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### Virology

journal homepage: www.elsevier.com/locate/yviro

# Nuclear export signal of PRRSV NSP1 $\alpha$ is necessary for type I IFN inhibition

Zhi Chen<sup>a</sup>, Shaoning Liu<sup>a,b</sup>, Wenbo Sun<sup>a</sup>, Lei Chen<sup>a</sup>, Dongwan Yoo<sup>c</sup>, Feng Li<sup>d</sup>, Sufang Ren<sup>a</sup>, Lihui Guo<sup>a</sup>, Xiaoyan Cong<sup>a</sup>, Jun Li<sup>a</sup>, Shun Zhou<sup>e</sup>, Jiaqiang Wu<sup>a,\*</sup>, Yijun Du<sup>a,\*</sup>, Jinbao Wang<sup>a,\*</sup>

<sup>a</sup> Shandong Key Laboratory of Animal Disease Control and Breeding, Institute of Animal Science and Veterinary Medicine, Shandong Academy of Agricultural Sciences, Sangyuan Road No. 8, Jinan 250100, China

<sup>b</sup> Shandong Institute of Veterinary Drug Quality Inspection, Shandong Key Laboratory for Quality Safety Monitoring and Risk Assessment of Animal Products, Huaicun Street No. 68, Jinan 250722, Shandong Province, China

<sup>c</sup> Department of Pathobiology, University of Illinois at Urbana-Champaign, 2001 South Lincoln Ave, Urbana, IL 61802, USA

<sup>d</sup> Department of Biology and Microbiology, Department of Veterinary and Biomedical Sciences, South Dakota State University, Brookings, SD 57007, USA

<sup>e</sup> College of marine science and engineering, Qingdao Agricultural University, Changcheng Road No. 700, Qingdao 266109, China

#### ARTICLE INFO

Article history: Received 16 March 2016 Returned to author for revisions 4 July 2016 Accepted 6 July 2016

Keywords: PRRSV NSP1α Type I IFN Nuclear export signal (NES)

#### ABSTRACT

The nonstructural protein  $1\alpha$  (NSP1 $\alpha$ ) of porcine reproductive and respiratory syndrome virus (PRRSV) is a nucleo-cytoplasmic protein that suppresses the production of type I interferon (IFN). In this study, we investigated the relationship between the subcellular distribution of NSP1 $\alpha$  and its inhibition of type I IFN. NSP1 $\alpha$  was found to contain the classical nuclear export signal (NES) and NSP1 $\alpha$  nuclear export was CRM-1-mediated. NSP1 $\alpha$  was shuttling between the nucleus and cytoplasm. We also showed that the nuclear export of NSP1 $\alpha$  was necessary for its ability for type I IFN inhibition. NSP1 $\alpha$  was also found to interact with CBP, which implies a possible mechanism of CBP degradation by NSP1 $\alpha$ . Taken together, our results describe a novel mechanism of PRRSV NSP1 $\alpha$  for type I IFN inhibition and suppression of the host innate antiviral response.

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#### 1. Introduction

Porcine reproductive and respiratory syndrome (PRRS) is an emerging and re-emerging swine disease that severely affects swine populations worldwide. The etiological agent is the PRRS virus (PRRSV), a member of the family *Arteriviridae* in the order *Nidovirales* (http://www.ictvonline.org/virusTaxonomy.asp). PRRSV possesses a single-stranded and positive-sense RNA genome of 15 kb in length, which includes at least 10 ORFs; namely, ORF1a, ORF1b, ORF2a, ORF2b, and ORFs 3–7, and ORF5a (Dokland, 2010; Fang and Snijder, 2010; Johnson et al., 2011; Ozato et al., 2008). ORF1a and ORF1b are comprised of 75% of the total genome and code for two polyproteins, pp1a and pp1b, which are proteolytically cleaved into 14 non-structural proteins (NSPs) by papain-like cysteine protease (PLP)  $\alpha$  in NSP1 $\alpha$ , PLP $\beta$  in NSP1 $\beta$ , poliovirus 3C-like cysteine protease (PLP2) in NSP2, and serine protease (SP) in NSP4. The remaining ORFs code for 8 structural proteins, namely, glycoprotein 2

\* Corresponding authors.

*E-mail addresses*: wujiaqiang2000@sina.com (J. Wu), duyijun0916@163.com (Y. Du), wangjb@saas.ac.cn (J. Wang).

http://dx.doi.org/10.1016/j.virol.2016.07.008 0042-6822/© 2016 Published by Elsevier Inc. (GP2), small envelope protein (E), GP3, GP4, GP5, GP5a, membrane (M) and nucleocapsid (N) proteins (Dokland, 2010; Johnson et al., 2011; Meulenberg, 2000; Ozato et al., 2008).

Virus infection of host cells leads to initiation of antiviral innate immune responses, which lead to expression of type I IFNs and pro-inflammatory cytokines. Type I IFNs (IFN- $\alpha/\beta$ ) are considered as key components of the innate immunity and provide the first barrier of defense against virus infections (Gale and Sen, 2009). During infection, viral pathogen-associated molecular patterns (PAMPs), mostly viral nucleic acids, are initially recognized by host pattern-recognition receptors (PRRs); subsequently, signaling pathways are activated, which lead to transcription of IFNs (Luo et al., 2008; Patel et al., 2010). Viruses have evolved strategies to inhibit aspects of PRRs-mediated signaling to evade the host antiviral mechanism. PRRSV is a weak inducer of IFNs in vitro and in vivo. IFNs are poorly expressed in PRRSV-infected MARC-145 cells and porcine alveolar macrophages (PAMs), which are the primary target cells of the virus (Miller et al., 2004; Sagong and Lee, 2011). Moreover, IFNs are negligible in the lungs of pigs, where PPRSV actively replicates in vivo (Gomez-Laguna et al., 2010). The molecular mechanism of PRRSV to inhibit type I IFN production has been studied; at least six viral proteins (NSP1 $\alpha$ ,





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NSP1 $\beta$ , NSP2, NSP4, NSP11, and N protein) were identified to possess an inhibitory effect on type I IFN production (Beura et al., 2010; Chen et al., 2014; Sagong and Lee, 2011).

As the first protein synthesized during infection, NSP1 $\alpha$  is generated through self-cleavage at Met180-Ala181 and plays important roles throughout the course of PRRSV replication. In addition to its function as an indispensable factor for genome replication and protease in replication, NSP1 $\alpha$  functions as an IFN antagonist; which blocks NF- $\kappa$ B activation via suppression of I $\kappa$ B phosphorylation (Song et al., 2010) and inhibits type I interferon transcription by degrading CREB-binding protein (CBP) (Han et al., 2013, 2014). Further analysis showed the nuclear localization of NSP1 $\alpha$  was related to its IFN-suppressive activity (Han et al., 2014).

In this study, the nucleo-cytoplasmic shuttling scheme of NSP1 $\alpha$  and its relationship to IFN inhibition were determined. The results revealed the shuttling scheme of NSP1 $\alpha$  and the importance of the nuclear export of NSP1 $\alpha$  for inhibition of its type I IFN.

#### 2. Materials and methods

#### 2.1. Cells, viruses, and chemicals

MARC-145 cells were grown in Dulbecco's modified Eagle's medium (DMEM) supplemented with 10% fetal bovine serum (HyClone, Logan, UT, USA), 2 mM L-glutamine, 100 U penicillin/ml and 100  $\mu$ g streptomycin/ml in a humidified incubator with 5% CO<sub>2</sub> at 37 °C. The PRRSV SD-JN strain was used to clone NSP1 $\alpha$  (Wu et al., 2009). MG132, leptomycin B (LMB), and cyclohexamide (CHX) were purchased from Beyotime (Jiangsu, China).

#### 2.2. Plasmids

The pGL3-promoter and pRL-TK were purchased from Promega (Madison, WI, USA). The pIFN- $\beta$ -luc plasmid was constructed by cloning – 281 to + 19 region of the IFN- $\beta$  promoter into the pGL3-promoter vector as described previously (Beura et al., 2010; Chen et al., 2014). The pEGFP-N1 and pCMV-HA were purchased from Clontech (Palo Alto, CA, USA). The NSP1 $\alpha$  gene of the PRRSV SD-JN strain (Wu et al., 2009) was amplified by RT-PCR and cloned in the mammalian expression vector pEGFP-N1 (Clontech) downstream of the green fluorescent protein (GFP) and named NSP1 $\alpha$ -GFP; or cloned in the pCMV-HA vector (Clontech) fused with the N-terminal HA-tag, and named HA-NSP1 $\alpha$  (Table 1). Plasmids with NES mutation or deletion from NSP1 $\alpha$ -GFP or HA-NSP1 $\alpha$  were

#### Table 1

Primers used in the study.

constructed by replacing eight leucine residues in NES (LSARSLLPLNLQVPELGVLGL) with alanine or deleting NES using the Fast Mutagenesis system according to the manufacturer's instructions (Trans, China). Primers used in cloning and mutations are listed in Table 1. The nuclear localization sequence (PKKKRKV) of SV40 large T antigen (Kalderon et al., 1984) was cloned into the mammalian expression vector pEGFP-N1 to obtain plasmid NLS-GFP. The NES sequence of the NSP1 $\alpha$  or MEK1 protein (Jaaro et al., 1997) was then inserted into the NLS-GFP plasmid (Figs. 1C and 2A). All constructs were sequenced to confirm the correct in-frame insertion of individual genes.

#### 2.3. Transfection and luciferase reporter assay

MARC-145 cells were seeded in 12-well plates and grown to 70–80% confluency. The cells were transfected with 250 ng of the plFN- $\beta$ -luc luciferase reporter plasmid, 2.5 ng of pRL-TK, and 250 ng of NSP1 $\alpha$ -GFP by using Lipofectamine<sup>TM</sup> 3000 according to the manufacturer's instructions (Invitrogen, Carlsbad, CA, USA). An empty vector was added to the transfection mixture to keep the total DNA amount constant. At 24 h post-transfection, the cells were transfected with 1 µg poly (I:C) (Sigma-Aldrich, St. Louis, MO, USA). After 12 h, luciferase assay was performed using a dual luciferase assay system (Promega). Inhibition of transcriptional efficiency was evaluated as relative luciferase activity, which was calculated by normalizing Firefly luciferase to *Renilla* luciferase activities according to the manufacturer's instructions. All assays were repeated at least three times, with each experiment performed in triple.

#### 2.4. Co-immunoprecipitation (Co-IP) assay

To determine the interaction between CRM-1 (karyopherin chromosome region maintenance-1) and NSP1 $\alpha$ , MARC-145 cells grown in a 10-cm dish were transfected with 5 µg HA-NSP1 $\alpha$  for 2 days. After LMB treatment for 10 h, the cells were washed twice with PBS and collected. The cells were then resuspended in lysis buffer [50 mM Tris (pH 7.4) containing 150 mM NaCl, 1% NP-40, 0.25% sodium deoxycholate and complete protease inhibitor (Roche, Rotkreuz, Switzerland)]. The cell lysates were clarified by centrifugation at 12,000g for 10 min at 4 °C. The supernatant was subjected to Co-IP experiments using HA-Tag IP/Co-IP kit (Thermo Scientific, Waltham, MA, USA) according to the manufacturer's instructions. After two washes with TBST [25 mM Tris (pH7.2) containing 150 mM NaCl and 0.05% Tween-20], Sepharose beads were incubated with cell lysis for 2 h at 4 °C, and washed with

Primer name	Sequence (5' – 3')	Purpose
HA-NSP1α-F	CG <u>GAATTC</u> CCATGTCTGGGATACTTGATCG ( <i>Eco</i> RI)	HA-Nsp1α plamid clone
HA-NSP1α-R	GGA <u>AGATCT</u> TCACATAGCACACTCAAAAGGGC (BgIII)	
NSP1α-GFP-F	TTT <u>GAATTC</u> CCATGTCTGGGATACTTGATCGGTGCACGT ( <i>Eco</i> RI)	NSP1α-GFP plasmid clone
NSP1α-GFP-R	GGG <u>GGATCC</u> CGCATAGCACACTCAAAAGGGCAAAAGTC (BamHI)	
MT-NSP1α-F	CCT <u>GC</u> GAAT <u>GC</u> CCAAGTTCCTGAG <u>GC</u> TGGGGTG <u>GC</u> GGGT <u>GC</u> ATTTTATAGGCCCGAAGA	Leu to Ala mutation in HA-NSP1 $\alpha$ and NSP1 $\alpha$ -GFP
MT-NSP1α-R	GGAACTTGG <u>GC</u> ATTC <u>GC</u> AGGA <u>GC</u> GG <u>C</u> AGACCGTGCACTGgcACATCGTGTGCAGTAGAC	
DT-NSP1α-F	TGCACACGATGTTTTTATAGGCCCGAAGAGCCA	NES of NSP1 $\alpha$ deletion in HA-NSP1 $\alpha$ and NSP1 $\alpha$ -GFP
DT-NSP1α-R	GGGCCTATAAAAACATCGTGTGCAGTAGACCT	
NLS-GFP-F	AAAAAGAAGAAAAGGTAGATCTCGAGCTCAAGCTT	NLS of SV40 Large T antigen insertion
NLS-GFP-R	CTTTCTCTTCTTTTTGGTGAGTCCGGTAGCGCTAG	
NLES-F	<b>GAAGCTGGAGGAGCTAGAGCTTGATGAG</b> CGAATTCTGCAGTCGACGGTACCGCGGGGCCCGGGATCC	NES of MEK1 insertion to NLS-GFP
NLES-R	CTAGCTCCTCCAGCTTCTTCTGCAAGGCCCATAAGCTTGAGCTCGAGATCTACCTTTCTCTTTTTTTG	
NES of NSP1α-F	CTCCAAGTTCCTGAGCTTGGGGTGCTGGGTCTACGAATTCTGCAGTCGACG	NES of NSP1α insertion to NLS-GFP
NES of NSP1α-R	GCTCAGGAACTTGGAGATTCAGAGGAAGGAGAGAGACCGTGCACTGAGAAGCTTGAGCTCGAGATC	

Restriction endonuclease sites were underlined in italics. The NLS of SV40 large T antigen, NES of MEK1, or NES of NSP1 $\alpha$  were both in italics and boldface. The mutated sites were underlined in boldface.

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