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Regulation and evasion of antiviral immune responses by porcine reproductive and respiratory syndrome virus



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ABSTRACT

Virus infection of mammalian cells triggers host innate immune responses to restrict viral replication and induces adaptive immunity for viral elimination. In order to survive and propagate, viruses have evolved sophisticated mechanisms to subvert host defense system by encoding proteins that target key components of the immune signaling pathways. Porcine reproductive and respiratory syndrome virus (PRRSV), a RNA virus, impairs several processes of host immune responses including interfering with interferon production and signaling, modulating cytokine expression, manipulating apoptotic responses and regulating adaptive immunity. In this review, we highlight the molecular mechanisms of how PRRSV interferes with the different steps of initial antiviral host responses to establish persistent infection in pigs. Dissection of the PRRSV–host interaction is the key in understanding PRRSV pathogenesis and will provide a basis for the rational design of vaccines.

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1. Introduction

Since described in USA in 1987, porcine reproductive and respiratory syndrome (PRRS) has now been one of the most important diseases in pigs, leading to significant economic losses in swine industry worldwide (Albina, 1997; Pejsak et al., 1997; Rossow, 1998). In 2005, the annual costs of PRRS for the American swine industry were approximately 560 million dollars (Neumann et al., 2005), and recently, the estimated costs are increased to about \$664 million per year in the United States (Jiang et al., 2013). In the past twenty-seven years, PRRS has emerged in almost all of the pig-producing countries (Bilodeau et al., 1991; Cho and Dee, 2006; Kuwahara et al., 1994). In 2006, a highly pathogenic PRRSV (HP-PRRSV) strain with discontinuous 30 amino acid depletion in nsp2 protein associated with porcine high fever syndrome (PHFS) was reported in China, and overwhelmed swine industries in China and Vietnam (Huang and Meng, 2010; Li et al., 2007b; Tian et al., 2007). The clinical symptoms of typical PRRS are reproductive failure in sows and severe respiratory disease and poor growth performance in piglets (Done and Paton, 1995; Pejsak et al., 1997). For the high

fever syndrome, it is characterized by high fever, high morbidity, and high mortality (Tian et al., 2007).

The causative agent, porcine reproductive and respiratory syndrome virus (PRRSV), was identified in 1991 in the Netherlands (Wensvoort et al., 1991) and 1992 in the United States (Morrison et al., 1992). According to the sequence analysis, PRRSV is grouped into two genotypes, the type 1 European PRRSV (the prototype is Lelystad virus (LV)) and the type 2 North American PRRSV (the prototype is VR2332). PRRSV is an enveloped positive single-stranded RNA virus and belongs to the genus *Arterivirus*, family *Arteriviridae*, order *Nidovirales*. The genus *Arterivirus* also includes equine arteritis virus (EAV), lactate dehydrogenase-elevating virus (LDV), and simian hemorrhagic fever virus (SHFV) (Cavanagh, 1997; Plagemann and Moennig, 1992; Snijder and Meulenberg, 1998). PRRSV genome is approximately 15.4 kb in length and has at least 10 open reading frames (ORFs) (Yun and Lee, 2013). ORF1a and ORF1b, which constitute about 75% of the genome, encode two polyprotein precursors: pp1a and pp1ab. pp1a and pp1ab are considered to be cleaved into at least 16 nonstructural proteins (nsp1 α , nsp1 β , nsp2-6, nsp2TF, nsp2N, nsp7a, nsp7b and nsp8-12) upon infection by viral proteases nsp1 α , nsp1 β , nsp2, and nsp4. ORF2a, ORF2b, ORF3-7, and ORF5a encode eight structural proteins: a small, non-glycosylated E protein, five glycosylated membrane proteins (GP2-GP5 and GP5a), a non-glycosylated membrane protein (M), and the nucleocapsid protein (N) (Dokland, 2010; Fang and Snijder, 2010; Fang et al., 2012b; Li et al., 2014; Wei et al., 2013). These PRRSV proteins are involved in virus entry, replication and

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viral particle assembly processes. In addition, some of the proteins are multi-functional and shown to play modulatory roles in host immune responses.

In this review, we will focus on the interaction between host immune system and PRRSV, and describe the molecular mechanisms used by PRRSV and its proteins to modulate host immune responses and signaling pathways, and discuss the implications that these modulations have on viral pathogenesis and the rational design of protective vaccines.

2. Host immune responses against virus infection

Virus infection results in the activation of pattern recognition receptors (PRRs) by recognizing specific pathogen-associated molecular patterns (PAMPs) to initiate antiviral signaling cascades, triggering the production of cytokines including interferons (IFNs) and chemokines (Kawai and Akira, 2006; Pichlmair and Reis e Sousa, 2007; Tenover and Maniatis, 2006; Yan and Chen, 2012). The induction of critical cytokines is essential for antiviral innate immunity to control virus infection in the early phase and facilitate the adaptive immune system (Hoebe et al., 2004; Kabelitz and Medzhitov, 2007).

Type I interferons are important antiviral cytokines that represent one of the first lines of defense to limit viral replication and spread, thus contributing to the protection of host from infections. The induction of type I IFNs depends on sensors detecting viral nucleic acid, which is generated as genome or intermediates of viral transcription or replication (Akira et al., 2006). Two intracellular PRRs, the retinoic acid inducible gene-1 (RIG-I) and melanoma differentiation associated gene 5 (MDA5), act as sentinels for detecting viral RNA in the cytoplasm (Loo and Gale, 2011; Takeuchi and Akira, 2008). Activated RIG-I and MDA5 recruit virus-induced signaling adaptor (VISA, also known as MAVS, Cardif, and IPS-1) via CARD-CARD (caspase recruitment domain) interaction (Kawai et al., 2005; Seth et al., 2005; Xu et al., 2005). VISA is localized in mitochondria and acts as a bridge to link RIG-I-like RNA helicase (RLH) and the TNF receptor associated factor 3 (TRAF3) complex, which subsequently activates transcriptional factors IRF3 and IRF7 in a TRAF family-member-associated NF- κ B activator (TANK) binding kinase 1 (TBK1)- and IKKi-dependent manner (Akira et al., 2006). VISA also interacts with TRAF2/6 complex, which is required for the activation of NF- κ B (Edwards et al., 2007). Alternative endosome-lysosome PRRs, TLR3 and TLR7 recognize double-stranded RNA and single-stranded RNA, respectively, leading to the dimerization of receptors and recruitment of adaptor TRIF or MyD88 (Diebold et al., 2004; Kawai and Akira, 2010; Oshiumi et al., 2003). The stimulation triggers the assembly of signaling complexes and initiation of signaling cascades, resulting in the activation and nuclear translocation of IRF3/IRF7, NF- κ B, and AP-1 to induce the transcription of type I IFNs (Honda et al., 2006). The crucial effort of type I IFNs on antiviral responses results from the activation of JAK/STAT signaling, leading to the expression of interferon-stimulated genes (ISGs) (Stark and Darnell, 2012; Takaoka and Yanai, 2006). These ISGs are involved in the amplification and regulation of the IFN responses, and interfere with several steps of the viral life cycle (Sadler and Williams, 2008; Schoggins and Rice, 2011; Schoggins et al., 2011).

The activation of PRRs also triggers the inflammatory cytokine and chemokine productions (Takeuchi and Akira, 2010). Recognition of viral molecules by TLRs recruits specific adaptor to the receptors, resulting in the production of proinflammatory cytokines via the TRAF6-TAK1-NF- κ B pathway (Deng et al., 2000; Wang et al., 2001). Simultaneously, TGF- β -activated kinase 1 (TAK1) activates the MAPK (JNK, p38, and ERK) pathway, leading to the activation of AP-1. The adaptor of RIG-I like receptors

(RLRs), VISA, also interacts with the Fas-associated death domain protein (FADD) to induce NF- κ B activation and modulate the transcription of proinflammatory cytokines such as IL-1 β , IL-6 and TNF α (Takahashi et al., 2006). Different from IL-6 and TNF α , the production of secreted IL-1 β requires the cleavage of pro-IL-1 β by a protease, caspase-1, which is activated independent of TLR and RLR signaling. Inflammasome, which is composed of nucleotide oligomerization domain (NOD)-like receptors, apoptosis-associated speck-like protein containing a CARD (ASC) adaptor and caspase-1, induces caspase-1 activation to mediate the maturation of pro-IL-1 β (Rathinam et al., 2012). The secretion of proinflammatory cytokines is responsible for amplifying the innate immune responses to virus infection and shaping the adaptive immune responses to follow.

3. Modulation of immune responses by PRRSV

Epidemiologic studies have revealed that conventional strains of PRRSV often develop a persistent infection after an acute infection lasting for 3–4 weeks (Cho and Dee, 2006; Rossow, 1998; Wills et al., 1997). During persistent infection, viremia is absent and virus replication is restricted in some immune privileged lymphoid tissues (Beyer et al., 2000; Rowland et al., 2003). The persistence of the virus within pigs and herds is often associated with the recurrence of secondary viral and bacterial infections (Albina et al., 1994; Stevenson et al., 1993). This reflects the fact that PRRSV has evolved mechanisms to evade and suppress host immune responses.

3.1. Escape from innate immunity

3.1.1. Suppression of type I IFN induction and signaling

Interferons have various functions in activating innate immune responses against viral infection (Theofilopoulos et al., 2005). In particular, type I IFNs block viral replication and spread by inducing multiple antiviral proteins that interfere with every step of the viral infection. Previous studies have shown that PRRSV is sensitive to interferons, and recombinant porcine IFN β or synthetic double stranded RNAs can inhibit PRRSV replication and protect pigs from PRRSV infection (Albina et al., 1998; Miller et al., 2004; Overend et al., 2007). In order to propagate and spread in hosts, PRRSV has evolved several strategies to antagonize type I IFN responses (see Table 1). These strategies include delaying the PRR detection, interfering with detection and signaling pathways of IFN induction, inhibiting IFN-mediated signaling pathways, and blocking the action of IFN-induced genes with antiviral activity.

3.1.1.1. Delaying the PRR detection. Invading agents are detected by cell membrane or intracellular PRRs. RNA sensors including

Table 1
Antagonism of type I IFN responses by PRRSV.

Viral proteins	Function
nsp1	Inhibits IRF3 phosphorylation and nuclear translocation Mediates CBP degradation Inhibits NF- κ B-responsive promoter activation Induces degradation of karyopherin- α 1 and inhibits nuclear translocation of ISGF3
nsp2	Prevents the polyubiquitination and degradation of I κ B α Suppresses activation of IRF-3
nsp4	Interferes with ISG15 conjugation to cellular proteins Mediates the cleavage of NEMO and suppresses NF- κ B activation
nsp11	Inhibits NF- κ B and IRF3 promoter activation
N	Inhibits poly(I:C)-mediated IRF3 phosphorylation and nuclear translocation

endosome–lysosome TLR3 and TLR7, cytosol RIG-I and MDA5, may play vital roles in recognizing and responding to PRRSV infection. Many viruses such as swine transmissible gastroenteritis virus (TGEV) and Sendai virus (SeV) induce activation of PRR signaling within hours of virus infection (Albina et al., 1998). However, virulent PRRSV strains, especially highly pathogenic strain JXwn06, appear to delay the activation of PRR, which is of benefit to the viral replication within cells during the early stages of infection (Huang et al., 2014). Previous publications have shown that SARS-CoV (also belonging to the order Nidovirales) infection leads to the formation of double membrane vesicles (DMVs) and proteins involved in virus replication (nsp3, nsp5, and nsp8) are located mainly outside of DMVs (Knoops et al., 2008; Perlman and Netland, 2009). These vesicles contribute to viral replication and help hide the viral RNA from cellular recognition and delay the antiviral IFN production. Similarly, in arterivirus life cycle, open reading frame 1a (ORF1a)-encoded subunits of the arterivirus replicase induce endoplasmic reticulum-derived DMVs, which scaffold the viral replication complex (Kroese et al., 2008; Pedersen et al., 1999). These reports suggest that hiding the viral RNA from PRR recognition of nidoviruses delays IFN induction. However, the precise mechanisms by which PRRSV evades PRRs detection need to be determined.

3.1.1.2. Inhibition of IFN production. The production of type I IFNs depends on activation of the transcription factors IRF-3/7, NF- κ B and AP-1 through either TLRs or RLRs pathways. In PRRSV-infected macrophages and PBMCs, IFN α is undetectable when cells are superinfected with TGEV, a known inducer of Type I IFNs (Albina et al., 1998). Moreover, PRRSV has been reported to repress the ability of porcine pDC to mount type I IFN responses to itself as well as to TGEV, and a TLR9 agonist, ODN D19 (Calzada-Nova et al., 2011). Five PRRSV proteins have been identified and characterized as IFN antagonists, including one structural protein (N) and four non-structural proteins (nsp1, nsp2, nsp4 and nsp11).

Nsp1 has been considered as the strongest antagonist to inhibit IFN β production. PRRSV nsp1 can be auto-cleaved into two proteins nsp1 α and nsp1 β , each of which includes a papain-like cysteine protease domain, called PCP α and PCP β , respectively (den Boon et al., 1995; Ziebuhr et al., 2000). Nsp1 α and nsp1 β have been shown to be involved in suppressing IFN β luciferase activity (Chen et al., 2010). IRF3 (Ser 396) phosphorylation and nuclear translocation are inhibited by nsp1 β (Beura et al., 2010). Nsp1 expression also inhibits the activation of NF- κ B-responsive promoter (Song et al., 2010). Furthermore, nsp1 mainly localizes into the cell nucleus after 10 h post-infection (Chen et al., 2010), indicating that the nuclear form may interact with the host factors in the nucleus. Kim et al. have reported that nsp1 inhibits IRF3 association with CREB-binding protein (CBP) in the nucleus and mediates CBP degradation to block the recruitment of CBP for enhanceosome assembly, leading to the inhibition of IFN transcriptional activation. However, CBP degradation is not due to nsp1 PCP activity but rather mediated via the proteasome-dependent degradation pathway (Kim et al., 2010).

Nsp2 is the largest and the most variable non-structural protein in PRRSV, with only ~32% identity between subtypes (Allende et al., 1999). The highly pathogenic PRRSV reported in 2006 outbreaks in China contains two non-contiguous deletions (30 amino acids) in the nsp2 hypervariable region (Li et al., 2007b; Tian et al., 2007), and these deletions serve as genetic markers for differentiation from other conventional PRRSV. Nsp2 is a papain-like protease belonging to the ovarian-tumor domain deubiquitinase superfamily (Frias-Staheli et al., 2007; Makarova et al., 2000). Previous study has shown that nsp2 antagonizes IFN β induction by interfering with the NF- κ B signaling pathway in HEK-293T cells (Sun et al., 2010). The precise mechanism is that the nsp2 OTU domain, which

possesses ubiquitin–deconjugating activity, has the ability to inhibit NF- κ B activation by interfering with the polyubiquitination process of I κ B α , leading to the prevention of I κ B α degradation. Nsp2 also inhibits IFN β production by suppressing the activation of the IRF-3 pathway induced by SeV and the cysteine protease domain (PL2) is required for this function (Li et al., 2010). On the contrary, Fang et al. have found that nsp2 of HP-PRRSV strain WUH3 activates NF- κ B in MARC-145 and HeLa cells through inducing I κ B α degradation and p65 translocation to the nucleus, leading to the expression of IL-6, IL-10 and COX-2. Further studies have demonstrated that 30-aa deletion of HP-PRRSV is not associated with NF- κ B induction, but the hypervariable region (HV) is essential for NF- κ B activation (Fang et al., 2012a). Our results have also revealed that nsp2 of HP-PRRSV strain JXwn06 has no inhibitory effect on IFN β production induced by poly(I:C) in HeLa cells (Huang et al., 2014). The possible explanation for these seemingly opposite results is that nsp2 sequence varies among different strains. However, the effect of nsp2 on host innate immunity needs to be further investigated.

PRRSV nsp4, which belongs to the member of the chymotrypsin-like serine proteases (3CLSP), is a multifunctional protein that participates in polypeptide protein process and viral replication (Fang and Snijder, 2010; Snijder et al., 1996). Nsp4 contains a canonical catalytic triad that is composed of Ser118, His39, and Asp64, and cleaves specific substrate of the 3C-like cysteine proteases, a subgroup of chymotrypsin-like enzymes named after the picornavirus 3C proteases (Tian et al., 2009). Previous studies have revealed that the 3C protease participates in a number of biological processes. For example, it can inhibit host cell polyadenylation by mediating the cleavage of CstF-64, a critical factor for 3' pre-mRNA processing in a cell nucleus (Weng et al., 2009), trigger apoptosis through caspase activation, and suppress type I IFN expression by cleaving key factors of the signaling pathways (Belsham et al., 2000; Lei et al., 2013; Li et al., 2002; Mukherjee et al., 2011). Beura et al. have shown that PRRSV nsp4 inhibits IFN β promoter activity activated by IRF3 overexpression in HeLa cells (Beura et al., 2010). Recently, we have found that nsp4 antagonizes IFN β and NF- κ B activation in HeLa and porcine CRL-2843 cells by inhibiting I κ B α phosphorylation and p65 translocation to the nucleus. The inhibition depends on 3C-like serine protease catalytic activity of nsp4, and site or deletion mutants abolish its inhibitory property. We further show that nsp4 mediates the cleavage of NF- κ B essential modulator (NEMO), a regulatory subunit of IKKs complex, leading to the suppression of NF- κ B activation and IFN β production (Huang et al., 2014). Chen et al. have also found that nsp4 suppresses IFN β transcription by blocking NF- κ B activation, and the amino acid at residue 155 in nsp4 is essential for the effect (Chen et al., 2014). In addition, they show that nsp4 from different pathogenic PRRSV strains has differential ability to inhibit IFN β expression. In agreement with this observation, our results show that nsp4 of HP-PRRSV JXwn06 has greater inhibitory effect on IFN β induction than nsp4 from the less pathogenic PRRSV CH-1a. These data imply that the inhibitory property on IFN β induction by PRRSV nsp4 may be correlated with PRRSV pathogenicity.

Nsp11 contains the nidovirus uridylylate-specific endoribonuclease (NendoU) activity, a genetic marker unique to Nidoviruses (Nedialkova et al., 2009). Nsp11 has been examined for its inhibition role in IFN β production. In MARC-145 cells, nsp11 overexpression inhibits poly(I:C) or IKK ϵ -induced activations of IFN β promoter and IRF3 dependent promoter, and NendoU activity in nsp11 is essential for the suppression (Shi et al., 2011). Beura et al. have found that nsp11 is able to inhibit NF- κ B promoter activation (Beura et al., 2010). These results have also been confirmed by another report (Sun et al., 2014). All of these are in support of the opinion that nsp11 functions in IFN down-regulation. However, the precise mechanisms for nsp11 to interact with host immune responses remain to be further elucidated.

The nucleocapsid (N) protein is a small basic protein with 123 amino acids, and possesses a N-terminal RNA-binding domain and a C-terminal dimerization domain (Yoo et al., 2003). N is the structural component of the viral capsid and participates in nucleocapsid assembly and virus infectivity. Similar to nsp1, N protein is localized in the cytoplasm and the nucleus (Rowland et al., 1999), suggesting that the nuclear translocation of N may have effects on the modulation of host antiviral responses. Supporting this note, the ability of N to circumvent the innate immunity by suppressing type I IFN induction has been verified. N protein suppresses IFN β expression by inhibiting poly(I:C)-mediated IRF3 phosphorylation and nuclear translocation in immortalized porcine alveolar macrophages (Sagong and Lee, 2011). However, whether the nuclear localization of N protein is critical for its ability to modulate the IFN responses by inhibiting IRF3 activation needs to be investigated.

3.1.1.3. Inhibition of IFN responses. The binding of type I IFNs to the IFNAR on the surface of cells that secrete type I IFNs or nearby cells triggers the activation of the JAK/STAT signal pathway, resulting in the expression of a wide variety of interferon-stimulated genes (ISGs) that can establish antiviral and immune-regulatory states in host cells. However, PRRSV is shown to efficiently inhibit the downstream signal transduction of type I IFNs. IFN α -induced ISG15 and ISG56 production is suppressed in PRRSV-infected MARC-145 cells and PAMs. IFN α stimulation increases the expression of STAT2, whereas STAT2 protein in PRRSV-infected cells after IFN α treatment remains at the control level (Patel et al., 2010). PRRSV and its viral protein nsp1 β have the ability to block nuclear translocation of ISGF3 heterotrimers. The mechanism is that the N-terminal domain of nsp1 β induces degradation of karyopherin- α 1 (KPNA1, also known as importin- α 5), which mediates nuclear import of ISGF3 (Wang et al., 2013b). Nsp1 β of different PRRSV strains has variable effect on JAK/STAT signaling pathway. Two PRRSV strains VR-2332 and VR-2385 infections result in KPNA1 reduction, whereas an avirulent strain Ingelvac PRRS MLV does not. However, MLV reduces the level of ISG15 and ISG56 transcripts induced by IFNs in MARC-145 cells, implying that other mechanisms might be responsible for the suppression of IFN signaling. Many viruses are able to inhibit type I IFN signaling by inducing negative regulators of JAK/STAT signaling (Bode et al., 2003; Pauli et al., 2008; Yokota et al., 2004). However, little is known about the effects of PRRSV infection on up-regulation of these negative regulators.

3.1.1.4. Impairing functions of antiviral ISG. PRRSV can target individual downstream ISGs to interfere with host antiviral responses. ISG15, an ubiquitin-like protein, is one of the highly expressed proteins that function as an effector molecule in host cell responses to viral infection (D'Cunha et al., 1996; DCunha et al., 1996; Zhao et al., 2013). ISG15 conjugation (ISGylation) to substrate proteins follows a process similar to that of ubiquitin conjugation by utilizing an ubiquitin-activating enzyme (Ube1L, E1) (Pitha-Rowe et al., 2004), an ubiquitin-conjugating enzyme (UbCH8, E2) (Zhao et al., 2004), and an ubiquitin ligase (HERC5, E3) (Wong et al., 2006). ISG15 and/or ISGylation of cellular proteins play important roles in establishing an antiviral state in infected cells. In MARC-145 cells, overexpression of ISG15 interferes with PRRSV replication. PRRSV infection induces ISG15 expression in a relative short time but returns to a near-baseline level after 24 h post infection and seems to inhibit ISG15 conjugation, suggesting that PRRSV counters the antiviral effect of ISG15 and ISGylation. PRRSV nsp2 protein, which has a PLP2-DUB domain possesses deISGylation activity, is responsible for interfering with ISG15 conjugation to cellular proteins (Sun et al., 2012).

3.1.2. Modulation of other cytokines production

3.1.2.1. Up-regulation of IL-10. Interleukin-10 (IL-10), also known as human cytokine synthesis inhibitory factor (CSIF), is a crucial immuno-regulatory cytokine and can be produced by several cell types, including monocytes/macrophages, dendritic cells (DCs), and T and B cells (Conti et al., 2003; Ouyang et al., 2011; Saraiva and O'Garra, 2010). IL-10 can inhibit the production of numerous inflammatory cytokines and counter adaptive immunity, such as antigen presentation and cell-mediated immune responses (Moore et al., 2001; Sabat et al., 2010). Accumulating evidence has revealed that PRRSV significantly induces IL-10 expression in vivo and vitro (Flores-Mendoza et al., 2008; Suradhat and Thanawongnuwech, 2003; Suradhat et al., 2003; Thanawongnuwech and Thacker, 2003; Wang et al., 2011). Zhou et al. have found that inoculation with recombinant adenoviruses (rAds) expressing nsp1 (rAd-nsp1) increases IL-10 secretion and decreases IFN γ secretion in pigs, implicating that nsp1 induces IL-10 expression in vivo (Zhou et al., 2012). Previous studies have also shown that IL-10 gene expression is up-regulated in MoDCs and PAMs transfected with the plasmid encoding N protein. Furthermore, recombinant N protein induces IL-10 expression and increases the number of IL-10-producing cells in cultured PBMCs and MoDCs (Wongyanin et al., 2012). Our laboratory shows that PRRSV CH-1a strain activates IL-10 production in PAMs, BMDMs, and MDMs at both mRNA and protein levels. We find that PRRSV-stimulated IL-10 production is dependent on p38 MAPK and NF- κ B signaling pathways. By screening PRRSV non-structural and structural proteins, GP5 is identified as an IL-10 inducer. Overexpression of GP5 induces the phosphorylation of p38 (Hou et al., 2012b). These results are also confirmed by another lab at the same time (Song et al., 2013). The authors find that HP-PRRSV strain WUH3 induces IL-10 production at both mRNA and protein levels in PAMs, and the TLR-MyD88-NF- κ B signaling cascade may be required for PRRSV-induced IL-10 expression (Song et al., 2013).

3.1.2.2. Down-regulation of TNF α . Tumor necrosis factor α (TNF α) is a proinflammatory cytokine secreted by a wide variety of cells including macrophages and activated T cells. The pleiotropic function of TNF α is attributed to the promotion of an antiviral state in uninfected neighboring cells, recruitment of lymphocytes to the foci of infection, selective cytolysis of virus-infected cells, and modulation of apoptosis/survival of cells (Natoli et al., 1998; Smith et al., 1994; Toews, 2001). Previous study has revealed that addition of recombinant porcine TNF α to cultures clearly reduces PRRSV replication (Lopez-Fuertes et al., 2000). Therefore, it is unsurprising that PRRSV has evolved anti-TNF strategies.

Increasing evidence has demonstrated the inhibitory effect of PRRSV on TNF α production. In acute phase of PRRSV-infected pigs, TNF α is poorly expressed (Gomez-Laguna et al., 2010). The induction of TNF α by LPS and PMA is significantly suppressed by PRRSV in porcine macrophages (Hou et al., 2012a; Lopez-Fuertes et al., 2000). PRRSV selectively inhibits TNF α expression activated by porcine pDC exposed to TGEV or a TLR9 agonist (Calzada-Nova et al., 2011). It has also been demonstrated that the viral protein nsp1 is involved in the down-regulation of TNF α production. In this work, the authors find that both constitutive subunits (nsp1 α and nsp1 β) of nsp1 inhibit the activation of TNF α promoter by modulating the activities of transcription factors NF- κ B and Sp1, respectively (Subramaniam et al., 2010). Our study also reveals that HP-PRRSV impairs TLR4- and TLR3-stimulated TNF α release through altered ERK regulation. Furthermore, HP-PRRSV strains, HV and JXwn06, are weaker inducers of TNF α production compared to the conventional strain CH-1a, which may partially contribute to the pathogenesis of HP-PRRSV (Hou et al., 2012a).

3.1.3. Modulation of apoptosis

Apoptosis, a process of programmed cell death in multicellular organisms, is a strictly regulated mechanism of cell death that involves a complex network of biochemical pathways (Hotchkiss and Nicholson, 2006; Tait and Green, 2010). The main role of apoptosis is the development and maintenance of homeostasis. Moreover, apoptosis also plays an important role in the pathogenesis of several viral infections (Rudin and Thompson, 1997), and is considered to be a crucial innate defense mechanism that inhibits viral replication and eliminates virus-infected cells (Thomson, 2001). Therefore, many viruses have evolved strategies to prevent or delay apoptosis during replication, ensuring cell survival until sufficient progeny virus is produced (Banadyga et al., 2009; Cai et al., 2011; Shen et al., 2013). PRRSV confers protection to PRRSV-infected PAMs against staurosporine-induced apoptosis, indicating that PRRSV stimulates anti-apoptotic pathways in macrophages at the early stage of infection. PRRSV replication might partially contribute to the inhibition of apoptosis in PRRSV-infected cells, because UV-inactivated virus induces low levels of anti-apoptosis (Costers et al., 2008). Another study shows that activation of JNK signaling pathway is important in apoptosis induction of the host cells in responses to PRRSV infection (Yin et al., 2012). However, at the early stage of PRRSV infection, p53 and Akt are activated as negative regulator of ER-dependent JNK activation, which is in favor of the virus replication (Huo et al., 2013). In cell line MARC-2a stably expressing GP2a, the percentage of apoptotic cells is significantly decreased, suggesting that GP2a protein likely plays a role in apoptotic inhibition exerted by PRRSV (Pujhari et al., 2014).

On the contrary, some viruses induce apoptosis to enhance virus transmission and avoid immune responses (Jan et al., 2000; Medigeshi et al., 2007; Metz et al., 2014). Apoptosis induction in host cells is an important cellular event in the pathogenesis of PRRSV (Suarez, 2000). Apoptosis has been observed in the lungs and thymus of PRRSV-infected pigs (Labarque et al., 2003; Wang et al., 2014). PRRSV also triggers apoptosis in PAMs and MARC-145 cells at the late stage of infection (Costers et al., 2008). A key event in the induction of apoptosis signals is the activation of a family of pro-apoptotic proteases termed caspases (Budihardjo et al., 1999). The data generated by our laboratory show that PRRSV nsp4 is a critical apoptosis inducer and has effect on the activation of caspase-3, -8, and -9 (Ma et al., 2013), which is in agreement with the previous publication that PRRSV infection activates caspase cascades (Costers et al., 2008). The ability of nsp4 to induce apoptosis is significantly impaired by His39, Asp64, and Ser118 mutations in nsp4, revealing that 3C-like protease activity is essential for nsp4 to trigger apoptosis. We also find that apoptosis occurs in both infected and non-infected cells, suggesting that apoptogenic cytokines, such as TNF α , may be induced and involved in this process. Yin et al. have shown that PRRSV infection activates JNK pathway in MARC-145 cells, and PRRSV-induced JNK activation is associated with ROS generation (Huo et al., 2013). Further studies have demonstrated that Bcl-2 family anti-apoptotic proteins Bcl-xl and Mcl-1 are down-regulated by PRRSV, which is dependent on JNK activation (Yin et al., 2012). Furthermore, PRRSV infection also activates IRE1 phosphorylation, one of the arms of the unfolded protein responses (UPR, also known as ER stress responses), which may contribute to JNK-mediated apoptosis (Huo et al., 2013). These studies have shown that JNK signaling pathway might play a vital role in PRRSV-induced apoptosis of host cells.

3.1.4. Escape from immune responses utilizing miRNAs

MicroRNAs (miRNAs) are a class of small non-coding RNA molecules (~21–23 nt) that regulate gene expression post-transcriptionally through degradation of mRNAs or inhibition of translation (Krol et al., 2010). These molecules have emerged as critical gene regulators in complex life, including differentiation,

development, cellular proliferation and death, immune responses and virus infection. Recent studies have provided compelling evidence that multiple miRNAs including miR-146a, miR-155 (Vigorito et al., 2013), miR-21, miR-23b (Zhu et al., 2012), miR-126 (Agudo et al., 2014), miRNA-181a (Ebert et al., 2009; Li et al., 2007a; Xie et al., 2013; Zietara et al., 2013), and miR-17–92 clusters (Jiang et al., 2011; Khan et al., 2013; Wu et al., 2012) are involved in the regulation of innate and adaptive immune response, including the release of inflammatory mediators, the development and activation of B and T cells and the proliferation of monocytes and neutrophils (Contreras and Rao, 2012; David, 2010; Lindsay, 2008; Nahid et al., 2011; O'Neill et al., 2011). Not surprisingly, during viral infection, host miRNAs can affect viral replication by regulating host immune responses to generate a less permissive environment for viral replications. In the case of miR-155, it is induced during viral infection and inhibits virus infection by positively regulating innate immune responses (Su et al., 2011). For example, during VSV infection, miR-155 is induced to inhibit VSV infection by enhancing type I interferon responses via targeting suppressor of cytokine signaling 1 (SOCS1) (Wang et al., 2010). Similarly, miR-155 induced by Japanese encephalitis virus (JEV) infection in microglial cells suppresses JEV replication through positively modulating innate immune responses by targeting SH2-domain-containing inositol-5-phosphatase 1 (SHIP1) (Pareek et al., 2014; Thounaojam et al., 2014). In addition, as a critical modulator of CD8⁺ T cell responses, miR-155 is induced in CD8⁺ T cells in responses to lymphocytic choriomeningitis virus (LCMV) infection and is critical for the antiviral CD8⁺ T cell responses to acute and chronic LCMV infection (Dudda et al., 2013).

On the other side, many viruses have evolved to induce miRNAs, which act as negative regulators of immune responses to facilitate viral infection. Different from miR-155, miR-146a is reported to facilitate virus replication by dampening interferon induction by targeting TNFR-associated factor 6 (TRAF6) and IL-1R-associated kinase 1 (IRAK1). A previous report has shown that Enterovirus 71 (EV71)-induced miR-146a facilitates viral infection and pathogenesis by suppressing IFN production (Ho et al., 2014). Similar to miR-146a, miR-21 is demonstrated to be induced by HCV and contributes to evasion of host immune system by targeting MyD88 and IRAK1. It's worth noting that virus-derived miRNAs actively participate in evasion of immune responses to facilitate viral replication (Cullen, 2013; Skalsky and Cullen, 2010). For example, a human herpesvirus miRNA attenuates interferon signaling and help maintain viral latency by targeting IKK ϵ (Liang et al., 2011). Another example is the human torque teno virus (TTV), which encodes a microRNA (TTV-tth8-miR-T1) that inhibits interferon signaling by targeting N-myc and STAT interactor (NMI), a positive modulator of STAT signaling pathways (Kincaid et al., 2013).

During PRRSV infection, many miRNAs are found to be altered, suggesting that miRNAs might be involved in PRRSV infection (Hicks et al., 2013). Although little is known about the exact role of miRNAs in PRRSV pathogenesis, two recent studies may give some hints. miR-125b is found to reduce PRRSV replication by decreasing NF- κ B expression through stabilizing κ B-RAS2, which serves as a negative regulator of NF- κ B. Moreover, miR-125b is down-regulated by PRRSV infection and this may be a strategy for PRRSV to evade host immune responses by inhibiting the NF- κ B signaling pathway (Wang et al., 2013a). In our recently published paper, we demonstrate that miR-23, a miRNA induced by poly(I:C), can suppress PRRSV replication by promoting the expression of type I IFNs. PRRSV infection suppresses the expression of poly(I:C)-induced miR-23, implying that this antagonism might be a strategy used by PRRSV to evade the miRNA-mediated immune responses induced in TLR3 pathway (Zhang et al., 2014). Notably, during PRRSV infection, the well-characterized immune-modulator miR-146a is up-regulated. Since miR-146a is a negative regulator of immune

responses, it is likely that the up-regulation of miR-146a might facilitate viral infection by suppressing IFN production. Moreover, as type I IFN production and signaling is severely crippled during PRRSV infection, it is important to investigate whether any of the miRNAs is involved in the evasion of host immune responses by regulating the production or signaling of IFNs. And this clarification might help us understand the pathogenesis of PRRSV.

3.2. Escape from adaptive immunity

3.2.1. Impairing antigen presentation

Dendritic cells (DCs), the most potent of the prominent antigen presenting cells (APCs), play important roles in the generation of T-cell responses and the maintenance of immune responses (Banchereau and Steinman, 1998; Steinman, 2012). Upon PRRSV infection, these cells are activated and undergo maturation, and then migrate to the lung-draining lymph nodes where they present viral epitopes to naïve T cells (Freigang et al., 2005). This process results in proliferation and differentiation of naïve T cells into effector cells, triggering adaptive immune responses. To impair immune responses, PRRSV have evolved defense mechanisms to inhibit the antigen presentation function of DCs. The reduced expression of MHC class I and II molecules are observed in PRRSV-infected monocyte-derived dendritic cells (Mo-DCs) (Wang et al., 2007) and bone marrow-derived dendritic cells (BM-DCs) (Chang et al., 2008; Peng et al., 2009; Weesendorp et al., 2013). The expression of co-stimulatory molecule CD80/86 varies possibly because of using different strains. Another strategy used by PRRSV to counter DCs function is the induction of cell death via both apoptosis and necrosis mechanisms (Rodriguez-Gomez et al., 2013). The down-regulation of the cell surface molecules and cell death of DCs lead to a failure in the onset of an efficient adaptive immunity. T cell responses are reported to appear at 4–8 weeks and CD4⁺- and CD8⁺-T cells remain low and constant after infection, indicating that cell-mediated immunity (CMI) is transient and delayed in PRRSV infection (Bautista and Molitor, 1997; Feng et al., 2002; Lopez Fuertes et al., 1999; Xiao et al., 2004).

3.2.2. Activation of immunosuppressive regulatory T cells

Immunosuppressive regulatory T cells (Tregs) are responsible for balancing the immune responses and maintaining immune homeostasis by controlling or inhibiting the functions of immunocompetent effector cells. Tregs are divided into natural and inducible Tregs, which are developed in the thymus or generated in the periphery from naïve CD4⁺ T cells, respectively (Belkaid, 2007; Miyara and Sakaguchi, 2007). Based on the cytokines they produce, inducible Tregs can be classified into three subsets that are described in humans and mice, including Treg 1 cells (Tr1) which secrete IL-10, T helper 3 cells (Th3) which secrete TGF- β , and CD8⁺ Tregs (Belkaid, 2007; Shevach, 2006). In pigs, two main Tregs are identified and described as CD4⁺CD8⁻CD25⁺Foxp3⁺ and CD4⁺CD8⁺CD25⁺Foxp3⁺ (Kaser et al., 2008).

Tregs are commonly recognized as a key contributor in regulating the magnitude of the host immune responses to viral infection, thus protect against excessive inflammation and tissue damage. However, many viruses including human immunodeficiency virus (HIV), Epstein-Barr virus (EBV), and hepatitis C virus (HCV) induce proliferation and activation of Tregs to escape the immune responses and establish persistent infection (Kinter et al., 2004; Smyk-Pearson et al., 2008; Vahlenkamp et al., 2005; Voo et al., 2005). In recent years, several studies have also revealed that PRRSV activates Tregs both in vitro and in vivo (Cecere et al., 2012; LeRoith et al., 2011; Manickam et al., 2013; Wongyanin et al., 2010). Silva-Campa and colleagues have shown that Tregs are induced by PRRSV-infected DCs, which is dependent on the production of TGF β (Silva-Campa et al., 2009). Subsequently, they have identified

that PRRSV infection induces the proliferation of Tregs with the phenotype CD4⁺CD8⁺CD25⁺Foxp3^{high} (Silva-Campa et al., 2012). This team has also demonstrated that American genotype PRRSV strains are able to induce Tregs and up-regulate TGF β expression, but neither TGF β nor Tregs are induced by European genotype PRRSV (Silva-Campa et al., 2010). Furthermore, up-regulation of IL-10 gene expression and induction of Tregs have been observed when using N protein-pulsed porcine Mo-DCs, indicating that N protein might play a significant role in the induction of IL-10 and Tregs (Wongyanin et al., 2012). The ability of PRRSV to induce Tregs likely contributes to the persistence in host and may be in favor of secondary infection.

3.2.3. Antibody-dependent enhancement (ADE)

The humoral immune responses to PRRSV have been studied. In PRRSV-infected pigs, specific IgM antibodies are detectable in serum by day 5–7 post-infection (PI), and reach a peak at day 14 PI and then decline (Yoon et al., 1995). Concentrations of IgG antibodies reach a peak at 21–49 days PI (Loemba et al., 1996; Vezina et al., 1996). At the early stage of infection, these antibodies are directed against N, M, GP5 and nsp2 proteins (de Lima et al., 2006). However, these rapid antibody responses do not correspond to neutralizing antibodies (NAs). NAs appear by 4 weeks PI or later and are mainly directed against GP5 protein, which contains the major neutralizing epitopes located in the N-terminal ectodomain of GP5 (Ostrowski et al., 2002; Plagemann, 2004; Yoon et al., 1994). NAs play an important role in the protection against PRRSV infection, but maintain at low levels (Lopez and Osorio, 2004). The inefficient humoral immune responses cannot eliminate virus from host.

Besides the common CD163 receptor-dependent mechanism of cellular attachment (Welch and Calvert, 2010), PRRSV relies on antiviral antibodies for its entry into host cells, such as macrophages and monocytes (Yoon et al., 1996). This phenomenon is known as antibody-dependent enhancement (ADE). Previous studies have shown that the yield of progeny PRRSV significantly increases in PAMs in the presence of diluted anti-PRRSV antisera, and viremia is much severer in pigs injected with sub-neutralizing antibodies before virus infection than that in animals injected with normal IgG, indicating that ADE facilitates the entry of PRRSV into target cells through Fc receptor-mediated endocytosis (Halstead et al., 2010; Mateu and Diaz, 2008). Qiao et al. have found that the enhancement of PRRSV infection is inhibited by anti-porcine Fc γ RII antibody when MARC-poFc γ RII cells and PAMs are infected in the presence of anti-PRRSV antibody (Qiao et al., 2011). This result suggests that poFc γ RIIb, an inhibitory Fc γ R, mediates ADE of PRRSV infection.

In addition, ADE also interferes with innate signaling responses. Previous study has indicated that pretreatment with Fc γ RIIb-specific IgG up-regulates the transcriptional levels of IFN α and TNF α , but down-regulates IL-10 in PRRSV-infected PAMs (Zhang et al., 2012). The expression of TNF α and IFN β is suppressed in the presence of anti-PRRSV antibodies. Moreover, qPCR analysis shows that mRNA levels of transcriptional factors, NF- κ B, IRF1 and IRF3 are greatly inhibited in PRRSV-Ab-infected macrophages (Bao et al., 2013). Thus, these results demonstrate that ADE signaling alters innate antiviral responses by modulating the expression of key antiviral factors.

4. Implications for vaccine development

Both killed and modified live PRRS vaccines have been developed soon after PRRS outbreak. PRRS killed virus vaccine is safe but induces poor immune responses and has poor protection against either homologous or heterologous PRRSV (Charemtantanakul, 2012). On the other hand, commercial PRRS modified-live virus

(MLV) vaccine has been widely used and shown some efficacy in reducing viremia and virus shedding (Murtaugh et al., 2002). However, MLV elicits delayed humoral and cell-mediated immunity and has only partial protective efficacy against genetically heterologous PRRSV strains (Charerntantanakul, 2012). Thus, development of effective PRRSV vaccine must consider and conquer the high genetic and antigenic variability of PRRSV and its ability to manipulate the host immune system.

MLVs can be developed by deletion and transformation of the key virulence factors using reverse genetics techniques. Genetic manipulations of influenza viruses that express truncated forms of the NS1 protein, a strong inhibitor of type I IFNs (Hale et al., 2010), are shown to be defective in suppressing IFN responses and induce reduction of replication in animal models (Richt and Garcia-Sastre, 2009). The recombinant mouse hepatitis virus (MHV) lacking nsp1 gene induces robust type I IFN and is strongly attenuated in mice (Zust et al., 2007). As outlined above, PRRSV has evolved a number of strategies to modulate host immune responses, especially antiviral type I IFNs. Several PRRSV proteins (nsp1, nsp2, nsp4, nsp11 and N) are involved in inhibiting type I IFN responses. Previous study reveals that MLV nsp1 β has no effect on mediation of KPNA1 degradation, and does not inhibit IFN-mediated signaling, which is in contrast with VR2332 nsp1 β because of the difference in amino acids (Wang et al., 2013b). Thus, recombinant PRRSV that changes the immune-regulatory function of these proteins to restore IFN responses may provide a strategy for the development of PRRSV vaccines.

PRRSV has the ability to impair antigen presentation function of APCs. APC-target strategies can be used to strengthen the efficacy of vaccines against PRRSV. Fusion of antigens with cytotoxic-T-lymphocyte-associated protein 4 (CTLA4) enhances immune responses to a model DNA vaccine, because CTLA4 binds to APCs (Boyle et al., 1998). In our study, we construct a fusion expression plasmid expressing CTLA4 and PRRSV GP5, which contains T-cell epitopes and induces neutralizing antibodies. Mice immunized with the fusion expression plasmids show more production of neutralizing antibodies (NAs), IFN γ , IL-4, and the lymphocyte proliferation activity than mice immunized with GP5 expression plasmid, indicating that CTLA4 fused with GP5 can enhance GP5 immunogenicity (Wang et al., 2013c).

For RNA virus, antigenic variability and rapid replication are also effective ways to evade host immune responses. To attenuate virus replication, de-optimization of codon pair bias is a valid strategy (Coleman et al., 2008; Mueller et al., 2010). Ni et al. have attenuated PRRSV by codon-pair deoptimized GP5 gene using synthetic attenuated virus engineering (SAVE) (Ni et al., 2014). In our recent study, nsp2 and nsp9 genes of HP-PRRSV have been codon-pair deoptimized and the recombinants HP-PRRSV HV-nsp9^{min} and HV-nsp29^{min} are rescued (unpublished data). These recombinant viruses are remarkably attenuated in PAMs and in vivo. Furthermore, vaccination with HV-nsp29^{min} has ability to protect pigs from lethal challenge with wild-type HP-PRRSV isolates. Our results suggest that the codon pair bias de-optimized HV-nsp29^{min} has the potential to be used as a live vaccine candidate against HP-PRRSV.

5. Conclusion

Strategies of immune evasion and modulation used by PRRSV affect both innate and adaptive immune responses. In infected cells, PRRSV sequesters itself to limit PRRs detection, suppresses type I IFN production and signaling, manipulates the cytokine responses and modulates apoptosis. PRRSV structural protein (N) and nonstructural proteins (nsp1, nsp2, nsp4 and nsp11) play significant roles in attenuating signaling through the IFN induction and JAK/STAT pathway. In addition, PRRSV evolves mechanisms to

inhibit the process of antigen presentation and induce proliferation and activation of Tregs, causing deficiency of subsequent adaptive immune responses. The effect of ADE also facilitates the entry and propagation of PRRSV. Even though the fact that PRRSV and its viral proteins interfere with host immune responses has been described, the exact molecular mechanisms and structural bases for the antagonism between viral components and host key factors are still unclear and require extensive investigations. These insights will help us understand the PRRSV pathogenesis and develop more effective and broadly protective vaccines.

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