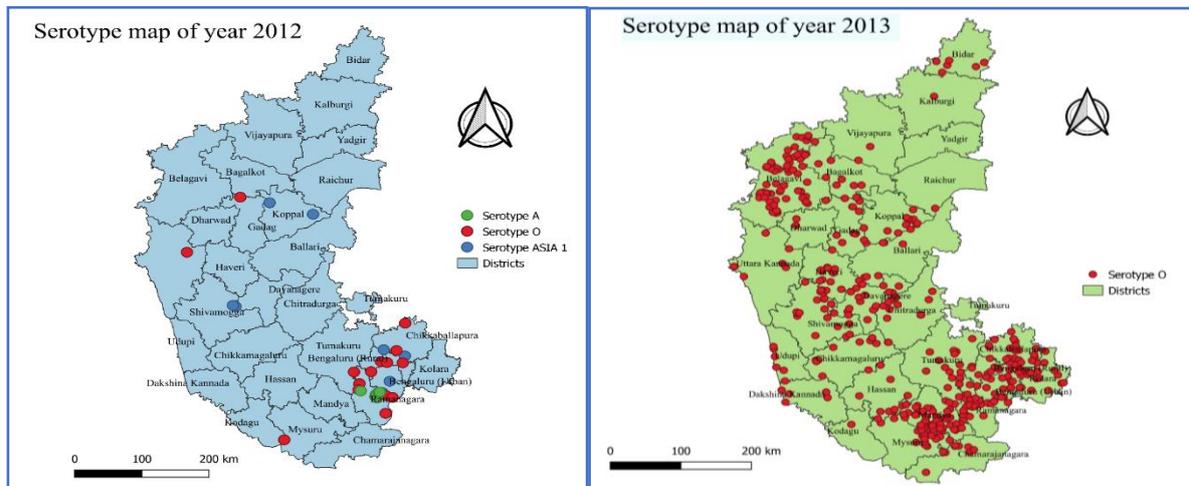


Fig 2 Serotype maps for the years 2012 and 2013

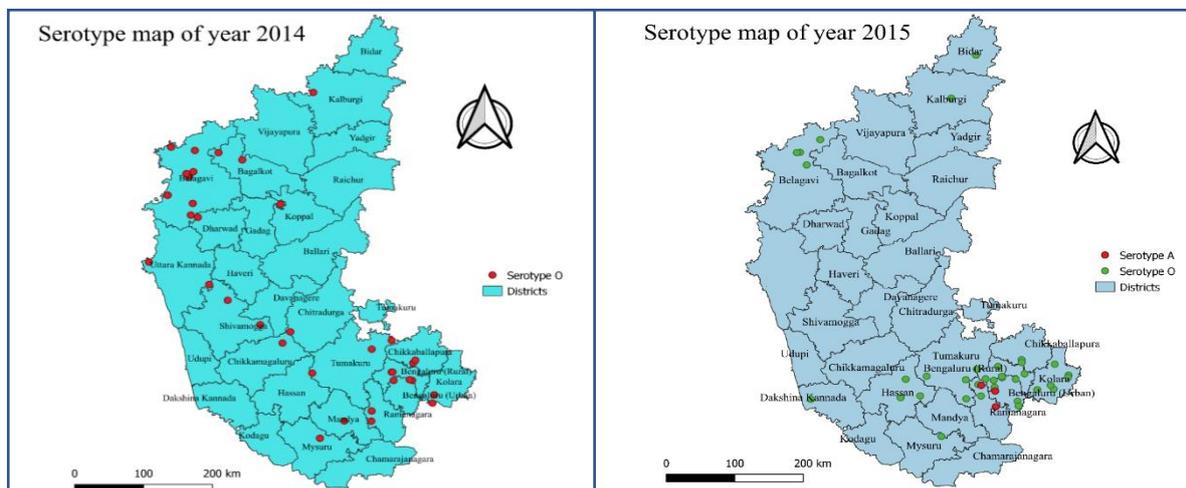


Fig 3 Serotype maps for the years 2014 and 2015

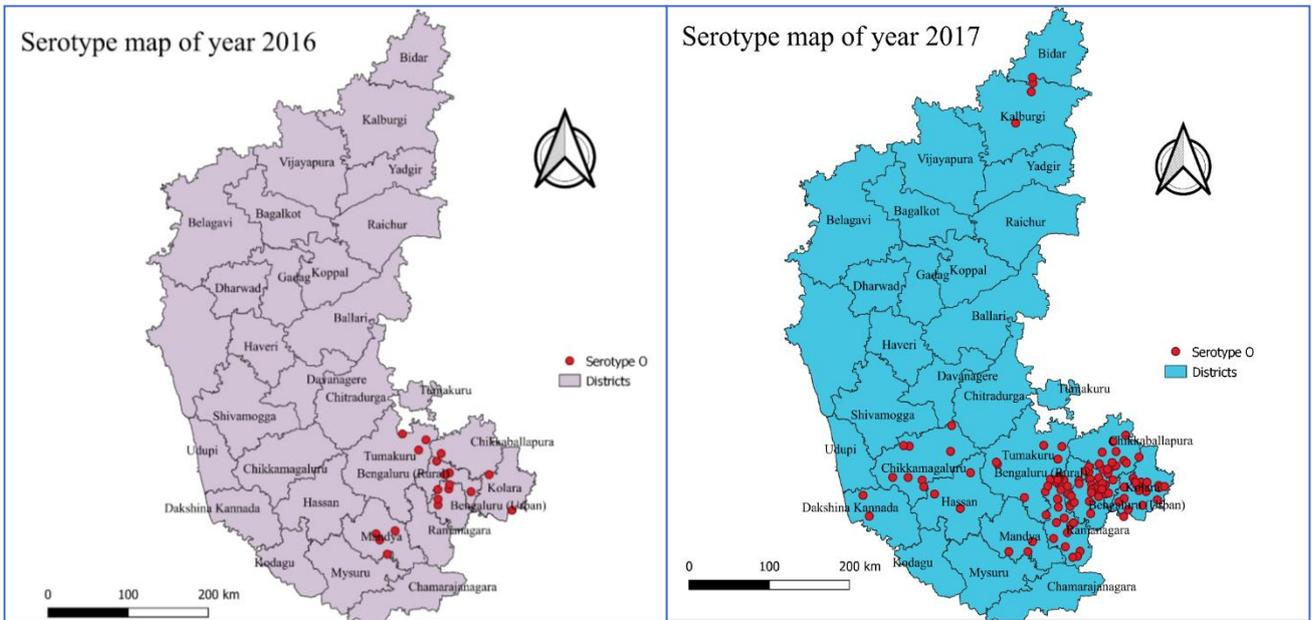


Fig 4 Serotype maps for the years 2016 and 2017

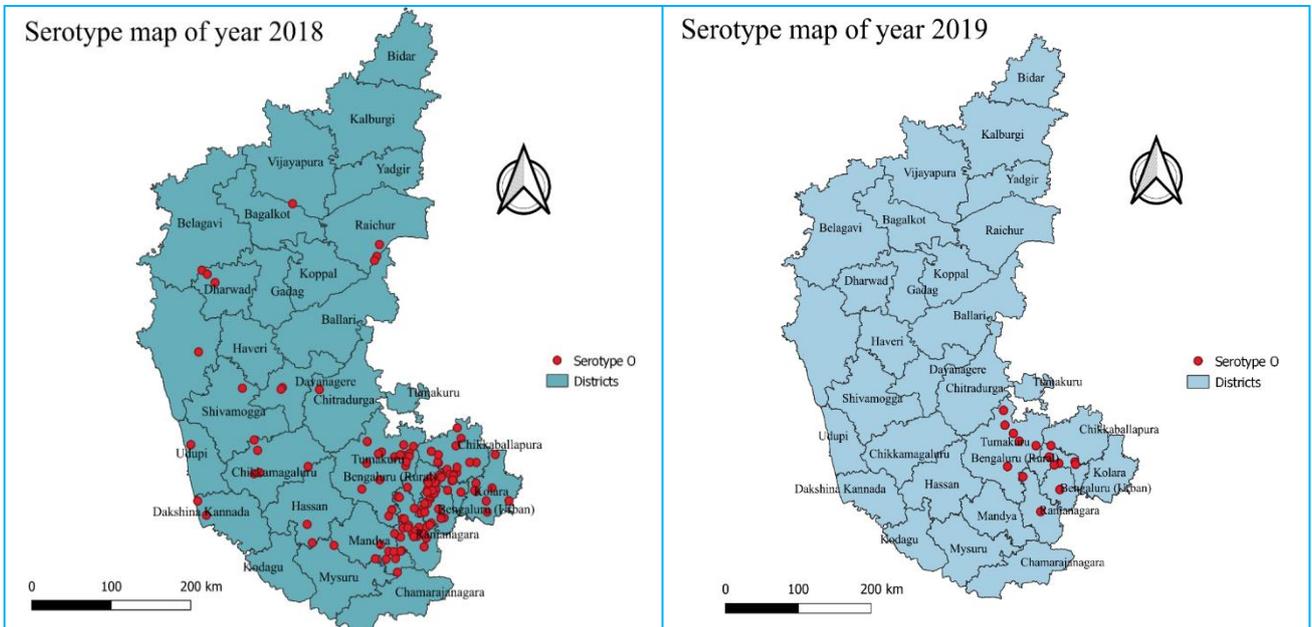


Fig 5 Serotype maps for the years 2018 and 2019

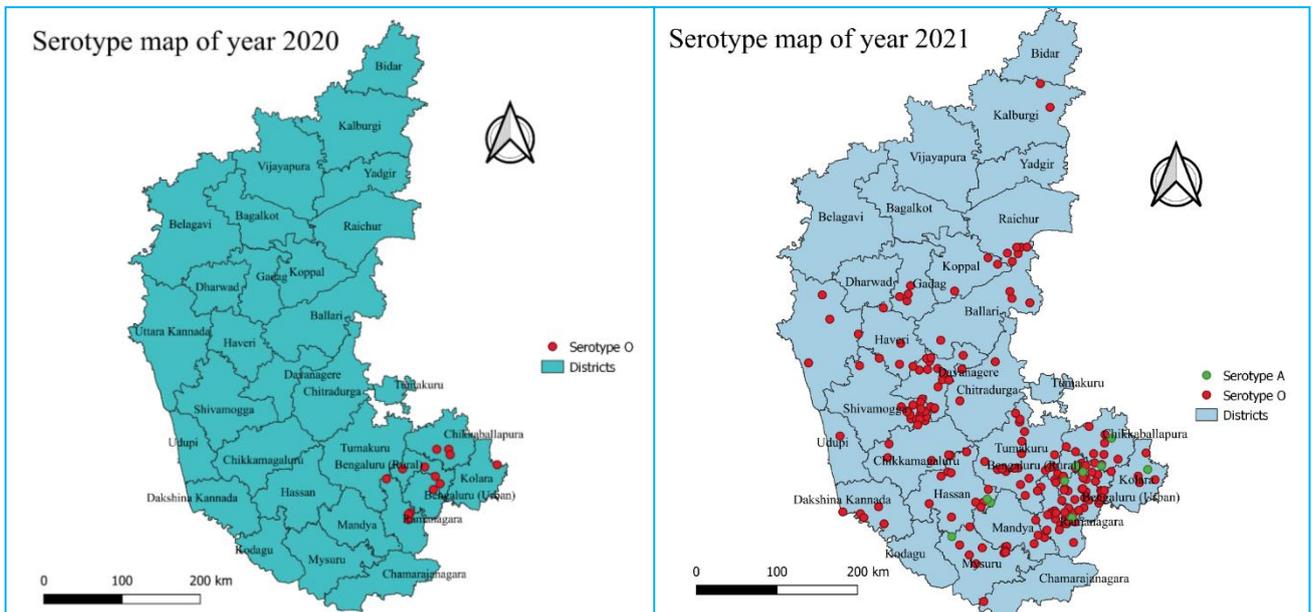


Fig 6 Serotype maps for the years 2020 and 2021

The Serotype A distribution is less prevalent compared to Serotype O. Serotype O and A have the widest global distribution and have been responsible for outbreaks in Europe, America, Asia and Africa. It was noticed in East Asia, South East Asia, Indian subcontinent, Southern Asia, Arabian Peninsula, Western Asia, Central Asia, North Africa [31]. Asia 1 serotype is primarily found in the Indian subcontinent, it has also been sporadically reported in countries to the west and east of this region. Periodically, the serotype has spread into the Middle East and occasionally reached Europe. However, it has not been reported from Africa or the Americas [32-35]. The Asia 1 serotype was first detected in samples collected in India in 1951 through 1952 [36] and later in Pakistan in 1954 [37]. The Asia 1 serotype was reported from West Bengal state of India [38]. The Asia 1 serotype was also observed in Karnataka during the year 2012 [30]. It was first detected in early 1920s in Europe and mainly affected pigs and cattle with less infection. However, in 2004, four small outbreaks of serotype C were detected in the Amazon region [39]. The last report of Serotype C was noticed in Ethiopia during 2005 [40]. In India there were

no reports of Asia 1 since 1996 [38]. Only sub-Saharan Africa is affected by the SAT 1-3 serotypes.

CONCLUSION

Analysis of Foot and Mouth disease serotype data in Karnataka for the period of 2012-2021 was carried out and revealed that the serotype O is the main serotype in the state. We found that 97% of the outbreaks occurred with serotype O. The yearly trends of Foot and mouth disease (FMD) shown that the year 2013 was noticed maximum number of outbreaks and least number of outbreaks in the year 2020 (n=13). Bengaluru rural and Ramanagar districts reported maximum serotype O outbreaks and needs targeted surveillance and studies to identify factors responsible for variation in the distribution of outbreaks in other districts. The GIS maps will be helpful for policy makers to visualize the spatial distribution of FMD outbreaks due to different serotypes and plan for intervention strategies for effective prevention and control of disease in Karnataka state.

LITERATURE CITED

1. Carrillo C, Tulman ER, Delhon G, Lu Z, Carreno A, Vagnozzi A, Kutish GF, Rock DL. 2005. Comparative genomics of foot-and-mouth disease virus. *Jr. Virology* 79(10): 6487-6504.
2. Klein J. 2009. Understanding the molecular epidemiology of foot-and-mouth-disease virus. *Infection, Genetics and Evolution* 9(2): 153-161.
3. Pattnaik B, Subramaniam S, Sanyal A. 2012. Foot-and-mouth disease: Global Status and future road map for control and prevention in India. *Agric. Research* 1: 132-147.
4. Valarcher JF, Knowles NJ, Zakharov V, Scherbakov A, Zhang Z, Shang YJ. 2009. Multiple origins of foot-and-mouth disease virus serotype Asia 1 outbreaks, 2003-2007. *Emerg. Infect. Diseases* 15: 1046-1051.
5. Norström M. 2001. Geographical Information System (GIS) as a tool in surveillance and monitoring of animal diseases. *Acta Vet. Scand.* 42(Suppl 1): S79. <https://doi.org/10.1186/1751-0147-42-S1-S79>
6. González Gordon L, Porphyre T, Muhanguzi D, Muwonge A, Boden L, Bronsvort BMC. 2022. A scoping review of foot-and-mouth disease risk, based on spatial and spatio-temporal analysis of outbreaks in endemic settings. *Transbound Emerg. Dis.* 69(6): 3198-3215.
7. Rout M, Senapati MR, Mohapatra JK, Dash BB, Saniyal A, Pattnaik B. 2014. Serosurveillance of foot-and-mouth disease in sheep and goat population of India. *Prev. Vet. Med.* 113: 273-277.
8. Lin YL, Jong MH, Huang CC, Shieh HK, Chang PC. 2010. Genetic and antigenic characterization of foot-and-mouth disease viruses isolated in Taiwan between 1998 and 2009. *Veterinary Microbiology* 145(1/2): 34-40.
9. Zheng H, He J, Guo J, Jin Y, Yang F, Lv L, Liu X. 2012. Genetic characterization of a new pandemic Southeast Asia topotype strain of serotype O foot-and-mouth disease virus isolated in China during 2010. *Virus Genes* 44: 80-88.
10. Knowles N, Nazem Shirazi M, Wadsworth J, Swabey K, Stirling J, Statham R, Li Y, Hutchings G, Ferris N, Parlak Ü. 2009. Recent spread of a new strain (A-Iran-05) of foot-and-mouth disease virus type A in the Middle East. *Transboundary and Emerging Diseases* 56(5): 157-169.
11. Hui RK, Leung FC. 2012. Evolutionary trend of foot-and-mouth disease virus in Hong Kong. *Veterinary Microbiology* 159(1/2): 221-229.
12. Valdazo-González B, Knowles NJ, King DP. 2014. Genome sequences of foot-and-mouth disease virus O/ME-SA/Ind-2001 lineage from outbreaks in Libya, Saudi Arabia, and Bhutan during 2013. *Genome Announcements* 2(2): e00242-00214.
13. Khounsy S, Conlan J, Gleeson L, Westbury H, Colling A, Paton D, Knowles N, Ferris N, Blacksell S. 2008. Foot and mouth disease in the Lao People's Democratic Republic: I. A review of recent outbreaks and lessons from control programmes. *Rev. Sci. Tech.* 27(27): 839-849.
14. Nguyen T, Lee KN, Ko YJ, Lee HS, Nguyen VC, Mai TD, Do TH, Kim SM, Cho IS, Park JH. 2010. Molecular characterization of serotype A foot-and-mouth disease viruses circulating in Vietnam in 2009. *Veterinary Microbiology* 144(1/2): 58-66.
15. Nguyen T, Park JH, Kim SM, Ko YJ, Lee HS, Nguyen VC, Mai TD, Do TH, Cho IS, Lee KN. 2010. Heterogeneity and genetic variations of serotypes O and Asia 1 foot-and-mouth disease viruses isolated in Vietnam. *Veterinary Microbiology* 145(3/4): 220-229.
16. Abdul-Hamid NF, Hussein NM, Wadsworth J, Radford AD, Knowles NJ, King DP. 2011. Phylogeography of foot-and-mouth disease virus types O and A in Malaysia and surrounding countries. *Infection, Genetics and Evolution* 11(2): 320-328.
17. Lee KN, Nguyen T, Kim SM, Park JH, Do HT, Ngo HT, Mai DT, Lee SY, Nguyen CV, Yoon SH. 2011. Direct typing and molecular evolutionary analysis of field samples of foot-and-mouth disease virus collected in Viet Nam between 2006 and 2007. *Veterinary Microbiology* 147(3/4): 244-252.
18. Jamal SM, Ferrari G, Ahmed S, Normann P, Belsham GJ. 2011. Genetic diversity of foot-and-mouth disease virus serotype O in Pakistan and Afghanistan, 1997-2009. *Infection, Genetics and Evolution* 11(6): 1229-1238.
19. Upadhyaya S, Ayelet G, Paul G, King DP, Paton DJ, Mahapatra M. 2014. Genetic basis of antigenic variation in foot-and-mouth disease serotype A viruses from the Middle East. *Vaccine* 32(5): 631-638.

20. Di Nardo A, Knowles N, Paton D. 2011. Combining livestock trade patterns with phylogenetics to help understand the spread of foot and mouth disease in sub-Saharan Africa, the Middle East and Southeast Asia. *Revue Scientifique et Technique-OIE* 30(1): 63.
21. Mohapatra J, Pawar S, Tosh C, Subramaniam S, Palsamy R, Sanyal A, Hemadri D, Pattnaik B. 2011. Genetic characterization of vaccine and field strains of serotype A foot-and-mouth disease virus from India. *Acta Virologica* 55(4): 349.
22. Mohapatra JK, Subramaniam S, Pandey LK, Pawar SS, De A, Das B, Sanyal A, Pattnaik B. 2011. Phylogenetic structure of serotype A foot-and-mouth disease virus: global diversity and the Indian perspective. *Journal of General Virology* 92(4): 873-879.
23. Nandi SP, Rahman MZ, Momtaz S, Sultana M, Hossain M. 2015. Emergence and distribution of foot-and-mouth disease virus serotype A and O in Bangladesh. *Transboundary and Emerging Diseases* 62(3): 328-331.
24. Sanyal A, Subramaniam S, Mohapatra JK, Tamilselvan RP, Singh NK, Hemadri D, Pattnaik B. 2010. Phylogenetic analysis of Indian serotype Asia1 foot-and-mouth-disease virus isolates revealed emergence and reemergence of different genetic lineages. *Veterinary Microbiology* 144(1/2): 198-202.
25. Subramaniam S, Mohapatra JK, Sharma GK, Das B, Dash BB, Sanyal A, Pattnaik B. 2013. Phylogeny and genetic diversity of foot and mouth disease virus serotype Asia1 in India during 1964–2012. *Veterinary Microbiology* 167(3/4): 280-288.
26. Subramaniam S, Sanyal A, Mohapatra JK, Sharma GK, Biswal JK, Ranjan R, Rout M, Das B, Bisht P, Mathapati BS. 2013. Emergence of a novel lineage genetically divergent from the predominant Ind2001 lineage of serotype O foot-and-mouth disease virus in India. *Infection, Genetics and Evolution* 18: 1-7.
27. Ullah H, Siddique M, Al Amin M, Das B, Sultana M, Hossain M. 2015. Re-emergence of circulatory foot-and-mouth disease virus serotypes Asia1 in Bangladesh and VP1 protein heterogeneity with vaccine strain IND 63/72. *Letters in Applied Microbiology* 60(2): 168-173.
28. Ullah H, Siddique MA, Sultana M, Hossain MA. 2014. Complete genome sequence of foot-and-mouth disease virus type A circulating in Bangladesh. *Genome Announcements* 2(3): e00506-00514.
29. Yuvaraj S, Madhanmohan M, Nagendrakumar S, Kumar R, Subramanian BM, Mohapatra JK, Sanyal A, Pattnaik B, Srinivasan V. 2013. Genetic and antigenic characterization of Indian foot-and-mouth disease virus serotype O isolates collected during the period 2001 to 2012. *Infection, Genetics and Evolution* 13: 109-115.
30. Hegde R, Gomes AR, Giridhar P, Kowalli S, Shivashankar BP, Sudharshana KJ, Nagaraj K, Sesharao R, Mallinath KC, Shankar BP, Nagaraj D, Seema CM, Khan TA, Nagaraj GV, Srikala K, Dharanesh NK, Venkatesha MD, Renukaprasad C. 2014. Epidemiology of foot and mouth disease in Karnataka state, India: a retrospective study. *Virusdisease* 25(4): 504-509. <https://doi.org/10.1007/s13337-014-0239-3>
31. Brito B, Rodriguez L, Hammond J, Pinto J, Perez A. 2017. Review of the global distribution of foot-and-mouth disease virus from 2007 to 2014. *Transboundary and Emerging Diseases* 64(2): 316-332.
32. Ansell D, Samuel A, Carpenter W, Knowles N. 1994. Genetic relationships between foot-and-mouth disease type asia 1 viruses. *Epidemiology and Infection* 112(1): 213-224.
33. Islam M, Rahman M, Adam KH, Marquardt O. 2001. Epidemiological implications of the molecular characterization of foot-and-mouth disease virus isolated between 1996 and 2000 in Bangladesh. *Virus Genes* 23: 203-210.
34. Schumann KR, Knowles NJ, Davies PR, Midgley RJ, Valarcher JF, Raoufi AQ, McKenna TS, Hurtle W, Burans JP, Martin BM. 2008. Genetic characterization and molecular epidemiology of foot-and-mouth disease viruses isolated from Afghanistan in 2003–2005. *Virus Genes* 36: 401-413.
35. Valarcher JF, Leforban Y, Rweyemamu M, Roeder P, Gerbier G, Mackay D, Sumption KJ, Paton DJ, Knowles NJ. 2008. Incursions of foot-and-mouth disease virus into Europe between 1985 and 2006. *Transboundary and Emerging Diseases* 55(1): 14-34.
36. Dhanda M, Gopalakrishnan V, Dhillon H. 1957. Note on the occurrence of atypical strains of foot-and-mouth diseases virus in India. *Ind. Jr. Vet. Science* 27: 79-84.
37. Brooksby J, Rogers J. 1957. Methods used in typing the virus of foot-and-mouth disease at Pirbright, 1950–55. *Methods of typing and cultivation of foot-and-mouth disease virus, European Productivity Agency of the Organisation for European Economic Co-operation, Project*. 31: 34.
38. Bhattacharya S, Banerjee R, Ghosh R, Chattopadhyay A, Chatterjee A. 2005. Studies of the outbreaks of foot and mouth disease in West Bengal, India, between 1985 and 2002. *Revue Scientifique et Technique (International Office of Epizootics)* 24(3): 945-952.
39. Paton DJ, Di Nardo A, Knowles NJ, Wadsworth J, Pituco EM, Cosivi O, Rivera AM, Kassimi LB, Brocchi E, de Clercq K. 2021. The history of foot-and-mouth disease virus serotype C: the first known extinct serotype? *Virus Evolution* 7(1): veab009.
40. Rweyemamu M, Roeder P, Mackay D, Sumption K, Brownlie J, Leforban Y, Valarcher JF, Knowles N, Saraiva V. 2008. Epidemiological patterns of foot-and-mouth disease worldwide. *Transboundary and Emerging Diseases* 55(1): 57-72.