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REVIEW ARTICLE

Persistence, Emergence and Distribution of Foot and Mouth Disease Virus (FMDV); Global and Pakistan Perspectives

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ABSTRACT
Foot-and-mouth disease (FMD) is a serious infectious animal health problem in many parts of the world. The risk that imported livestock and their products may introduce foot-and-mouth disease virus (FMDV) restricts trade in these commodities from parts of the world where FMDV has not been eradicated. Foot-and-mouth disease can be controlled but there are few difficulties like the existence of multiple serotypes of the causative virus, multiple host species including wildlife and extreme contagiousness. This review focuses on the persistence, emergence and distribution of FMDV in comparison of global and Pakistan perspectives. All these factors are much more important to know before we can formulate any control strategy for FMD on national and regional level.

Foot and mouth disease is one of the most important disease and biggest trade barrier for animals and animal products (Rufael et al., 2008; Perry et al., 2007). FMDV is highly transmissible and causes high morbidity outbreaks with moderate to low mortality in most cases (Grubman et al., 2004).

FMD is a vesicular disease; the clinical severity of disease depends on the infecting dose and strain of virus. FMD virus have seven serotypes, O, A, C, South African Territories (SAT 1, SAT 2, SAT 3) and Asia 1. All FMD serotypes are immunogenically different and vaccination with one serotype does not develop immunity to against other serotype or subtypes of a serotype (Paton et al 2005; Callis et al., 1968).

Various studies revealed that infected animals can excrete virus shortly before showing of any clinical signs and highest excretion occurs after showing clinical signs. All secretions of an infected animal such as saliva, milk, nasal fluid and feces have highest amount of virus which can cause disease outbreak. FMD virus also transmits through air; the airborne virus enters in respiratory track by inhalation, virus may also enter through oral ingestion and damaged epithelium. In some ruminants virus is not completely cleared from the pharynx, that animals are act as carriers for disease, which can further infect healthy animals (Alexandersen et al., 2003).

FMDV Transmission

FMD virus transmits through direct contact with infected animals; virus enters in susceptible animals through damaged epithelium, cuts or abrasions and mucosal membrane or by the deposition of droplets in respiratory tract. In pigs, FMD virus transmits through physical contact with infected secretions containing large amount of virus. Besides, as pigs are commonly kept on concrete floor, pre-existing damage to the integument may increase the chance of being infected (Alexandersen and Donaldson, 2002).

Transmission can take place by directly or indirectly contact with infected animals and contaminated fomites; virus spread through inhalation of aerosolized virus, contaminated feed, and the virus enters through skin abrasions or mucous membranes. Different routes of transmission vary with the species. For example, sheep and cattle were more susceptible to aerosolized virus than other animals (Fiebre, 2007).

The disease can also be transmitted indirectly through contaminated vehicles; persons that are working in diseased area and through all other activities, such as shearing, de-worming, blood sampling. Under certain conditions, including climatic and geographic factors, FMDV can be transmitted over a long distance in an airborne manner. Pigs excrete highest amount of airborne virus as compared to other ruminants. Conditions that prompt the long distance transmission of FMDV include a high relative humidity, usually 55 % or higher, minimal mixing of air by turbulence and convection. These conditions are possibly seen in areas that have consistent slow wind and cloudy weather (Alexandersen and Donaldson, 2002).

The airborne transmission of virus plays a major role in some FMD outbreaks (Christensen et al., 2005; Smith et al., 1969). In UK 2001 outbreak, the FMD virus was spread through transport of unrecognized FMD infected animals to FMD free area (Gloster et al., 2003).

The animal from which live FMD viruses can be isolated after twenty eight days contact with infection is called carrier animal. Those animals were fully susceptible which can develop disease, in which virus persists subsequent recovery, or a vaccinated animal can becomes a carrier. In the carrier animals, virus persists in the pharyngeal region. Carrier Sheep and goats can carry FMD virus for up to nine months and cattle and African buffalo for up to three and five years respectively; wildlife ungulates carry virus for only a relatively short period and pigs don't carry the carrier state (Salt, 1993). There was some epidemiological evidence that the origin of acute disease outbreaks in suspected animals is due to contact with carrier animals. This mode of transmission was confirmed experimentally for FMD serotype SAT (Vosloo et al., 1995). The epidemiological studies of FMD virus are difficult and complex, it depends on different factors that are related to the virus, host and environmental conditions (Pereira, 1981).

FMDV Persistence

FMD virus persists in the light zones of germinal centers in lymph nodes associated with the pharyngeal region, while these tissues did not develop infective virus (Juleff et al., 2008). The carrier state was well characterized in all ruminants, and there is an only one report finding that supports the carrier state in pigs (Alexandersen et al., 2003; Alexandersen et al., 2001; Mezencio et al., 1999).

The virulence of virus is different for different hosts like, amount of virus excretion, severity of lesions and long term persistence of virus in animal body. The severity and persistence of disease depends on different environmental conditions and the virus multiplication and spread depends on host specie, population density, contacts between wild and domestic animals, animal movement and nutritional status. The environment can promote virus transmission or can also act as geographical barrier in virus distribution it depends on different environmental conditions (Sobrino and Domingo, 2001; Ferguson et al., 2001).

Global Distribution of FMD

In the beginning of 20th century, FMD outbreaks occurred periodically in Europe but these outbreaks have devastating effects (Barteling and Vreeswijk, 1991). In 1950s, some western European countries were experiencing more than hundred outbreaks in a year (Brown, 1992). In 1968, FMD outbreaks were reported in UK in which very high number of animals was slaughtered (Gloster et al., 2005). After that only few outbreaks have occurred in Europe, in Denmark in 1983 and in Italy in 1993, Latter it observed that the virus was closely related to viruses that earlier circulating in Middle East (Nunez et al., 2006; Christensen et al., 2005). In 2001, FMD was suspected in pigs in East England that was confirmed by World Reference Laboratory (WRL) and it was identified as serotype O Pan-Asia O/UK/2001 strain (Knowles et al., 2001). In 2001 UK outbreak, the main cause of severity of outbreak is due to extensive movement of animals around the UK and to other neighbor countries. Total four million animals were slaughtered in UK outbreak and it regained its FMD free status in start of 2002 (Scudamore and Harris, 2002).

FMD outbreaks have occurred in every country which has livestock except some countries that have disease free status. This disease did not change its distribution significantly till the last 30 years. It remained endemic in South America, sub-Saharan Africa, India, Middle/ Far East but the member of Mercasur (Argentine, Paraguay, Brazil, and Uruguay) have control and improve their status through vaccination programmes. Due to poor surveillance, less diagnostic facilities and control programmes are the main sources FMD spread in cattle in African countries, like Tunisia, Morocco, Algeria. It is very difficult to in Asian countries because they have a large number of ruminants and poverty, due to which FMD outbreaks occurred again and again continuously where it had been, controlled (Malaysia, Philippines, Japan) previously. It is impossible to control FMD in these countries due to uncontrolled movement of livestock, but Brazil has partially controlled it. The whole inactivated virus was used to immunize the animals in Europe. It has successfully achieved and stopped vaccination till 1991. This decision was followed for sake of trade agreements, for remaining European countries to control imports (Kitching, 1998).

In 2010, Japan and Korea lost their FMD free status, FMD A and O serotype viruses affected these countries. The FMD viruses that caused outbreaks were originated from Southeast Asia that was endemic for FMD serotypes O and A (Knowles et al., 2012). FMD is

endemic in Southeast Asian countries; Cambodia, Laos, Malaysia, Myanmar, the Philippines, Thailand, and Vietnam. FMD serotypes O, A, and Asia 1 were detected from these countries and serotype C only reported in Philippines between 1976 and 1994. FMD vaccination reduced the reports of outbreaks in Philippines and no outbreaks have occurred since 2005, while some countries of this region also have FMD free status without vaccination (Abdul-Hamid et al., 2011; Lee et al., 2011; Gleeson et al., 2003). Recently, Ahmed et al. (2012) described the molecular characterization of SAT 2 FMD viruses that have caused widespread field outbreaks of FMD in Egypt during February and March 2012. Phylogenetic analysis showed that viruses from these outbreaks fell into two distinct lineages within the SAT 2 topotype VII, which were distinct from a contemporary SAT 2 lineage of the same toptype from Libya. These were the first FMD outbreaks due to this serotype in Egypt since 1950.

Foot and Mouth disease is endemic in Pakistan, India and Afghanistan, FMD serotypes A, O and Asia 1 is prevalent in these countries but FMD O serotype has been responsible of high number of outbreaks in Pakistan (Abubakar et al., 2012; Jamal et al., 2011; Schumann et al., 2008). The rates of three FMD serotypes in Pakistan are 70%, 25% and 4.7% for type O, Asia 1 and type A, respectively (Zulfiqar, 2003). According to Abubakar et al. (2009), in Pakistan, FMDV serotype 'A' and 'Asia-1' were predominant strains in the samples from Sindh province while 'O' and 'A' were the major serotypes in samples from Punjab province. Similarly in India, Subramaniam et al., (2012) described the status of FMD for five fiscal years and claimed that three serotypes of FMD virus (O, A and Asia1) are prevalent. Serotype O was responsible for 80% of the confirmed outbreaks/cases, whereas Asia1 and A caused 12% and 8%, respectively. There is a need to adopt better control policy, monitoring policy for all prevalent serotypes and subtypes in FMD endemic countries. It will help to select most appropriate vaccine for that serotype (Knowles et al., 2005).

Occurrence of FMDV Serotypes; Global and Pakistan Perspective

Foot and mouth disease serotypes are not equally prevalent in different regions of world; while some regions also have disease free status. In endemic settings such as the Indian subcontinent, this variability has resulted in the emergence of pandemic strains that have spread widely and caused devastating outbreaks in disease-free areas (Brito et al., 2012).

FMD have seven serotypes and subtypes within a serotype these all serotypes are prevailing in Africa while only four serotypes (O, A, Asia 1, C) are occurred in Asia and in South America with only three serotypes (O, A, Asia 1). FMD serotypes SAT-1, SAT-2 and SAT-3 were endemic only in African countries (Rweyemamu et al., 2008).

Serotype A

FMDV serotype A is the most genetically and antigenically diverse among the seven FMDV serotypes and more than thirty subtypes have been identified. However, the origin of the recombinant virus remains unclear. FMD Serotype A control is very difficult by vaccination because it is considered to be as most diverse serotype antigenically and genetically (Kitching, 2005). Sequence analysis revealed that the origin of FMDV serotype A probably lay in South America. Phylogenetic analysis of complete VP1 gene sequence revealed that type A virus isolated from Africa is highly diverse and grouped into three genotypes: Euro-SA, Asia and Africa. Serotype A outbreaks were reported in Afghanistan, turkey, India, Bhutan, Malaysia, Yemen in 2011 and in Myanmar 2010 (OIE 2011). FMD type A Iran-05 was detected in Pakistan and Egypt, two outbreaks in Kazakhstan and Thailand in 2012 (WRLFMD, 2012)

Serotype O

Genetic diversity of FMDV serotype O is also high in comparison to type A, and it allows the classification of the viruses into many distinct lineages. The lineages are Cathay, ME-SA (Middle East-South Asia), SEA (South-East Asia), Euro-SA (Europe-South America), ISA-1 (Indonesia-1), ISA-2 (Indonesia-2), EA (East Africa) and WA (West Africa) (Knowles et al., 2001). FMD Serotype O is widely distributed all around the world, especially in south Asia and Middle East countries (Valarcher et al., 2004). FMD serotype O Pan-Asia lineages were reported in Japan, Korea, Mongolia, Russia, the United Kingdom, France, and South Africa in year 2000–2006 (Cottam et al., 2006).

In Southeast Asia O serotype reported in Taiwan, China, Hong Kong, Thailand and Myanmar, in central Asia reported in Pakistan during 2009. In Middle East O serotype outbreaks were reported in Yemen, Egypt and UAE during 2009 (WRLFMD, 2009). O serotype outbreaks were reported by OIE in Turkey, Oman, Afghanistan, Pakistan, India, china, Korea in 2010-2011 (OIE, 2011). In 2011, serotype O outbreaks were continued to occur in China, South Korea, Japan, Mongolia, Russia, and North Korea (Knowles, 2012).In Bangladesh type A and type O viruses were isolated between 1987 and1997 and again between 1998, 2000 and 2009 (Loth et al., 2011; Islam et al., 2001). The FMD type O virus was isolated in Pakistan during 2002-2006 belonged to pak-98, Iran-2001 Pan Asia or Pan-Asia-II 2006 lineages (Waheed et al., 2010; Saeed et al., 2009; Abubakar et al., 2009; Klein et al., 2008; Knowles et al., 2005). WRLFMD reported O serotype Pan Asia II lineage in Iran, Bahrain, Afghanistan, Israel, Pakistan, Egypt and Taiwan during 2011-2012 (WRLFMD, 2012).

Serotype Asia 1

FMD serotype Asia 1 was firstly reported in a sample originated from Pakistan in 1954 (Brooksby and Rogers, 1957). FMD Asia 1 outbreak has been reported in Europe and Greece in 1984, the nucleotide sequence of this virus was closely related to the Middle East virus isolated in 1983. This serotype is not as highly variable as other FMD serotypes and all viruses shared more than 85% nucleotide similarity (Ansell et al., 1994). In 1970s, serotype Asia 1 virus move from Pakistan to Afghanistan, Iran, Iraq and Turkey (Firoozi et al., 1974).

Serotype Asia 1 outbreak was continuously occurring in Indian subcontinent and in neighboring countries (Valarcher et al., 2009). In 2004, serotype Asia 1 outbreak was reported in Kyrgyzstan, Tajikistan and in year 2005-2006 outbreaks were detected in Eastern Russia, Mongolia and in some regions of China (Valarcher et al., 2005). Phylogenetic analysis of FMD virus VP1 gene these outbreaks revealed that virus belongs to sixth group within the Asia 1 serotype (Valarcher et al., 2009). In 2011 FMD serotype Asia 1 outbreak were reported in Turkey, India and Afghanistan (WRLFMD, 2012).

Serotype C

FMDV serotype C spreads to limited areas as compared to other serotypes, its outbreaks was detected in Europe, South America, East Africa, North Africa, Angola and southern Asia. FMD type C virus were controlled and eradicated by vaccination in Europe and South America, and it also become extinct in Africa and other Asian countries.FMD serotype C FMD virus has not been detected in Asia after 1995 and this leads to optimism that FMD serotype C virus is no more present in Asia. Type C FMD virus was detected in the Philippines for many years but last outbreak was recorded in 1991 onwards to 90s no FMD serotype C outbreak detected in this country. Molecular characterization of type C virus revealed that it belongs to evolving topotype Philippines C, originally from South America in the 1970s (Rweyemamu et al., 2008). In 1954, for the first time Serotype C was detected in Pakistan at a military farm, where both cattle and buffaloes were affected. Further, FMD serotype C outbreak was detected in buffaloes during 1963 in northern Pakistan (NWFP). The last outbreak of type C virus detected in eastern part of Pakistan in 1995 (Jamal et al., 2010).

Serotypes SAT (South African Territories-1,2,3)

The SAT serotypes of FMD were prevalent in southern and eastern Africa and are endemic to African buffalo populations in sub-Sahara Africa (Vosloo et al., 1995). The FMDV serotypes SAT are normally confined to sub-Saharan Africa. The natural host for the SAT viruses is the African buffalo which is persistently infected with multiple serotypes. There are three SAT serotypes: SAT1, SAT2 and SAT3. Several studies in Southern Africa have confirmed the African buffalo can sustain FMD virus in their body as a carrier for serotypes SAT-1, SAT-2 and SAT-3 (Voslooand Thomson, 2004). Egypt has reported 20 outbreaks of Foot and Mouth Disease (FMD) serotype SAT-2 in cattle and buffaloes in several regions and Libya reported 23 outbreaks of FMD O, A and SAT-2 during 2012 (WRLFMD, 2012).

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