Chapter 13
Peste Des Petits Ruminant Virus

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Abstract The *peste des petits ruminant* (PPR) virus is a small ruminant morbillivirus (SRMV), formerly known as PPR virus, belonging to the family *Paramyxoviridae*, and the genotype of the virus is clustered into four lineages, based on the nucleoprotein (N) and fusion (F) gene-based sequence and phylogenetic analysis. The PPR virus causes highly contagious, OIE notifiable and economically important transboundary animal viral disease of domestic and wild small ruminants, known as "plague of small ruminant". PPR is clinically manifested by high fever, nasal and ocular discharges, oral necrotising and erosive ulcers, gastroenteritis, and diarrhoea with respiratory distress followed by bronchopneumonia and death. The most important epizootiological risk parameters of PPR in sheep and goats are the introduction of animals to the flock from the unknown source, along with other management factors and rearing patterns. Though natural transmission occurs in cattle, buffaloes and camels, the clinical form of the disease is generally not observed. PPR can be diagnosed based on the clinical signs, pathological lesions and specific detection of the virus antigen or antibodies or genomic nucleic acid by various serological or molecular assays. With the availability of effective and safe vaccine and enabling of institutional mechanism, many countries implemented the vaccination programme to control the disease. PPR is one of the foremost constraints in enhancing the productivity of sheep and goats in developing countries, particularly affecting the economy of the poor landless, and small or marginal farmers. Considering the importance of sheep and goats in food security and socio-economic growth, Food and Agricultural Organization (FAO) and the World Organisation of Animal Health (OIE) jointly launched an international plan for control and eradication of PPR by 2030. This chapter delivers structures of the PPR virus and its genome organisation and functions, disease transmission, epidemiology and risk factors of the disease, diagnosis, prevention and control measures with perspectives.

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13.1 Preamble

The husbandry of small ruminants plays an important role in maintaining the sustainable livelihood of the small, marginal and landless rural farmers in underdeveloped and developing countries in the world. Sheep and goats are the "Any Time Money—ATM" of the poor landless farmers, and it generates self-employment and income for their livelihood throughout the year. Peste des petits ruminants (PPR), otherwise called as "plague of small ruminants" or "goat plague", is concomitant with considerable morbidity and mortality in sheep and goats and causes a serious threat to the economy of the endemic countries. PPR is an acute, extremely contagious, transboundary animal viral disease (TAD) of domestic sheep and goats and small wild ruminants. It causes severe socio-economic implications to livestock owners and is reported to cause an economic loss of USD 1.45–2.1 billion annually (OIE and FAO 2015). The disease was first reported in Côte d'Ivoire, West Africa, during 1942 (Gargadennec and Lalanne 1942) and then spread to other parts of Africa, the Arabian Peninsula, the Middle East and Asia (Balamurugan et al. 2014a; Muthuchelvan et al. 2015; Parida et al. 2015b; Baron et al. 2016). Clinically, PPR is manifested by depression, high fever, nasal and ocular discharges, oral necrotic ulcers, necrotising gastroenteritis, and diarrhoea with respiratory distress followed by bronchopneumonia.

The small ruminant morbillivirus (SRMV), otherwise known as PPR virus (PPRV) (Gibbs et al. 1979) (http://ictvonline.org/virusTaxonomy.asp), causes disease, and the virus is a single negative-stranded RNA genome of single genotype (Adombi et al. 2017) and clustered into four lineages based on the analyses of the nucleocapsid (N) and fusion (F) gene sequences (Shaila et al. 1996; Balamurugan et al. 2010b). Generally, lineages I to III circulate in Africa, while lineage IV (Asian lineage) circulates in Asian continents. However, a recent emergence of Asian lineage IV virus in African countries (Morocco, Marmara Region of Turkey) (Banyard et al. 2010; Kwiatek et al. 2011) and African lineage to China (Zhou et al. 2018) challenges the risk of PPR being introduced to Europe as well (Kwiatek et al. 2011; Baazizi et al. 2017), as lately PPR outbreaks were reported in Bulgaria (Altan et al. 2019). Therefore, the disease spread to various countries in African, Asian and European continents with an association of different lineages is a cause of worldwide concern (Kwiatek et al. 2011; Balamurugan et al. 2014a; Kumar et al. 2014; Parida et al. 2015b; Shatar et al. 2017; Niyokwishimira et al. 2019).

Thus, the transboundary nature of SRMV is expected to accentuate the disease spread to wider geographical region affecting the livestock productivity, especially in developing and underdeveloped countries. As of today, a total of 76 countries with ~1.7 billion of sheep and goats in Africa and Asian continents are in threat of the

disease (http://www.fao.org/ppr/en/). Considering the sheep and goats in food security and socio-economic growth in the underdeveloped and developing countries of the globe, Food and Agricultural Organization (FAO) and the OIE jointly initiated a worldwide programme for control and eradication of PPR by 2030 (OIE and FAO 2015; http://www.fao.org/news/story/en/item/282397/icode; Parida et al. 2019).

13.2 History

The first report of "small ruminants plague" was described in Ivory Coast, West Africa, during 1942 (Gargadennec and Lalanne 1942). They reported an epidemic disease in small ruminants, which was the resemblance to rinderpest (RP), without the involvement of in-contact cattle. After that, the disease spread to Nigeria, Senegal, Ghana, Sudan and other countries in Africa until 1984. Further, disease spread to various countries in the African and Asian continents. In India, the first outbreak was reported from South India during 1987 (Shaila et al. 1989) and thereafter from other parts of northern India, and as of now the disease is enzootic, and outbreaks are regularly occurring throughout the year (Balamurugan et al. 2014a). Based on the analyses of the reports of the outbreak in the National Animal Disease Referral Expert System (NADRES) (http://www.nadres.res.in) from 1991 to 2017, PPR is the topmost disease reported in sheep and goats in India (Balamurugan et al. 2016). PPR is of snowballing status and extends its topographical spreading across the enzootic country. Further, evidence of infection has been reported from several other countries from time to time. Spread of disease to different countries in Africa, Asia and Southern Europe with an association of different lineages of the virus is a cause of animal health alarm (Kwiatek et al. 2011; Balamurugan et al. 2014a; Banyard et al. 2010), as outbreaks were reported in Bulgaria during June 2018. As of today, PPR is enzootic in various countries with the expansion of the range and several outbreaks are being reported recurrently from diverse countries in Africa, Asia and Europe with the involvement of different lineages of virus (Banyard et al. 2015).

13.3 Peste Des Petits Ruminants Virus

PPR virus is an envelope small ruminant morbillivirus (SRMV), which belongs to the genus *Morbillivirus* in the family *Paramyxoviridae* and the order *Mononegavirales* (Gibbs et al. 1979; http://ictvonline.org/virusTaxonomy.asp). On account of its genetic similarity with other members of the genus, PPRV is a relatively recently identified virus. Therefore, most of our understanding of virus structure and molecular biology is based on the comparison with other morbilliviruses (Baron 2015). PPRV is immunologically cross-reactive with other *Morbillivirus*es, namely measles virus (MV), rinderpest virus (RPV), canine distemper virus (CDV), dolphin and porpoise morbillivirus (DMV) and phocine distemper virus (PDV) (Barrett et al. 1993). The PPRV is pleomorphic with an envelope lipoprotein membrane and a

ribonucleoprotein core, which contains non-segmented single-stranded negative RNA genome (Haffar et al. 1999) of ≈16 kb length (Chard et al. 2008). It has an envelope of about 8–15 nm thickness, with spikes of 8.5–14.5 nm length. The herringbone-like structured ribonucleoprotein strand measures ≈4–23 nm. The genome follows the *"rule of six"* and the order of coding genes and their arrangements are as follows: 3′ N–P/C/V–M–F–H–L 5′ (Bailey et al. 2005). While studying the evolutionary dynamics of PPRV, an evolutionary rate of 2.61×10^{6} nucleotide substitutions per site per day was estimated (Bao et al. 2017). Each transcriptional unit is separated by conserved intergenic trinucleotides. The viral genome is separated into six transcriptional elements encoding six structural proteins (fusion (F) and haemagglutinin (H), matrix protein (M), nucleoprotein (N), large (L) and phosphoprotein (P)) and two non-structural (V, C) proteins. The N and P proteins form the enzyme complex in connotation with large (L) protein. Generally, morbilliviruses are classified into two groups: one group comprises CDV and PDV, and another group consists of RPV, MV and PPRV, based on nucleotide (nt) and amino acid (aa) sequences of N protein (Diallo 1990). The close antigenic relationship between the three (N, V and H) proteins of PPRV with DMV has also been reported (Bailey et al. 2005). The conserved 3′ and 5′ termini sequences of the virus are complementary and play an important role as regulatory elements in replication, transcription and packaging of the genome (Banyard et al. 2010). The PPRV leader sequence with 3′ UTR of N gene produces the virus genome promoter (GP) and similarly trailer sequence with 5′ UTR of L gene constitutes the anti-genome promoter (AGP) (Muniraju et al. 2014).

13.3.1 Nucleocapsid (N) Protein

The N protein of virus is the most abundant, antigenically well-conserved and foremost constituent of the nucleocapsid core of virion and plays an important role in transcription and replication. The nucleocapsid is the much conserved immunogenic core protein and expressed at a high level in the infected cells as compared to the other viral proteins. This protein is a noble target candidate for diagnosis assay (Munir et al. 2013) due to its antigenic stability and contains both type-specific and cross-reactive epitopes. It is highly immunogenic, but nucleocapsid antibodies are not protective due to its internal location. The genetic diversity of the N gene sequences was used for classification of SRMV into different lineages by phylogenic analysis. The N gene is located at 3′ end of the genome and encodes for the most transcribed N protein among all the genes of SRMV. The N protein has 525 amino acids (aa) and is possible to interact with other N protein (N–N interaction), P protein (N–P interaction) and L polymerase protein (P–L interaction) for involving in the replication of the virus. Even though sequences essential for self-assembly of N proteins are mapped, evidence of two domains {N-terminus (at 1–120aa) and central region (at 146–241aa)} was established for N–N self-assembly with a short peptide (at 120–145aa) essential for the stability of nucleoprotein. Recently, Ma

et al. (2018) identified PPRV viral synonymous codon usage at the two transition boundaries in PPRV N protein and suggested that tRNA abundance of host variation might have potential effects on the formation of the secondary structure of PPRV N protein. Further, the amino acids in the region (at 106–210aa) are essential for suppressing the nuclear translocation of IRF3 (IFN regulatory factor 3) and IFN-β production, and the region (at 140–400aa) of IRF3 was identified as the crucial region for the N protein-IRF3 interaction (Zhu et al. 2019). Therefore, PPRV N protein as an extremely important antagonistic viral factor that plays a vital role in the suppression of IRF3 function and type I IFN production by interacting with IRF3 and abrogating the phosphorylation of IRF3, and interfering with the TBK1-IRF3 complex formation and thereby inhibiting IFN production (Zhu et al. 2019). Protein plays a vital role in the replication, as silencing of the mRNA can block the production of transcripts and further it right away hinders the synthesis of M protein, which results in inhibition of virus progeny.

13.3.2 Matrix (M) Protein

It is the most conserved and one of the smallest proteins, possesses an inherent ability to bind to lipid membranes and is situated inside the viral envelope (Haffar et al. 1999). It plays a key role in the assembly of virus and in the formation of new virion and release from the cells by budding as well as is adequate for assembly and release of virus-like particles (Wang et al. 2017). M protein has 335aa with an MW of 37.8 kDa. The highly conserved nature of the protein plays a critical role in the progeny virus formation and interacts with glycoproteins in the cell membrane. Further, it mediates the virus budding process favourably at specialised areas of the host membrane. It constitutes the internal coat of the virus envelope and acts as a link to connect F and H proteins with RNP core. For example, MV budding occurs at the apical microvilli due to greatly concentrated actin filaments, which are required for cellular transport. Moreover, the motif (at FMYL 50–53aa) is required for the localisation of the protein to enable the budding in Nipah virus as that of SRMV. Nevertheless, it is not well known whether these viruses share functional homologies. The defected M protein of MV and CDV prevents the formation of infectious virus, which leads to persistent infection, and Liu et al. (2015) showed inhibition of virus replication in vitro and increased virus-mediated fusogenicity by targeting mRNA of M protein by SiRNA approaches.

13.3.3 Surface Glycoproteins

The surface glycoproteins (H and F) of the virus facilitate attachment and penetration. The 137 kDa protein is coded by a conserved F gene and the highly immunogenic F protein have an MW of 59 kDa (Bailey et al. 2005). F protein is embedded in the lipid bilayer envelope as spikes (Diallo et al. 2007). The virulence of the virus

depends on the cleavage of F protein, which is synthesised as a precursor (F0), and cleaved into F1 and F2 subunits, linked by a disulphide bond. Cleavage is mandatory for the virus to become fusogenic and infective and F2 subunits of morbillivirus contain a highly conserved glycosylation NXS/T site. Though the mechanism is not well understood, SRMV has RRTRR (at 104–108aa) (Chard et al. 2008), which is recognisable by the trans-Golgi-associated furin endopeptidase reliable to the cleavage RRX1X2R (X1-any aa, X2—either arginine or lysine) site of morbilliviruses. The F1 subunit of SRMV has four conserved motifs, namely N-terminus fusion peptide, heptad repeat 1 and 2 and a transmembrane domain. The identically structured heptad repeats have a fusion mechanism, which is likely to play a role in budding. Further, anchoring the fusion peptide domain in the membrane and dimerisation of heptad repeat lead to fusion (Rahaman et al. 2003). A conserved leucine zipper motif (at 459–480aa in PPRV) is accountable for enabling the oligomerisation and fusion of the protein through the mysterious process. The F protein of virus is needed for penetration and cell-to-cell spread and plays a crucial role in virus-induced cytopathology, haemolysis (Devireddy et al. 1999) and fusion and hemifusion activities (Seth and Shaila 2001).

The H protein facilitates the virus to bind to the cellar receptor, CD 150 or SLAM (Tatsuo et al. 2001). H and F are equally involved in the fusion activity of the F protein. The ORF of H protein gene (7376–9152 nucleotides) encodes at least conserved 67 kDa H protein (haemagglutinin–neuraminidase). H protein of PPRV and RPV shares only 50% amino acid identity, even though both viruses have 609aa residues that reflects the virus specificity for cell tropism and host range. The H protein of the virus plays a fundamental role in the progression of viral infection and specific binding to the host cell membrane and generation of virus-neutralising antibodies in the host. Moreover, it is the vital antigenic determinant and a major determinant of cell tropism in MV and is the main cause of cross-species pathogenesis. Further, H protein of PPRV requires a homologous F protein for its exact function during replication, and it possesses haemadsorption and neuraminidase activities (Seth and Shaila 2001) whereas in some paramyxoviruses surface proteins can cause haemagglutination and can carry neuraminidase activities. In PPRV, it agglutinates the erythrocytes from diverse mammalian and avian hosts, including the PPRV-infected cell cultures that readily haemadsorb chicken erythrocytes. Further, identification of epitopes and their motifs advances our understanding of the antigenic features of H protein of SRMV and provides a foundation for the progress of epitope-based diagnostic assays and multiple epitope vaccines (Yu et al. 2017).

13.3.4 Large (L) Protein

The RNA-dependent RNA polymerase is the largest, conserved and least abundant protein among morbilliviruses. L protein of SRMV is 2183aa long with an MW of 247.3 kDa identical to that of rinderpest virus (Bailey et al. 2005). L protein is a multifunctional catalytic protein that executes transcription and replication of the genomic RNA, besides capping, methylation and polyadenylation of viral mRNA

including RNA triphosphatase (RTPase), guanylyltransferase (GTase) and methyltransferase activities (Ansari et al. 2019). Three functional motif sequences have been identified, though the direct actions of this protein are not investigated for PPRV (Munir et al. 2013). The binding site sequences (at 9–21aa) for P and L proteins for P–L interaction are conserved in paramyxoviruses, except first valine amino acid in PPRV (Chard et al. 2008). Further, though significant functions of the protein are not yet defined, it will be possible to determine the multifunctional activities of L protein of PPRV using the reconstituted system (Yunus and Shaila 2012). Further, Ansari et al. (2019) identified RTPase domain in the C-terminal region (at 1640–1840aa) of the L protein, which exhibits RTPase activity as well as RTPase-associated nucleotide triphosphatase activity (NTPase).

13.3.5 Phosphoprotein (P) Protein

The P, V and C proteins of morbillivirus are encoded by the overlapping ORF sequences of P gene (Mahapatra et al. 2003). The P protein of PPRV is least conserved and is acidic due to the abundance of serine and threonine and undergoes intensive post-translational phosphorylation. The P protein has a varied length of amino acids from 506 to 509 among morbilliviruses, and PPRV has the longest and plays a role at multiple levels in both viral replication and transcription and immune regulation (Mahapatra et al. 2003). C-terminus of the P protein is more conserved than the N-terminus and is involved in the N–P interaction, which is required for cell cycle control, regulation of transcription and translation. The interactive motifs in the P protein of PPRV are conserved and required for the P–N interaction and are also a vital element of the polymerase complex and a key determinant of cross-species pathogenicity.

13.3.6 Accessory Proteins

The accessory non-structural C and V proteins are synthesised from the ORF of the P gene through the utilisation of alternative start codons and RNA editing mechanism, respectively, in virus-infected cells. The C-terminus of C protein of morbillivirus is highly conserved (Mahapatra et al. 2003) and plays a vital role in viral replication and also inhibits interferon-beta (IFN-β) production by blocking the transcription factors of IFN-β activation. This molecular machinery of C protein of RPV inhibition still needs further investigation. The biological function of the C protein is not known in PPRV, whereas in MV infection it is a virulence factor. The V protein of the virus is generated from mRNA of the phosphoprotein gene by adding one or more non-template G residues by RNA editing. The amino acid length of V protein is highly variable among morbilliviruses, and the N-terminus of V protein shares amino acid residues to the P protein with different cysteine-rich residues at C-terminus. Like P protein, the V protein undertakes phosphorylation and has 60%

of the serine residues. The V protein plays a regulatory role in the transcription and replication of the virus, is a potent inhibitor of IFN and blocks IFN signalling through interference and suppression of STAT-mediated signalling (Ma et al. 2015).

13.3.7 Molecular Biology of Virus

The foremost elements of the host range and tissue tropism of PPRV are the cellular receptors. The virus uses the cellular SLAM or Ovine Nectin-4 molecule (Birch et al. 2013). The continuous cell line such as Vero (African green monkey kidney) (Lefevre and Diallo 1990), marmoset B-lymphoblastoid-B95a (Sreenivasa et al. 2006) and VeroNectin-4 (Fakri et al. 2016) cells can be used for isolation and propagation and titration of the viruses in vitro. Pawar et al. (2008) observed that association exists among replication of PPRV in PBMC of livestock species and the level of SLAM mRNA, and they inferred that the virus uses SLAM receptors of the unnatural host at abridged efficiencies. Generally, the virus exhibits classical cytopathic effect (CPE) in infected cells, like the rounding of the cells or grape-bunch-clusters, vacuolation, granulation and syncytia within 3–5 days of infection. Further, the CPE of virus-infected PBMCs was characterised by degeneration, ballooning, rounding and clumping of cells without syncytia (Mondal et al. 2001), but syncytia were also observed in B95a cells 2–3 days postinfection (pi) (Sreenivasa et al. 2006). Generally, the virus is fragile and sensitive to the ether, but is comparatively stable at pH 5.8–10.0 and inactivated at 50 °C for 60 min (OIE 2013).

The first step in the replication cycle of the virus is the attachment on the surface of the cell membrane and fusion to release genetic materials into the cytoplasm. After the binding and entry of the virus in the endometrial epithelial cells, it intensely affects early cellular gene expression (Yang et al. 2018a, b). The H protein of virus is accountable for attachment to the sialic acid on the cell membrane (Munir et al. 2013) surface through either SLAM or CD 150 (Pawar et al. 2008) or nectin-4 (Birch et al. 2013) receptor. Attachment activates the fusion of the F protein, enabling a fusion of the envelope with cell membrane and release of genetic materials into the cell. Replication of the morbilliviruses occurs solely in the cytoplasm of host cells. The viral genome is never found as naked RNA and is encapsidated by the N protein to form the helical ribonucleoproteins (RNP). This complex contains the encapsidated RNA, in conjunction with the P and L proteins, forming the mini replicative unit (Parida et al., 2015b). The polymerase complex acts on the viral genome, binds to the genome promoter and starts transcribing short leader RNAs and subsequently transcribing each gene, which leads to the building up of a transcriptional gradient. At certain points, the polymerase complex switches its action from mRNA production to full-length positive-sense RNA, which is thought to be linked to the accumulation of viral proteins, although the precise mechanism remains unclear (Parida et al. 2015a, b). Following the production of a full-length anti-genome RNA, the polymerase binds to the anti-genome RNA at the anti-genome promoter (3′) and generates nascent full-length sense genome. The synthe-

sised viral components finally lead to viral egress from the host cell. The M protein of virus plays a significant role in bringing the nascent RNPs and viral glycoproteins to the host cell membrane, which results in the packaging, budding and release of nascent virions (Parida et al. 2015a, b).

Further, Chaudhary et al. (2015) observed that receptor tyrosine kinase (RTK) signalling regulates virus replication and PVRL4 (nectin-4), tumour-associated marker, plays a vital role in pathogenesis and promises its use in cancer therapies (Delpeut et al. 2014). Moreover, Balamurugan et al. (2008) proved the antiviral effect of aqueous extract of *Acacia arabica* on in vitro virus multiplication, whereas Khandelwal et al. (2015) reported that SNPs proficiently inhibited the multiplication of the virus. Further, Kumar et al. (2019) demonstrated that sarco/endoplasmic reticulum calcium-ATPase (SERCA) could regulate virus replication by using SERCA-specific inhibitor (Thapsigargin) to block viral entry into the target cells as well as synthesis of viral proteins. Further, Qi et al. (2018) investigated the roles of host microRNA in PPR virus replication and pathogenesis. Yang et al. (2018a, b) reported that virus infection in caprine endometrial epithelial cells activates an autophagy response, mediated by C and N proteins of the PPRV, and induced autophagy inhibits caspase-dependent apoptosis and thus contributes to the enhancement of viral replication and maturity in host cells.

Molecular characterisation and phylogenetic analyses of different PPRV isolates/strains from various countries in African and Asian continents (Padhi and Ma 2014; Baron 2015; Banyard and Parida 2015) defined the prevalence of four lineages of the virus (Shaila et al. 1996; Dhar et al. 2002). During the 1970s, lineage I virus was initially isolated from Nigeria and Senegal countries in West Africa and later from Cote d'Ivoire, Guinea, Senegal and Burkina Faso. Subsequently, lineage II viruses were isolated in the 1980s from different countries in West Africa (Dundon et al. 2018) and as of now this African lineage did not cross the Red Sea to Asian continents. Further, lineage III viruses have been reported from Meilig, Ethiopia, Yemen, Sudan, Oman and Burundi (Niyokwishimira et al. 2019), whereas the Asian lineage IV viruses have been reported from Arabian Peninsula, the Middle East and southeast part of Asia. Moreover, recently, lineage IV was also reported in African countries and Southern Europe (Altan et al. 2019). Further, co-circulation of different lineages of the virus in Nigeria (Woma et al. 2016) and China (Liu 2018) with the emergence of lineage IV virus in Ethiopia (Muniraju et al. 2014) has also been reported. In India, since the first PPR report so far involves only PPRV lineage IV strains/isolates (Balamurugan et al. 2010b; Muthuchelvan et al. 2014), and one isolate of lineage III (PPR TN/92) (Shaila et al. 1996).

13.4 Prevalence of Disease

The prevalence of virus antibodies and detection of virus antigen/genome in small ruminants are reported from different countries in the world (Singh et al. 2004a; Balamurugan et al. 2011, 2012b, 2015; Khan et al. 2008; Mbyuzi et al. 2014; Gari et al. 2017; Balamurugan 2017; Ali et al. 2019) including cattle, buffaloes and cam-

els (Govindarajan et al. 1997; Abraham et al. 2005; Balamurugan et al. 2012a, 2014b; Sen et al. 2014; Omani et al. 2019). The presence of PPRV antibodies in small and large ruminants (Abubakar et al. 2017; Woma et al. 2016) infers subclinical/inapparent/non-lethal infection, as vaccination is irregularly practiced or restricted in the endemic settings of underdeveloped and developing countries in the world. Moreover, antibodies in small adult ruminant animals are not constantly indicative of PPR. Cattle and swine are the seroconverters to the virus, but they neither exhibit clinical symptoms nor transmit the infection. However, recently, Schulz et al. (2018) reported that suids are the likely source of infection. Moreover, cattle are dead-end hosts and do not play an epizootiological role in the maintenance and spread of the virus (Couacy-Hymann et al. 2019). All these studies revealed that PPR could also be transmitted from small ruminants to large ruminants and provided machinery for the survival of the virus in the environment outside the host. In unnatural hosts, PPRV may have a vital role to restrict the disease spread in certain topographical niche (Balamurugan et al. 2012a, 2014b), where small and large ruminants are reared together in the farming systems (Balamurugan et al. 2014b), which might be due to the fortuitous of adaption and alteration in the virulence of the virus. However, it needs further confirmation, based on the virus survival, host susceptibility of the host, virus mutation, variation in the disease severity, etc.

The role of wildlife in the epizootiology of the disease has been emphasised in literature (Taylor 1984), especially in wildlife species (e.g. in vulnerable wild small ruminants (Marashi et al. 2017), wild ungulates (Rahman et al. 2018), wild and domestic animals (Li et al. 2017)) which could be of substantial significance for the spread of the virus. There is a likelihood of wildlife-domestic interactions for feed and water reservoirs through grazing pastureland (Mahapatra et al. 2015), resulting in the spillover of the infection to wildlife (Rahman et al. 2016). However, the definite role of the wildlife on the epizootiology of PPR remains uncertain at present and to be investigated (Banyard et al. 2010; Balamurugan et al. 2015). Additionally, the presence of PPRV antibodies in the bovines and wild ruminants besides sheep and goats divulges the natural transmission (Abraham et al. 2005; Balamurugan et al. 2015). Moreover, the detection of PPRV in wildlife has not yet been described except in gazelles, camels (Khalafallaa et al. 2010; Zakian et al. 2016), wild bharal and chousingha (*Tetracerus quadricornis*), a member of the subfamily Bovinae (Jaisree et al. 2018). Further, PPRV in the nasal swabs of dogs by microarray screening (Ratta et al. 2016) and detection of virus genomes in the tissue of lion (Balamurugan et al. 2012c) provided new insight into the possible crossing of the species barrier. Because of the risk of PPR, vaccination should be adopted to circumvent the virus, and the circulation between wild and domestic small ruminants.

13.5 Risk Factors

The virus primarily affects domestic sheep and goats and rarely camels and other wildlife. Many researchers stated that though PPRV infects small ruminants severity is more in goats (Tripathi et al. 1996; Singh et al. 2004a; Balamurugan et al.

2015). Even though there is no evidence of carrier state (Furley et al. 1987), the infected animals excrete the PPRV in the secretions and excretions from the 3rd day to 26th day postinfection or even up to 16 weeks after infection (Balamurugan et al. 2006, 2010a; Liu et al. 2014; Wasee Ullah et al. 2016), and thus they play a vital role as a source of silent infection in the epizootiology of PPR. Toll-like receptors and cytokines have played a role in the differential susceptibility of species/breed to PPRV (Dhanasekaran et al. 2015) and analysing these factors with host genetic factors might provide further understanding on polymorphisms in the host and its susceptibility. Breed of the animals may also have a different outcome of disease (Lefèvre and Diallo 1990). Besides breeds, there exists a relationship between disease and age of the animals (6 months to 1 year), i.e. between the severity of the disease and the young animals. Young animals below 1 year of age are the significant predictors in rural systems or pastoral settings (Huyam et al. 2014; Gitonga 2015) and the passive immunity in offspring disappears after 4–5 months in endemic settings (Balamurugan et al. 2012d). Gowane et al. (2016) reported that the presence of maternal antibodies affects the vaccination response and inferred that the moderate estimate of heritability for vaccine response predicts the selection of goats for the greater vaccine response.

Moreover, response to the PPR vaccine in sheep and goats is extremely variable and influenced by environmental and genetic constituents, including MHC class II (Gowane et al. 2016, 2017, 2018). In general, the species, age and sex of the animals and the herd size have been identified as risk factors for PPR (Teshale et al. 2018). Further, the seasonal incidence of PPR was associated with the movement of the small ruminants and climate factors. However, in enzootic settings, PPR occurs around the year with more frequency in the lean period (Balamurugan et al. 2011, 2012b, 2016). Generally, small ruminants are raised by the small or marginal farmers on free-range grassland, shrubs and forest areas, and these animals frequently travel for long distances in the lean period for the search of fodder and water, thus causing a considerable upsurge of PPR incidence (Balamurugan et al. 2016). Most researchers have related the outbreaks with the introduction of new animals from the strange sources to the flocks as a major risk factor. Further, Kardjadj et al. (2015) reported abortion and associated risk factors in small ruminants for PPR. In general, the epidemiological risk parameters of PPR in sheep and goats are the young animals aged between 4 months and 1 year that are being severely affected. This warrants the need for public awareness of biosecurity management in the flocks (Almeshay et al. 2017).

Feeding pattern including stall feeding and grazing was not found to be a significant risk factor as reported (Rahman et al. 2016), although this variable has been considered as a risk factor for acquiring infectious diseases. However, stall feeding might have other management practices like the purchase of animals that upsurge the risk of transmission. Even though grazing was not a substantial risk factor, there is a quiet likelihood of domestic animal interfaces in pastures and aquatic sources for feed and water reservoirs for spillover of the disease. Rony et al. (2017) identified the determinants and space-time clusters of PPR while conducting hospital-based case-control study design and stated that vaccination should focus prior to the

onset of winter and monsoon on the disease hotspot areas, especially on high-risk groups (young animals aged 4–24 months), to raise their immunity level in the lean periods. Differences in PPRV seropositivity depending on species, sex, age, season and geographical location have previously been described (Abubakar et al. 2008). However, Khan et al. (2008) stated that significantly greater proportions of seropositive female animals were observed compared to male in their study. This may be related to the physiological differences between female and male, where females reveal some degree of infection resulting from stress due to milk production and pregnancies. Due to the significance of productivity potential, females sustained for a longer period as compared to males, thus increasing the likelihood of female animals being exposed to PPRV over time. PPRV actively circulated in the endemic regions and the migration of animals was the main source of spreading the disease in these regions (Almeshay et al. 2017).

13.6 Pathobiology

The disease occurs by the entry of the PPRV through the upper respiratory tract (URT) epithelial cells (Parida et al. 2015a). Pope et al. (2013) demonstrated that the initial site for the virus replication is within the tonsillar tissue and lymph nodes draining the site of inoculation. They proposed that immune cells transport the PPRV to lymphoid tissues where primary virus replication occurs, and then virus enters circulation (primary viraemia), and subsequently clinical signs appear according to the multiplication of the virus in the target cells/tissues (Truong et al. 2015). The virus proliferation and its pathogenicity are relational to those of many epizootiological determinants of the host (Munir et al. 2013; Balamurugan et al. 2015) including genetics and non-genetic determinants (Gowane et al. 2016, 2017). Kumar et al. (2004) reported the detection of the PPRV antigen in the respiratory epithelial syncytial cells. An affinity of the virus to the lung parenchymatous cells and lymphocytolysis was observed in Peyer's patches and mesenteric lymph nodes and further the virus was also detected in the ileal epithelial cells as dark brown granules. Nevertheless, various researchers have demonstrated the viruses in various tissues and organs, including epithelial crypts in the intestine. The details of the pathogenesis and involvement of immune cells during PPRV infection have been described (Balamurugan 2017). The transient leucocytosis was considered as a response to stress and immune activation and speculated the activation of B cells during secondary viraemia. Moreover, PPRV infection induces IFN-β weakly and transiently, and the virus can actively block the induction of IFN-β for protection (Sanz Bernardo et al. 2017). Kinetics of immune response has also been deliberated in vaccinated sheep and goats (Singh et al. 2004b, 2004c; Rajak et al. 2005) and protective antibodies persist for 3–6 years after a single vaccination (Saravanan et al. 2010; Zahur et al. 2014). The immunological study conducted by Rojas et al. (2019) indicated that F and H viral antigens are natural antibody-dependent cell-mediated cytotoxicity targets during infection and they stated a novel effector

immune mechanism against PPRV in the host that could contribute to virus clearance. Both humoral and cell-mediated immune responses are involved in the immune suppression (Rajak et al. 2005). However, the precise mechanism of suppression by the activation of the host RIG-I-like receptor (RLR) pathway has yet to be elucidated. Moreover, Zhu et al. (2019) demonstrated an antagonistic mechanism of PPRV that significantly suppressed the RLR pathway activation and type I IFN production by suppressing IFN-β- and IFN-stimulated gene (ISG) expression. Jagtap et al. (2012) reported that immunosuppressed animals had a short period of viraemia, and more extensive and severe disease progression with high mortality than the non-immunosuppressed one. Further, Mondal et al. (2001) demonstrated virus-induced apoptosis in PBMCs whereas Kumar et al. (2002) reported apoptotic lymphoid cells in PBMCs from infected animals. Nevertheless, genomic and transcriptomic analysis of host and virus revealed 985 differently expressed genes and transcription factors modulating immune-regulatory pathways with involvement of genes in regulation, spliceosomal and identified apoptotic pathways that are dysregulated (Manjunath et al. 2015). They identified PPRV-induced miR-21-3p, miR-320a and miR-363 transcriptome, which might act cooperatively to increase viral pathogenesis by downregulating several immune response genes. Manjunath et al. (2017) predicted induction of ISGs by IRFs in an interferon-independent manner to activate a strong immune response based on the transcriptome analysis and qRT-PCR validation. Further, Baron et al. (2015) specified constant decrease in CD4+ T cells during pathogenesis in goats, while Truong et al. (2015) reported that the predominant sites of virus replication are the lymph nodes, lymphoid tissue and GI tract organs.

13.7 Transmission

For the spread of infection, the virus requires nearby contact of the infected and susceptible host due to the low resistance or labile of the virus outside the environment (Balamurugan 2017). During infection, substantial quantities of viruses have been excreted in the discharges, secretion and excretion of the infected animals that are the important source of infection (Balamurugan 2017). Transmission occurs primarily between closely contacted animals especially by direct contact with neighbouring animals by inhalation of the fine infectious aerosol droplets. These virus particles indirectly spread through contaminated water and feed troughs, bedding materials, fomites, etc. This method appears to be less significant since the virus does not survive outside the host for a long period (Lefèvre and Diallo 1990). Further, trade at local marketplaces where animals from multiple sources are brought into close contact provides better likelihood for spread. Besides sheep and goats, virus transmission to wild ruminants and unnatural hosts, namely cattle, buffaloes, camels, swine, etc., provides outside mechanism for the survival of the virus (Abraham et al. 2005) and the presence of PPRV antibodies in these unnatural hosts and wild ruminants suggests the natural transmission (Abraham et al. 2005;

Balamurugan et al. 2012a). Recently, Şevik and Oz (2019) investigated the possible role of the *Culicoides* spp. in the transmission of the virus. Even though seroconversion has been reported, clinical disease/signs in these unnatural hosts have not been reported (Sen et al. 2014). Migrating small ruminants will often come into close contact with other infected animals (Singh et al. 2004a) and spread the infection. Kivaria et al. (2013) reported that the spread and persistence of PPRV infection with epizootiological patterns and predictions in developing and underdeveloped countries are required for a better understanding of transmission. Hence, animal movement plays a pivotal part in the disease spread and the conservation of PPRV in the environment. Recently, Fournié et al. (2018) estimated the required immune population to be more than 37% in at least 71% of rural village populations in an endemic setting to prevent the virus spread by fitting a metapopulation-simulating model.

13.8 Clinical Manifestations

Clinical symptoms of the disease in small ruminants are manifested by high fever, discharges from the eye and nasal orifices, oral necrotic ulcers, gastroenteritis, diarrhoea and respiratory distress and bronchopneumonia (Balamurugan 2017). In camels, clinical symptoms are similar with additional manifestations of keratoconjunctivitis and oedema of the abdomen (Omani et al. 2019). PPR manifests as either peracute or acute or mild forms relying on the disease severity (OIE 2013; Balamurugan 2017), which depends on the virulence of lineage of virus (Couacy-Hymann et al. 2007), host, breed, age and immune status of the species, etc. PPR exhibits 4–5 different phases/stages during the infection, viz. (i) short incubation, which ranged from 3 to 10 days; (ii) prodromal feverish/febrile stage; (iii) mucosal stage with high fever, conjunctivitis, discharges from eye and nasal orifices (Fig. 13.1a, b), and erosions of the oral mucosa especially on the tongue, palate, lips and other parts (Fig. 13.1c); (iv) diarrhoeal phase (Fig. 13.1d), with pneumonia, dehydration and death; and (v) recovery phase, especially for non-fatal stage, in which animals develop lifelong immunity. Studies on the clinical symptoms and its complications in the manifestation of the disease have been discussed (Tripathi et al. 1996).

13.9 Diagnosis

PPR is diagnosed by specific clinical signs and characteristic pathological lesions in the affected animals, which include consolidation of lungs; enlarged spleen and intestinal mesenteric lymph nodes; streaks of haemorrhages on the mucosa of large intestines, etc. (Fig. 13.1e, f); and confirmative diagnosis by an array of laboratory techniques. A surfeit of diagnostic assays is available for the detection of either viral antigen or antibodies or genome. In general, the confirmatory conventional assays/tests including the gold standard virus isolation are not rapid, are less sensitive, are tedious, require technical expertise and culture facilities, and may not be useful for

Fig. 13.1 (**a**–**f**) PPRV-infected sheep showing congestion of mucosa in the eye (reddened eye with mild conjunctivitis) (**a**); mucopurulent discharges from nostrils (**b**); ulcers (diphtheritic–plaques) and necrotic lesions in the gum (**c**); severe diarrhoea with solid hind quarters (Frank diarrhoea) (**d**); post-mortem lesions of PPR-affected sheep's lungs showing congestion and consolidation of lobes (**e**); and colon showing discontinuous streaks of congestion and haemorrhages on the mucosal folds (**f**)

primary diagnostics. For large-scale screening of samples, ELISA has widely been used for monitoring and surveillance of disease or even for diagnosis. Advanced understanding on the biology of the virus and molecular biological techniques leads to the development of rapid, highly specific and sensitive molecular assays (RT-PCR, real-time RT-PCR, and loop-mediated isothermal amplification (LAMP) assays) for the detection of the viral genome. Further, point-of-care diagnostics or on-the-field diagnostics tool, in the less equipped laboratory settings including lateral flow assay,

has also been developed, but its usage is not up to the expected levels (Raj et al. 2008). Further, recombinant DNA technology made the production of safe recombinant viral proteins easy, as a better alternative to live antigen, and its application as the diagnostic antigen in the immunoassay for disease diagnosis. Recently, various modern diagnostic approaches have been developed by different researchers for detection of PPRV antibodies in serum and PPRV antigen/nucleic acid in the secretion, blood and tissue samples including milk (Clarke et al. 2018) and are summarised in Table 13.1. Parida et al. (2019) reported that nasal swabs are the most suitable to sample when considering the molecular diagnosis. These diagnostics can be efficiently applied at different stages in the PPR control and eradication phases based on the resource availability and the number of samples to be screened (Libeau 2015; Santhamani et al. 2016).

The differential diagnoses to be carried out with other diseases having similar clinical signs are contagious caprine pleuropneumonia (CCPP), pasteurellosis, bluetongue, contagious ecthyma (ORF), foot and mouth disease (FMD), etc. Sometimes, coexisting/concurrent or mixed infection with other viruses causing diseases has also been described (Balamurugan 2017; Kumar et al. 2016; Maan et al. 2018; Adedeji et al. 2019; Malik et al. 2011). Hence, identification of epizootiological and economically significant sets of these viruses or mixed infections could also support in establishing better guidelines for animal trade that could transmit further infection and epizootics (Kumar et al. 2016).

13.10 Socioeconomic Impact of PPR

Sheep and goat rearing provide social, financial and economic security to landless, marginal and small farmers in developing and underdeveloped countries. PPR in sheep and goats devastates the security fabric of the farmers who are already in distress due to various socio-economic-climate-associated risk factors in these regions. Epizootics of PPR can cause 50–80% mortality in naive small ruminants. The disease primarily causes mortality resulting in direct production loss. Further, live weight loss, milk loss and few abortion cases are also visible in the affected flocks. To control the disease, the farmers incur expenditure for treatment and labour cost to nurse the infected animals. In a few cases, distress sale is also pronounced, especially when a larger number of animals die on the farm. Further, at the macro level, the ripple effect on the entire small ruminant value chain and the spillover effects on various livestock interlinked sectors of the economy are evident if PPR outbreaks occur in wider geographical locations in large numbers. Some impacts are direct (production loss), and some are indirect (treatment cost, distress sale, market restrictions, etc.). Some impacts are tangible and easy to measure, but many are intangible and difficult to measure. The tangible impact variables include mortality, reduction in meat and milk, foregone revenue, etc. whereas intangibles include the reduction in functionality like asset building, diversification and income smoothing (de Haan et al. 2015). The consequent impacts of PPR on food access, consumption change, income and expenditure adjustment among the PPR-affected

Table 13.1 Diagnostic techniques for PPR diagnosis

Diagnostic techniques	Features
Gold standard test virus isolation	Primary bovine and sheep cells, Vero cell line, marmoset B-lymphoblastoid-B95 a, VeroNectin-4 (Fakri et al. 2016)
Virus or serum neutralisation test	Using cell culture facilities
Agar gel immunodiffusion test/ counter-immunoelectrophoresis	Tentative diagnosis
Haemagglutination	Simple, inexpensive and provides results within a few hours
Competitive ELISA/blocking ELISA/epitope-blocking ELISA	Neutralising monoclonal antibodies—MAb—H protein/N protein (Singh et al. 2004c; Bodjo et al. 2018)
Immuno-capture ELISA/ sandwich ELISA	Rapid differential identification and MAb—N protein (Singh et al. 2004b)
Indirect ELISA/combined indirect ELISA	PPRV antigen and polyclonal antibodies/G protein (Yousuf et al. 2015)
Simple and aqueous-phase ELISA (SNAP-ELISA)	RT-PCR/ELISA system
Immunohistochemical detection	Detection of antigens within tissues
Immunoperoxidase monolayer assay (IPMA)	IPMA an alternative method of VNT using BHK-21 cell line stably expressing the goat SLAM (Zhang et al. 2016)
Dot-ELISA	Using anti-M protein MAb/anti-N protein MAb
Immunofiltration/antigen-competition ELISA/lateral flow assay	Detection of antigen/antibodies in the clinical samples (Raj et al. 2008)
Recombinant antigen-based ELISA	Using N/H/F antigen (Balamurugan 2017; Basagoudanavar et al. 2018)
Nucleic acid hybridisation and RT-PCR	F gene, N gene or N and M gene in either one- or two-step procedure (Forsyth and Barrett 1995; Couacy-Hymann et al. 2002; Balamurugan et al. 2006)
PCR-ELISA	RT-PCR with ELISA (Saravanan et al. 2004)
Real-time RT-PCR	N or M gene-based SYBR Green/TaqMan real-time RT-PCR either in simplex or duplex format real-time or one-step multiplex (Bao et al. 2008; Balamurugan et al. 2010a, e; Polci et al. 2015; Settypalli et al. 2016)
Loop-mediated isothermal amplification (LAMP)	N gene-based assay (Li et al. 2010)
Luciferase immunoprecipitation system (LIPS)	Rapid detection and specific differentiation of PPRV antibodies (Berguido et al. 2016)
Reverse transcription recombinase polymerase amplification assays (RT-RPA)	Targeting N gene sequences—conventional and real-time RT-RPA (Zhang et al. 2018; Li et al. 2018)
Real-time and lateral-flow strip RT-RPA assay	Real-time fluorescent detection by targeting the N gene of PPRV (Yang et al. 2017)
Lateral-flow immunoassay strip (LFIAS)	Fast and ultrasensitive test-strip system combining quantum dots (QDs) with a LFIAS using recombinant PPRV N protein (Cheng et al. 2017)

flocks and effect on other social variables like women participation, employment, asset loss and family education also need to be assessed to know the impact holistically. Further, the impact of the PPR in smallholder's perspective in the realm of the significance of small ruminants within agriculture and services is needed to implement appropriate interventions (de Haan et al. 2015). Hence, the disease cost associated with PPR is huge at the farm, regional, national and global level. PPR causes severe socio-economic implications to farmers and is reported to cause an estimated economic loss of USD 1.45–2.1 billion annually (OIE and FAO 2015).

The assessment of the impact of the disease in different countries/geographic regions, production environment and management types is essential for developing an appropriate PPR control plan for a region/country/sub-country level. It would be useful to convince the governments and international organisations to support and provide required funds to control PPR, eventually to plan and implement the global PPR eradication campaign. The estimated total cost for the global eradication of PPR is to the tune of US$3080 million (Jones et al. 2016), which includes costs associated with global, regional and national coordination; institutional development, epidemiology and surveillance; establishing diagnostic laboratories, vaccination implementation, training and research; socio-economics; contingency; and emergency response. In India, the recent estimate by Govindaraj et al. (2016) revealed loss to the tune of Rs. 1611 crore at 10% annual incidence level. The studies on the investment benefits of PPR control and eradication revealed considerable benefits to various stakeholders. Furthermore, eliminating PPR will benefit millions of landless, small and marginal farmers, in the most vulnerable societies in developing and underdeveloped countries in African and Asian continents.

13.11 Prevention and Control

Generally, control and eradication of the disease depend on the efficient and timely diagnosis, surveillance, monitoring and execution of vaccination against the disease in the susceptible populations. The available PPR vaccines in India (Sungri 96 Strain) and other countries in the world (Nigeria 75/1 strain) have been widely used for the prevention and control of PPR in sheep and goats. However, these vaccines do not favour the differentiation of infected and vaccinated animals. PPR has an enormous impact on sheep and goat production and restricts trade in endemic countries. Therefore its prevention and control are of high priority. Implementation of effective prophylactic measures is highly imperative for disease control. The terrestrial spread of PPR along with its epidemiological parameters and ways in which it spreads can be abridged through the facility of diagnostic aids (Taylor 2016). Among the available control measures, vaccination is a recommended tool to contain the disease in endemic settings. Even though isolation or quarantine and restriction on the movement of animals in the affected areas limit the spread of the disease, it is difficult to set up at field level due to concomitant problems in underdeveloped and developing countries in the world. Further, in PPR enzootic countries, hygienic

and phytosanitary control measures are problematic to sustain. Hence, mass vaccination is the only option available to control the disease effectively. Besides vaccination, quarantine of newly purchased animals for 2–3 weeks, understanding the health condition and the origin of purchased animals, continued monitoring of animals for illness, efficient cleansing of the contaminated places with disinfectants including equipment and clothing, etc. will pave the way for the control of the disease. There is no specific treatment available against PPR. The treatment regime of affected animals includes the use of broad-spectrum antibiotics plus fluid therapy along with vaccination of the affected flock during the first week of an outbreak in endemic settings (Abubakar et al. 2017).

13.11.1 Vaccination

Control strategies vary from different countries based on the prevalence of the disease. However, the choices are limited in underdeveloped and developing countries, as culling out policy is not feasible, owing to various socio-economic reasons. Vaccination is a recommended option for prevention and control of the disease to avoid an immediate economic loss to the farmers (Singh et al. 2009; Singh 2011; Balamurugan et al. 2016). In many countries, the success of rinderpest eradication provided the confidence to implement a similar programme for PPR. Scientific and technical experts, trained veterinarians, technical and para-veterinary staff for handling vaccines at various stages from production or procurement stages to vaccination in the field are paramount importance for the vaccination programme. Professional commitment from veterinarians and ancillary personnel involved in a mass immunisation programme is crucial to succeeding any vaccination programme (Singh et al. 2009). These prophylactic services are being gradually expanded by involving public-private partnership, especially the participation of non-governmental organisations, cooperatives and private veterinary practitioners in implementing and executing the disease control programme as stated (Singh et al. 2009). Further, setting up a network cum database would be of help in developing a coordinated approach towards effective implementation of the control programme. Some of the countries have already initiated PPR control measures either through their resources or with the help of international agencies to augment the small ruminant production (Singh and Bandyopadhyay 2015). Therefore, the launching of control and eradication programme appears to be a technically feasible, economically viable and practically attainable proposition (Singh et al. 2009).

PPR mass vaccination strategies include implementation of the campaign to achieve 80% flock immunity, by considering the dynamics population of small ruminants with the appearance of 30–40% naïve sheep and goat population every year, farming practices and agroclimatic conditions (Singh 2011; Woma et al. 2016). Thus, exhaustive vaccination of the whole population within a niche area in a specified period followed by vaccination of 3–4-month-old naïve animals (Singh 2011) is imperative to evade a window of susceptibility in newborn animals (Balamurugan

et al. 2012d). However, vaccination should also be targeted on the high-risk young ones, migratory or trade market flocks, etc. (Singh 2011); otherwise, rigorous vaccinations can also be done in the identified niche area to make "PPR-free zone" in enzootic settings. The prophylaxis and control measures, including vaccination strategies, planning of control and eradication programme, have been discussed in details (Balamurugan et al. 2016; Balamurugan 2017; Raj and Thangavelu 2015).

13.12 Perspectives

PPR is one of the transboundary animal viral diseases of small ruminants, and its control is essential for poverty alleviation in endemic underdeveloped and developing countries, as the existence of PPR can limit domestic and international trade and production. Disease epizootics affects farmers, the livestock industry and the national economy. However, the economic impacts of PPR are underestimated due to the occurrence of other diseases in mixed forms. Due to dynamic populations of sheep and goats, intensive vaccination needs to be carried out frequently for the control of the disease. As of today, PPR has been brought under control in some developing countries by safe and effective PPR vaccines. However, the rapid spread of disease in wider geographical locations necessitates the studies to be undertaken to understand the effect of agroclimatic changes on the disease occurrence in various regions including the mechanism of spread and transmission dynamics of disease and analysing the association between occurrence and risk factors and the formulation of the suitable models for forewarning and forecasting of the disease. Moreover, adapting vaccination strategies to the population dynamics and the specific features of the local epidemiological settings would effect the optimised allocation of limited resources and increase the likelihood of PPR eradication (Fournié et al. 2018). Also, national and international funding agencies' sponsored vaccination programmes revealed that final eradication could be attained with remarkable swiftness aimed at the culmination of the virus transmission if the origin of the PPRV infection was known (Taylor 2016). Further, research is needed for development and application of newer or latest or next-generation technologies for vaccines and diagnostics, but rather the cautious application of epidemiology and conventional virology to provide quantitative information to support for efficient control and eradication of the disease promptly (Baron et al. 2017). In the current RP-eradicated scenario, it gives the disease an even higher priority, as PPRV can infect large ruminants too. Further, FAO, OIE and other international agencies' cooperation, understanding, tools and experiences now on proposal advocate that PPR could be controlled and eliminated far more swiftly than rinderpest.

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