

Review of Different Strategies for Preventing and Controlling Classical Swine Fever

Dong, X.Y.,^{1,2} Zhao, M.Q.,¹ Tang, S.Q.,² Wang, J.Y.,¹ Pei, J.J.,¹ Liu, W.J.,¹ Ju, C.M.,¹ Luo, Y.W.,¹ and Chen, J.D.^{1,*}

¹ College of Veterinary Medicine, South China Agricultural University, Guangzhou 510642, China.

² College of Yingdong Agricultural Science and Engineering, Shaoguan University, Shaoguan 512005, China.

*Corresponding author: Dr. Jin-Ding Chen, Tel.: +86-20-8528 8017; Fax: +86-20-8528 0244. E-mail address: jdchen@scau.edu.cn.

ABSTRACT

Classical Swine Fever (CSF) caused by CSF virus (CSFV) which is single-stranded-RNA Pestivirus, belonging to the family Flaviviridae, leads to severe economic losses in the pig industry especially in developing countries. Many researchers have been involved in research in order to find better and strategies to control its outbreaks. Although prophylactic vaccination is banned within the European Union, emergency vaccination, allowing differentiation of vaccinated from infected animals, is still a key component of CSF control. Lessons learned from CSF epidemiology will expand our understanding of the ways in which virus co-opt host cells during the course of infection and help find approaches to control the disease. This review integrates research findings in CSF epidemiology and explores different strategies to prevent and control CSF.

Key words: Classical Swine Fever, CSFV, epidemiology, vaccination, control

INTRODUCTION

Classical Swine Fever (CSF), also called Hog Cholera or European Swine Fever, is one of the most important infectious diseases of pigs and wild boar, causing significant economic losses to the pig industry all over the world (1). Although eradicated from most European Union (EU) member states, CSF continues to cause serious problems in different parts of the world, including South-Eastern European countries (2, 3) and Asian countries (4, 5). Studies conducted over the past several decades have improved our knowledge of the mechanisms of CSFV translation and replication. New methodologies have facilitated advances in our understanding of the RNA elements and viral and host factors that modulate CSFV replication and translation. In recent years, with the development of molecular techniques, diagnosis of CSF has become more rapid and accurate, however the control of CSF is still in question due to many complex factors in Asia and several countries of Central and South America.

Antiviral drug (6), small interfering RNA (siRNA) (7), vaccination against CSF using inactivated or attenuated live virus vaccines (8) and marker vaccines (9) have been used to prevent CSF outbreaks or chronic infection in domestic pigs in these countries. CSF is a disease whose accurate diagnosis is difficult when based solely on clinical evidence. Thus, there is a growing demand for strategies that can provide timely clinical treatment and epidemiological control.

MOLECULAR EPIDEMIOLOGY OF CSF

Genetic typing of CSFV

Genetic typing of CSFV genotypes, subgroups and types shows a regional distribution and has proven to be a useful method for supporting epidemiological investigations. This information helps researchers to trace the origin of the virus and to follow the viral spread. Phylogenetic analysis of CSFV strains and isolates originating from different continents has

proved that CSFV can be divided into three groups with three or four subgroups: 1.1, 1.2, 1.3; 2.1, 2.2, 2.3; 3.1, 3.2, 3.3, 3.4; based on the partial sequences of the E2 and NS5B genes (10). Furthermore, different genotypes of CSFV are still spreading gradually and evolving worldwide.

Epidemics of CSFV

Molecular epidemiology based on nucleotide sequence diversity is a useful tool for tracing virus spread and for developing disease control strategies. For instance, epidemiological data from field investigations combined with genetic typing identified seven unrelated epidemics and a number of sporadic outbreaks in domestic pigs and in the wild boar population in Germany (11). Although not present in the United States, CSF is distributed worldwide. Several studies covering the molecular epidemiology of CSFV have been performed, including analysis of isolates from Asia, Europe and South America.

Europe

Several epidemics have occurred in the EU over the past decade. The phylogenetic tree shows that the Russian CSF virus isolates from outbreaks that occurred between 1994 and 1999 were all in subgroup 1.1 (12). Viruses of subgroup 2.1 only sporadically occurred in the EU in 1989, 1993, 1997, and 2000. The virus that occurred in 1993 in Austria was detected in wild boar meat illegally imported from China (13). The virus of The Netherlands in early 1997 was most probably newly introduced into the EU, as it belonged to subgroup 2.1 (14), which then spread from The Netherlands to Belgium in June 1997, starting a smaller epidemic (15). In 2000, CSFV was introduced into the United Kingdom. Genetic typing showed that the East Anglian CSFV also belonged to subgroup 2.1 (16).

In Germany, 424 outbreaks of CSF in domestic pigs and a great number of cases in wild boar were recorded between 1990 and 1998. Genetic typing of isolates from these outbreaks using the 5'NTR (150 nt) revealed the existence of seven regional groups of CSFV isolates within subgroup 2.1, 2.2, and 2.3 (17). A CSFV of subgroup 2.2 was responsible for CSF cases in wild boar in Switzerland (18), which also caused outbreaks in Austria (19). In Italy, viruses of subgroup 2.2 was occurred d between 1985 and 2000 in the wild boar population (20, 21) and sporadically caused outbreaks in domestic pigs (22). CSF viruses of genotype 2.3

were endemic in domestic pigs as well as in a unique wild swine population (23), most probably due to widely diffused Sardinian tradition of "free pig" farming, where reared pigs are allowed occasional contact with wild boars. As a result of large quantities of pig and wild boar meat imported in some parts of Italy (24) local strain was introduced into mainland Italy. The epidemics in 1988, 1990 and between 1993 and 1994 in Belgium were studied. Apart from one CSF virus isolate from 1988 which belonged to subgroup 1.1, the isolates formed a discrete cluster within subgroup 2.3 (25). The possibility of a long-term persistence of genotype 2.3 CSFV strains existing at an almost undetectable level in affected regions, even after long-term oral vaccination campaigns with intensive monitoring is a possibility. Hence, regional persistence in German wild boar populations has to be taken into account as an important factor in the continual outbreaks in affected areas (26). Molecular epidemiology of 97 CSF virus isolates available from these countries, from outbreaks that occurred between 1994 and 2007, was performed. The findings suggested that most of the isolates were from Romania and Bulgaria, and belonged to genotype 2.3 (27). The viruses isolated in the outbreak in Spain were 100 percent homologous and belonged to subgroup 2.3 (28). In Poland, Slovakia, Hungary, Estonia (29) and the Czech Republic (19), virus isolates also belonged to subgroups 2.3.

On the basis of the former findings, we may concluded that group 1 consists of all CSFV strains (30) prior to the 1980's, whereas all CSFV strains isolated from different European countries except Russia in the 1990's and recent epidemics in the EU belongs to one of the subgroups within group 2 (2.1, 2.2, or 2.3) (10-12,20,25,29,31). CSF is still currently endemic in various European countries.

Asia

In Asia, CSF epidemics are also fairly ubiquitous. Strains of genotypes 1, 2, and 3 have been isolated in different Asian countries (10,32). Furthermore, isolates belonging to group 3 seem to occur solely in Asia (12). In Taiwan, by analyzing the E2 sequences of CSFV from field outbreaks during 1993-2001, CSF viruses have been classified into two subgroups 3.4 and 2.1 (33, 34). Furthermore the Taiwanese strains of sub-genotype 2.1 were divided into two different genotypes termed 2.1a and 2.1b which may have be introduced from different origins (33). Another finding suggested that all Taiwanese CSFV strains were sub-genotypes 3.4 prior to

1996. However, genotype 2 strains of CSFV, identified as sub-genotype 2.1 or 2.2, have been isolated since 1994 and have gradually replaced the sub-genotype 3.4 strain (35). One hundred and ten clinical specimens representing 109 epizootic sites from 1986-1999 in China were also analyzed. A phylogenetic tree showed that 103 of the 110 field viruses were clustered within group 2 and subdivided into three subgroups, while the remaining seven viruses were clustered into subgroup 1.1 within group 1. It is evident that sub-groups 2.1 and 2.2 have predominated in the more recent epizootics in China, while group 1 viruses have caused only limited epizootics (36). A novel isolated CSFV in China in 2004 belonged to 2.3 topotype (37).

CSF is endemic in India. Phylogenetic analysis revealed that all CSFV isolates during 2005-2007 from domestic pigs in different districts of Assam belonged to group 1 and subgroup 1.1 in contrast to the situation in other Asian countries (38). Seventeen CSFV isolates recovered during the period of 3 years (2006-2008) from India could be grouped in to two subgroups, 1.1 and 2.2 (39). Another study demonstrated that CSFV field isolates from India 3 isolates belonged to genotype 2.1 and were closely related to European CSFV strains, and the remaining 6 isolates belonged to genotype 1 that contained old and new strains. It also indicated circulation of both genotypes 1 and 2.1 in north-eastern part of India (40). The findings above suggest that subgroup 1.1 CSF viruses are currently circulating in India, which is important for epidemiology and control of CSF. Furthermore, subgroup 2.1 or 2.2 viruses were also involved in a CSFV outbreak.

The CSFV isolates in Japan are divided into three genovars, CSFV-1, CSFV-2 and CSFV-3 (41). 24 isolates of CSFV obtained from CSF outbreaks during 1988 and 2003 in the Republic of Korea were genetically characterized for partial E2 gene, compared with CSF viruses reported by other countries. Phylogenetic analyses classified Korean field isolates between 1988 and 1999 into subgroup 3.2, and the viruses isolated during 2002-2003 CSF epidemics were classified into a different subgroup 2.1 (5).

South America

Although not present in the United States, CSF is distributed in Central and South America. Sporadic outbreaks of CSF are frequently recorded: For instance, Group 1 was reported to be isolated from Asian and South American in the 1980's (30). The origin and evolution of the CSF epizootic

that occurred in Cuba from 1993 to 1997 has been investigated by the analysis of E2 gene sequences from 15 representative viral isolates as well as the vaccine and the challenge strains used in this country. In the phylogenetic tree derived from these sequences, the Cuban isolates were located in a defined cluster within the previously reported genomic subgroup 1.2 (42).

PREVENTION AND CONTROL OF CSF

Cutting off transmission routes of CSF

CSF can spread via various routes. Direct transmission of CSF is undoubtedly the most efficient way of CSFV transmission. Epidemiological data found that most of primary CSF outbreaks were due to direct contacts with wild boar infected with CSFV or contaminated swill feeding (43). Trade of living infected pigs bears the highest risk of transmitting the virus; international trade especially may lead to the spread of the virus over long distances. Furthermore, neighborhood contacts to infected farms and other contacts via contaminated persons and vehicles are important modes especially in areas with high pig and pig farm density (44). However, the role of airborne transmission remains debatable (31). In EU Countries, boars for artificial insemination (AI) must be CSF-free. Furthermore, control of the influx of meat and meat products from countries, a commercial development towards more local marketing systems, the reduction of the pig density in critical areas and strict hygiene measures on pig farms as well as vehicles used for animal transportation would be also beneficial to avoid the spread of CSF.

CSF monitoring strategies in wild boars and domestic pigs

The wild boar population should be monitored for CSF outbreaks. The CSF status of wild boar populations is still unknown in several parts of Europe although a recommended monitoring program (oral immunization together with special hunting strategies) is available (45). When an outbreak of CSF in wild boar is detected, early measures must be taken to protect domestic pigs. The control of endemic infections in wild boar populations appears to be difficult. The basic requirement is the identification of both risk and surveillance zones, taking into account geographical conditions and the structure and the size of the wild boar populations. A complete ban on hunting activities was introduced in Switzerland

for 2 months after the detection of CSF in wild boar in order to limit movement of potentially infected animals outside their natural habitat (21).

Increased monitoring of the local domestic pig population should detect possible CSF outbreaks at an early stage. Surveillance programs aim to keep the number of infected herds as small as possible, by shortening the so-called “high risk period”. For instance, it was concluded leukocyte counts (31) could be an effective method for individual herds—but probably not for large-scale surveillance. It is probable that the Dutch CSF epidemic of 1997/1998 would have been detected earlier if routine serological surveillance had been applied (46). Additionally, computer-based models help to understand disease dynamics and can support decision-makers in case of an outbreak. Mass-action and state-transition models, branching processes and Monte Carlo methods (44), spreadsheet models (47) and spatial and stochastic models (48) have been used to study virus spread and to evaluate control strategies. However, due to changes in the biology of CSFV and pig trading schemes, it has become more difficult to completely control this disease, indicating that newer methods have to be developed for this purpose.

Eradication of CSF from wild boars and domestic pigs

Within the EU, different strategies are used for the eradication of CSF in wild boar and in domestic pigs. The combination of prophylactic mass vaccination and culling of infected pigs in endemic regions has made it possible to almost eradicate the disease in the EU. The control of CSF epidemics comprises of eradication of infected herds and preventive emptying of herds was effective within a radius of 750–1000 m of infected areas (49).

However, several epidemics which occurred in Europe during the last decade have pointed out that eradication according to the present legislation may be very costly and ethically unacceptable, particularly in areas with a high pig density (50,51). For example, CSF occurred in Netherlands from 1997 to 1998 where millions of pigs were slaughtered and direct losses were calculated to amount to 2 billion US dollars for eradication (14). The epidemiological characteristics of the 1997 CSF outbreak that occurred in the Limburg Province of Belgium between 30 June and 17 July 1997 resulted in a total of 46,561 pigs being slaughtered to control the spread of the infection. Another 27,579 pigs were slaughtered in the framework of the market support. The to-

tal direct costs of the episode were estimated at 10,893,337 Euros (15,52). Spain suffered an outbreak of CSF between June 14, 2001 and May 7, 2002; a total of 291,058 animals were slaughtered (28).

VACCINATION

Though many countries including EU member states pursue a non-vaccination stamping-out policy, however for some developing countries such as China, India and Africa, there is still a difficult method to eradicate this complex disease, even though vaccination against CSFV has been applied. Therefore, under certain conditions, emergency vaccination combined with control measures might be a future option for disease eradication and control (45).

Live attenuated virus strain vaccines

Massive vaccination with live attenuated vaccines, such as C-strain, developed in China in mid-1950s has been implemented routinely as a major control strategy in China as well as many other developing countries. The C-strain of the CSFV is considered as the gold standard vaccine for the control of CSF (53). The attenuated lapinized CSFV strains such as PAV-250, LPC, and HCLV, the attenuated CSFV by deletion of the viral N(pro) gene (54), can also induce virtually complete protection against the disease (55). The live CSFV strain vaccines mentioned above provide protection for pigs for CSF, however, they do not permit the serological discrimination between infected and vaccinated animals and its use can therefore impose severe trade restrictions. To solve these problems, advanced vaccines against CSF and discriminatory tests have been developed.

DNA-based Vaccines

A number of efforts are in progress to develop DNA vaccines in recent years. DNA vaccines are an attractive prospect because plasmid DNA can be highly purified and there is less opportunity for adventitious viruses to contaminate the vaccine preparation. Furthermore these vaccines are very stable at ambient temperatures and can be delivered in very small quantities under optimized route of injection. The vaccines developed were tested for safety and efficacy in animal models and claimed to be immunogenic and safe. The investigations showed that a DNA vaccine expressing the complete E2 protein of CSFV such

Table 1: Molecular epidemiology of CSF

Continent	Country	Group or subgroup	Time	Animal	Reference
Europe	Russia	2.1	1994-1999	DP	(12)
	Austria	1.1	1993	WB	(13)
		2.2	1992, 94	WB	(19)
	The Netherlands	2.1	1997	DP	(14)
	Belgium	2.1	1997	DP	(15)
		1.1	1988	DP	(25)
		2.3	1990,93,94	DP	(25)
	UK	2.1	2000	DP	(16)
	Germany	2.1,2.2,2.3	1990-1998	DP,WB	(17)
	Switzerland	32.2	1998	WB	(18)
	The Czech Republic	2.2	1991-1998	DP,WB	(19)
		2.3	1991-1998	DP,WB	(19)
	Italy	2.2	1985-2000	DP,WB	(20-22)
		2.3	1985-2000	DP,WB	(23-24)
	Germany	2.3	2010	WB	(26)
	Romania	2.3	1994-2007	DP	(27)
	Bulgaria	2.3	1997-2008	DP	(27)
	Kosovo	2.3	2006	DP	(27)
	Montenegro	2.3	2000	DP,WB	(27)
	Serbia	2.3	2000-2007	DP	(27)
	Croatia	2.1	1996-2007	DP	(27)
	Macedonia	2.2	2000	DP	(27)
	Spain	2.3	2001-2002	DP	(28)
	Estonia	2.3	1990s	DP	(29)
	Hungary	2.3	1990s	DP	(29)
	Poland	2.3	1990s	DP	(29)
	Slovakia	2.3	1990s	DP	(29)
Asia	Korea	3.2	1988- 1999	DP	(5)
		2.1	2002-2003	DP	(5)
	Lao People's Democratic Republic	2.1	1997	DP	(32)
		2.2	1999	DP	(32)
	Taiwan	3.4	Prior to 1994	DP	(33)
		2.1, 2.2	After 1994	DP	(34,35)
	China	1.1,2.1, 2.2	1986-1999	DP	(36)
		2.3	2004	DP	(37)
	India	1.1	2005-2007	DP	(38-40)
		2.2	2006-2008	DP	(39)
		2.1	2000-2004	DP	(40)
	Japan	1, 2, 3	Prior to 1999	DP	(41)
South America	Cuba	1.2	1993-1997	DP	(42)

WB: wild boar; DP: domestic pigs

as the Semliki Forest virus (SFV) replicon-derived DNA vaccine, conferred total protection against a severe viral challenge in domestic pigs immunized three times with 600 µg or twice with 100 µg (56-58). However, the results generated by scientists from different laboratories need to be pooled and evaluated scientifically to select a few

potential vaccine candidates for large-scale trials to proof efficacy and safety.

Marker vaccines

Marker vaccines against CSFV infection which allow differentiation of infected from vaccinated animals have been

Table 2: Development of vaccines based on glycoproteins of CSFV

Types of vaccine	Treatment	References
Recombinant virus vaccine	Vaccinia virus recombinants (VVR) expressing all CSFV structural proteins except for E2	(62)
	VVR expressing Erns and/or E2 protein	(73)
	Pseudorabies virus (PRV) recombinant virus expressing E2 or E1 protein	(74)
	A recombinant porcine adenovirus (rPAV) expressing E2 protein	(74)
	A recombinant parapoxvirus (PPV) Orf virus (ORFV) expressing E2 protein	(67)
	A recombinant baculovirus expressing Erns or E2 protein	(8,9)
	A recombinant human adenovirus type 5 expressing E2 protein	(75)
Live-attenuated vaccine	The 5' terminal half of the E2 and Erns gene of the C-strain was exchanged with the homologous gene of the BVDV strain	(69)
	The antigenic region of E2 and/or the complete Erns gene were replaced by the analogous sequence of BVDV II strain	(78)
	CSFV replicon particles lacking either the complete E2 gene or, alternatively, a stretch of 204 nucleotides encoding 68 amino acids located in the C-terminal region of the E2 glycoprotein	(60)
	Modification of the carboxyl-terminal domain of E1	(64)
	Modification of glycosylation of E2	(64)
	E2 without transmembrane region (E2-TMR)	(76)
	Erns deletion mutants	(65)
DNA vaccine	The Semliki Forest virus (SFV) replicon-derived DNA vaccine expressing the complete E2 protein	(56)
	Alphavirus replicon-derived DNA vaccine expressing glycoprotein E2	(58,69)
Subunit vaccine	E2 protein emulsified in Freund's adjuvant	(80)
	E2 protein in a water-oil-water adjuvant	(66)
Epitope-vaccine	E2 N-terminal CKEDYRY (aa693-699)	(71)
	E2 N-terminal antigenic units B/C	(79)
	B cell epitope at the N-terminus of the E2 protein	(63)
	Linear neutralizing epitopes have been mapped to envelope glycoprotein E2 and Erns	(68)

developed, including protective peptides, single expressed proteins and chimeric viruses (59-80) (Table 2).

CSFV glycoproteins E2, E(rns) and E1 are structural proteins detected on the external part of viral particles and play a major role in the initial stages of viral infection. Studies on these structural proteins have also opened a new ways to develop new vaccines. For example, the absence of the antigenic portion of glycoprotein E(rns), deletion of E2 gene, the

A-domain of E2 or E2-encoding region of classical CSFV can be used as non-transmissible, modified, live-attenuated marker vaccines which protects pigs from a lethal challenge dose of the highly virulent strain or differentiate between infected and vaccinated animals (59-62). In addition, the carboxyl-terminal domain of E1 glycoprotein provides the basis for a rationally designed and efficacious live-attenuated CSF vaccine (63-65).

Vaccination with the CSFV E2 subunit marker vaccine was an efficacious tool in the control program during an outbreak of CSF. Vaccination 10 days after outbreak significantly reduced the vertical transmission of moderate-virulent strain of CSFV from the pregnant sow to its offspring (66-69) and decreased the horizontal virus transmission of weaning piglets (53). However, another study showed that double vaccination with an E2 subunit marker vaccine only protected pregnant gilts from the clinical course of the disease but did not prevent horizontal nor vertical spread of the CSF virus (70). The E(rns) which possessed enzymatic activity and retained antigenicity might provide useful material for developing a marker vaccine (71,72).

An envelope glycoprotein D/E-negative Pseudorabies Virus (PRV) recombinant, Vaccinia Virus Recombinant (VVR) (62,73) or a recombinant Porcine Adenovirus (rPAV) (74,75) which expressed envelope glycoprotein E2 of CSFV was constructed as a biologically safe vaccine vector. Vaccination of pigs showed that the recombinant virus was able to protect pigs against CSF. The other observations demonstrated that a deletion of E2 protein in combination with a modified CTB (76), eukaryotic expression plasmid with only 5' signal sequence of E2 (77), synthetic peptide vaccine using E2 N-terminal antigenic units B/C (54,78) and a multi-peptide-vaccine (MPV) using aluminum adjuvant (79) or E2 emulsified in Freund's adjuvant (80) were all suitable to act as a candidate marker vaccine against CSFV.

Development of Antiviral drugs

A few effective antiviral drugs are currently available against CSFV infections (Table 3). At a concentration of 5 µg/ml,

Table 3. Application of antiviral drugs and siRNA

Application	Methods	Effects	References
Antiviral drugs	Prostaglandin (PgA1)	Inhibit the multiplication of CSFV in 99% in PK-15 cells	(81,82)
	Tunicamycin	Reduce CSFV spread in SK6 cells	(83)
	Uridine derivatives of 2-deoxy sugars, IW3 and IW7 mimicking part of tunicamycin	Reduce the formation of viral glycoproteins E2 and E ^{ms} and arrest viral growth	(84)
	Capsid protein (Cap) fused with the nuclease of <i>Staphylococcus aureus</i> (SN) in <i>Escherichia coli</i>	Inhibit the replication of CSFV	(85)
	Cap fused with an enzymatically inactive SN	No antiviral effects	(85)
	3D8 single-chain variable fragment (3D8 scFv)	Suppress CSFV replication at the viral RNA level	(86)
Small interfering RNA	Targeting nucleocapsid protein (C)	Inhibit viral replication	(7)
	Targeting Npro and NS5B genes	Reduce in viral genome copy number and suppress the production of infectious virus	(87)

prostaglandin (PGA1) was found to inhibit the multiplication of CSFV in 99% in cultures of PK-15 cells (81,82). Tyborowska *et al.* (2007) found that very low doses of tunicamycin drastically reduced CSFV spread and the virus yield in SK6 (swine kidney) cell cultures (83). Some glycosylation inhibitors, such as two of newly designed uridine derivatives of 2-deoxy sugars, IW3 and IW7 mimicking part of tunicamycin could effectively arrest viral growth without significant toxicity for mammalian cells. Moreover, IW3 and IW7 reduced the formation of viral glycoproteins E2 and E(rns) in a dose-dependent manner (84). Due to the observed antiviral effect accompanied by low cytotoxicity, these inhibitors are potential candidates for the inhibition of the spread of CSFV.

Capsid-targeted viral inactivation (CTVI) approach might be applicable to CSFV inhibition as a novel antiviral strategy. Zhou *et al.* (2010) found that the CSFV capsid protein (Cap) fused with the nuclease of *Staphylococcus aureus* (SN) in *Escherichia coli* could inhibit effectively the replication of CSFV in a dose-dependent manner, whereas the Cap fused with an enzymatically inactive SN (Cap-SN*) showed no nuclease activity or antiviral effects (85). Some proteins with ribonuclease (RNase) activity have been shown to suppress viral replication and may be valuable therapeutic approaches against CSFV. Exogenous treatment of 3D8 single-chain variable fragment (3D8 scFv) prior to or post-CSFV infection, could suppress CSFV replication at the viral RNA level (86).

Small interfering RNA (siRNA)

Small interfering RNA (siRNA) can be used to control genome replication and viral production (Table 3). For example, three species of siRNA, targeting different regions of CSFV: *Npro* and *NS5B* genes, were prepared by *in vitro* transcription. After transfection of PK-15 cells with each of the siRNAs followed by infection with CSFV, the results showed that treatment with the siRNAs caused a 4-12-fold reduction in viral genome copy number and suppressed the production of infectious virus by up to 467-fold for 72-84 h (87). The use of synthetic siRNA which corresponded to nucleotides 1130-1148 of the CSF virus strain Alfort, targeting the nucleocapsid protein (C) was investigated to inhibit viral replication (7). Therefore, the application of RNAi strategy for controlling CFSV could become a promising alternative to conventional eradication measures.

CONCLUSION

CSF epidemics in Asia and several countries of Central and South America have clearly shown that preventing the introduction of CSFV deserves high priority. Development of suitable marker vector vaccines to allow the vaccination of pigs, as well as better control strategies in disease outbreak countries is also important. Although many techniques and strategies have been developed for detection and control of CSF, there still remains many efforts that should be taken: 1) study of the efficacy and stability of vaccines against CSFV;

2) virological surveys to be carried out to establish the distribution of CSFV among domestic pigs and wild boar; 3) phylogenetic analyses and genealogical relationships among members of the CSFV; 4) the study of atypical infection in piglets; 5) the investigation of persistent infection even after vaccination and (6) the differentiation between vaccinated and infected pigs.

ACKNOWLEDGEMENTS

This work was supported by grants from the National Natural Science Foundation of China (Nos. 31072137, 31172321 and 30771611), the Key Project of Natural Science Foundation of Guangdong Province, China (No.S2011020001037), Special Fund for Agro-Scientific Research in the Public Interest (No.201203056) and Research Fund for the Doctoral Program of Higher Education of China (No.20114404110015).

REFERENCES

- Westergaard, J. M.: The classical swine fever in the EEC. In: Report on the Meeting of National Swine Fever Laboratories in the European Economic Communities. Commission of the European Communities. Brussels, Belgium, pp. 4-6, 1990.
- Edwards, S.: Survival and inactivation of classical swine fever virus. *Vet. Microbiol.* 73, 175-181, 2000.
- Vargas Terán, M., Calcagno Ferrat, N. and Lubroth, J.: Situation of classical swine fever and the epidemiologic and ecologic aspects affecting its distribution in the American continent. *Ann. N. Y. Acad. Sci.* 1026:54-64, 2004.
- Parchariyanon, S., Inui, K., Pinyochon, W., Damrongwatanapokin, S. and Takahashi, E.: Genetic grouping of classical swine fever virus by restriction fragment length polymorphism of the E2 gene. *J. Virol. Methods.* 87:145-149, 2000.
- Cha, S. H., Choi, E. J., Park, J. H., Yoon, S. R., Kwon, J. H. and Yoon, K. J.: Phylogenetic characterization of classical swine fever viruses isolated in Korea between 1988 and 2003. *Virus Res.* 126:256-261, 2003.
- Wang, Y. F., Wang, Z. H., Li, Y., Zhang, X. J., Sun, Y. and Li, M.: In vitro inhibition of the replication of classical swine fever virus by capsid-targeted virus inactivation. *Antiviral. Res.* 85:422-424, 2010.
- Porntrakulpipat, S., Supankong, S., Chatchawanchonteera, A. and Pakdee, P.: RNA interference targeting nucleocapsid protein (C) inhibits classical swine fever virus replication in SK-6 cells. *Vet. Microbiol.* 142:41-44, 2010.
- Wu, H. X., Wang, J. F., Zhang, C. Y., Fu, L. Z., Pan, Z. S. and Wang, N.: Attenuated lapinized Chinese strain of classical swine fever virus, complete nucleotide sequence and character of 3'-noncoding region. *Virus Genes.* 23:69-76, 2001.
- Li, N., Zhao, J. J., Zhao, H. P., Sun, Y., Zhu, Q. H. and Tong, G. Z.: Protection of pigs from lethal challenge by a DNA vaccine based on an alphavirus replicon expressing the E2 glycoprotein of classical swine fever virus. *J. Virol. Methods.* 144:73-78, 2007.
- Paton, D. J., McGoldrick, A., Belak, S., Mittelholzer, C., Koenen, F. and Vanderhallen, H.: Classical swine fever virus, a ring test to evaluate RT-PCR detection methods. *Vet. Microbiol.* 73:159-174, 2000.
- Fritzemeier, J., Teuffert, J., Greiser-Wilke, I., Staubach, C., Schlüter, H. and Moennig, V.: Epidemiology of classical swine fever in Germany in the 1990s. *Vet. Microbiol.* 77:29-41, 2000.
- Vlasova, A., Grebennikova, T., Zaberezhny, A., Greiser-Wilke, I., Floegel-Niesmann, G., Kurinnov, V., Aliper T. and Nepoklonov, E.: Molecular Epidemiology of Classical Swine Fever in the Russian Federation. *J. Vet. Med. B* 50:363-367, 2003.
- Hofman, M. A.: Molecular epidemiology of CSF, isolate Switzerland II/93 is closely related to a virus strain isolated from Chinese wild boar meat in Austria. In: Report on Annual Meeting of National Swine Fever Laboratories, Alghero, Sardinia, Italy 3-5 June, Directorate General for Agriculture, VI/B/II.2. Commission of the European Communities. Brussels, pp. 29, 1996.
- Terpstra, C. and de Smit, A. J.: The 1997/1998 epizootic of swine fever in the Netherlands, control strategies under a non-vaccination regimen. *Vet. Microbiol.* 77:3-15, 2000.
- Mintiens, K., Deluyker, H., Laevens, H., Koenen, F., Dewulf, J. and De Kruif, A.: Descriptive epidemiology of a classical swine fever outbreak in the Limburg Province of Belgium in 1997. *J. Vet. Med. B. Infect. Dis. Vet. Public. Health.* 48:143-149, 2001.
- Sandvik, T., Drew, T., Paton, D.: CSF virus in East Anglia, where from? *Vet. Rec.* 147:251, 2000.
- Greiser-Wilke, I., Depner, K., Fritzemeier, J., Haas, L. and Moennig, V.: Application of a computer program for genetic typing of classical swine fever virus isolates from Germany. *J. Virol. Methods.* 75:141-150, 1998.
- Hofman, M. A., Thuer, B., Vanzetti, T., Schleis, W., Schmidt, J. and Griot, C.: Klassische Schweinepest beim Wildschwein in der Schweiz. *Schweizer. Archiv. Tierheilkunde.* 141:185-190, 1999.
- Bartak, P. and Greiser-Wilke, I.: Genetic typing of classical swine fever virus isolates from the territory of the Czech Republic. *Vet. Microbiol.* 77:59-70, 2000.
- Lowings, J. P., Paton, D. J., Sands, J. J., De Mia, G. M. and Rutili, D.: Classical swine fever, genetic detection and analysis of differences between virus isolates. *J. Gen. Virol.* 75:3461-3468, 1994.
- Lowings, P., Ibata, G., Needham, J. and Paton, D.: Classical swine fever virus diversity and evolution. *J. Gen. Virol.* 77:1311-1321, 1996.
- Greiser-Wilke, I., Fritzemeier, J., Koenen, F., Vanderhallen, H., Rutili, D., De Mia, G. M., Romero, L., Rosell, R., Sanchez-Vizcaino, J. M. and San Gabriel, A.: Molecular epidemiology of a large classical swine fever epidemic in the European Union in 1997-1998. *Vet. Microbiol.* 77:17-27, 2000.
- Lowings, P., Ibata, G., De Mia, G. M., Rutili, D. and Paton, D.: Classical swine fever in Sardinia, epidemiology of recent outbreaks. *Epidemiol. Infect.* 122:553-559, 1999.
- Biagetti, M., Greiser-Wilke, I. and Rutili, D.: Molecular epidemiology of classical swine fever in Italy. *Vet. Microbiol.* 83:205-215, 2001.
- Vanderhallen, H., Mittelholzer, C., Hofmann, M. A. and Koenen, F.: Classical swine fever virus is genetically stable in vitro and in vivo. *Arch. Virol.* 144:1669-1677, 1999.

26. Leifer, I., Hoffmann, B., Höper, D., Bruun Rasmussen, T., Blome, S., Strebelow, G., Höreth-Böntgen, D., Staubach, C. and Beer, M.: Molecular epidemiology of current classical swine fever virus isolates of wild boar in Germany. *J. Gen. Virol.* 91:2687-2697, 2010.
27. Blome, S., Grotha, I., Moennig, V. and Greiser-Wilke, I.: Classical swine fever virus in South-Eastern Europe--retrospective analysis of the disease situation and molecular epidemiology. *Vet. Microbiol.* 146:276-284, 2010.
28. Allepuz, A., Casal, J., Pujols, J., Jové, R., Selga, I., Porcar, J., and Domingo, M.: Descriptive epidemiology of the outbreak of classical swine fever in Catalonia (Spain), 2001/02. *Vet. Rec.* 160:398-403, 2007.
29. Stadejek, T., Vilcek, S., Lowings, J. P., Ballagi-Pordány, A., Paton, D. J., Belák, S.: Genetic heterogeneity of classical swine fever virus in Central Europe. *Virus Res.* 52:195-204, 1997.
30. Björklund, H., Lowings, P., Stadejek, T., Vilcek, S., Greiser-Wilke, I., Paton, D. and Belák, S.: Phylogenetic comparison and molecular epidemiology of classical swine fever virus. *Virus Genes.* 19:189-195, 1999.
31. Stegeman, J. A., Bouma, A., Elbers, A. R. W. and Verheijden, J. H. M.: The white blood cell count is a valuable parameter for detection Classical Swine Fever (Leukocytentelling is een waardevol hulpmiddel voor het opsporen van klassieke varkenspest). *Tijdschr. Diergeneesk.* 125:511-518, 2000.
32. Blacksell, S. D., Khounsy, S., Boyle, D. B., Gleeson, L. J., Westbury, H. A. and Mackenzie, S.: Genetic typing of classical swine fever viruses from Lao PDR by analysis of the 5' non-coding region. *Virus Genes.* 31:349-355, 2005.
33. Deng, M. C., Huang, C. C., Huang, T. S., Chang, C. Y., Lin, Y. J., Chien, M. S. and Jong, M. H.: Phylogenetic analysis of classical swine fever virus isolated from Taiwan. *Vet. Microbiol.* 106:187-193, 2005.
34. Lin, Y. J., Chen, M. S., Deng, M. C. and Huang, C. C.: Complete sequence of a subgroup 3.4 strain of classical swine fever virus from Taiwan. *Virus Genes.* 35:737-744, 2007.
35. Pan, C. H., Jong, M. H., Huang, T. S., Liu, H. F., Lin, S. Y. and Lai, S. S.: Phylogenetic analysis of classical swine fever virus in Taiwan. *Arch. Virol.* 150:1101-1119, 2005.
36. Sun, J. F., Shi, Z. X., Guo, H. C., Su, L. and Tu, C. C.: Proteomic analysis of swine serum following highly virulent classical swine fever virus infection. *Virol. J.* 8:107, 2011.
37. Li, X., Xu, Z., He, Y., Yao, Q., Zhang, K., Jin, M., Chen, H. and Qian, P.: Genome comparison of a novel classical swine fever virus isolated in China in 2004 with other CSFV strains. *Virus Genes.* 33:133-142, 2006.
38. Sarma, D. K., Mishra, N., Vilcek, S., Rajukumar, K., Behera, S. P., Nema, R. K., Dubey, P. and Dubey, S. C.: Phylogenetic analysis of recent classical swine fever virus (CSFV) isolates from Assam, India. *Comp. Immunol. Microbiol. Infect. Dis.* 34:11-15, 2011.
39. Patil, S. S., Hemadri, D., Shankar, B. P., Raghavendra, A. G., Veeresh, H., Sindhoora, B., Chandan, S., Sreekala, K. and Gajendragad, M. R.: Genetic typing of recent classical swine fever isolates from India. *Vet. Microbiol.* 141:367-373, 2010.
40. Desai, G. S., Sharma, A., Kataria, R. S., Barman, N. N. and Tiwari, A. K.: 5'-UTR-based phylogenetic analysis of Classical swine fever virus isolates from India. *Acta. Virol.* 54:79-82, 2010.
41. Harasawa, R. and Giangaspero, M.: Genetic variation in the 5' end and NS5B regions of classical swine fever virus genome among Japanese isolates. *Microbiol. Immunol.* 43:373-379, 1999.
42. Díaz de Arce, H., Núñez, J. I., Ganges, L., Barreras, M., Teresa Frías, M. and Sobrino, F.: Molecular epidemiology of classical swine fever in Cuba. *Virus Res.* 64:61-67, 1999.
43. Thür, B. and Hofmann, M. A.: Comparative detection of classical swine fever virus in striated muscle from experimentally infected pigs by reverse transcription polymerase chain reaction, cell culture isolation and immunohistochemistry. *J. Virol. Methods.* 74:47-56, 1998.
44. Karsten, S., and Krieter, J.: Epidemiology of classical swine fever and models to analyze virus spread. A review. *Deut. Tier. W.* 112:180-188, 2005.
45. Anon: Monitoring of classical swine fever in wild boar in EU member states and candidate countries. In: Proceedings of the Seminar on the Control of Classical Swine Fever and the Evaluation of the Inter-laboratory Comparison Test, 2001. SANCO/1225/2001. Commission of the European Community. Brussels. pp. 85-95, 2001.
46. Crauwels, A. P. P., Nielen, M., Stegeman, J. A., Elbers, A. R. W., Dijkhuizen, A. A. and Tielen, M. J. M.: The effectiveness of routine serological surveillance, case study of the 1997 epidemic of classical swine fever in The Netherlands. *Rev. Sci. Tech. Off. Int. Epiz.* 18:627-637, 1999.
47. de Vos, C. J., Saatkamp, H. W., Huirne, R. B. and Dijkhuizen, A. A.: The risk of the introduction of classical swine fever virus at regional level in the European Union, a conceptual framework. *Rev. Sci. Tech.* 22:795-810, 2003.
48. Martínez-López, B., Ivorra, B., Ramos, A. M. and Sánchez-Vizcaino, J. M.: A novel spatial and stochastic model to evaluate the within- and between-farm transmission of classical swine fever virus. I. General concepts and description of the model. *Vet. Microbiol.* 147:300-309, 2010.
49. Mangan, M. J. J., Nielen, M. and Burrell, A. M.: Simulated effect of pig population density on epidemic size and choice of control strategy for classical swine fever epidemics in The Netherlands. *Prev. Vet. Med.* 56:141-163, 2002.
50. Horst, H. S., Meuwissen, M. P. M., Smak, J. A. and Van de Meijjs, C. C. J. M.: The involvement of the agriculture industry and government in animal disease emergencies and the funding of compensation in Western Europe. *Rev. Sci. Tech. Off. Int. Epiz.* 18:30-37, 1999.
51. Pittler, H., Fiedler, J., Jentsch, D., Hasselbach, P. and Kramer, M.: The problems and consequences of the swine fever epidemic during 1993/1994 in Germany. *Tierärztl. Umschau.* 50:522-530 (in German), 1995.
52. Elber, A. R., Stegeman, A., Moser, H., Ekker, H. M., Smak, J. A. and Pluimers, F. H.: The classical swine fever epidemic 1997-1998 in The Netherlands, descriptive epidemiology. *Prev. Vet. Med.* 42:157-184, 1999.
53. Dewulf, J., Laevens, H., Koenen, F., Mintiens, K. and de Kruif, A.: Efficacy of E2-sub-unit marker and C-strain vaccines in reducing horizontal transmission of classical swine fever virus in weaner pigs. *Prev. Vet. Med.* 65:121-133, 2004.
54. Dong, X. N., Wei, K., Liu, Z. Q. and Chen, Y. H.: Candidate pep-

- tid vaccine induced protection against classical swine fever virus. *Vaccine*. 21:167-173, 2002.
55. Gonzalez, C., Pijoan, C., Ciprian, A., Correa, P. and Mendoza, S.: The effect of vaccination with the PAV-250 strain classical swine fever (CSF) virus on the airborne transmission of CSF virus. *J. Vet. Med. Sci.* 63:991-996, 2001.
 56. Ganges, L., Barrera, M., Núñez, J. I., Blanco, I., Frias, M. T., Rodríguez, F. and Sobrino, F.: A DNA vaccine expressing the E2 protein of classical swine fever virus elicits T cell responses that can prime for rapid antibody production and confer total protection upon viral challenge. *Vaccine*. 23:3741-3752, 2005.
 57. Li, Y., Zhao, J. J., Li, N., Shi, Z., Cheng, D. and Zhu, Q. H.: A multiplex nested RT-PCR for the detection and differentiation of wild-type viruses from C-strain vaccine of classical swine fever virus. *J. Virol. Methods*. 143:16-22, 2007.
 58. Tarradas, J., Argilagué, J. M., Rosell, R., Nofrías, M., Crisci, E., Córdoba, L., Pérez-Martín, E., Díaz, I., Rodríguez, F., Domingo, M., Montoya, M. and Ganges, L.: Interferon-gamma induction correlates with protection by DNA vaccine expressing E2 glycoprotein against classical swine fever virus infection in domestic pigs. *Vet. Microbiol.* 142:51-58, 2010.
 59. Kortekaas, J., Vloet, R. P., Weerdmeester, K., Ketelaar, J., van Eijk, M. and Loeffen, W. L.: Rational design of a classical swine fever C-strain vaccine virus that enables the differentiation between infected and vaccinated animals. *J. Virol. Methods*. 163:175-185, 2010.
 60. Maurer, R., Stettler, P., Ruggli, N., Hofmann, M. A. and Tratschin, J. D.: Oronasal vaccination with classical swine fever virus (CSFV) replicon particles with either partial or complete deletion of the E2 gene induces partial protection against lethal challenge with highly virulent CSFV. *Vaccine*. 23:3318-3328, 2005.
 61. Reimann, I., Depner, K., Trapp, S. and Beer, M.: An avirulent chimeric Pestivirus with altered cell tropism protects pigs against lethal infection with classical swine fever virus. *Virology* 322:143-157, 2004.
 62. Rümenapf, T., Stark, R., Meyers, G. and Thiel, H. J.: Structural proteins of hog cholera virus expressed by vaccinia virus, further characterization and induction of protective immunity. *J. Virol.* 65:589-597, 1991.
 63. Liu, S., Tu, C., Wang, C., Yu, X., Wu, J. and Guo, S.: The protective immune response induced by B cell epitope of classical swine fever virus glycoprotein E2. *J. Virol. Methods*. 134:125-129, 2006.
 64. Risatti, G. R., Holinka, L. G., Lu, Z., Kutish, G. F., Tulman, E. R. and French, R. A.: Mutation of E1 glycoprotein of classical swine fever virus affects viral virulence in swine. *Virology*. 343:116-127, 2005.
 65. Widjoatmodjo, M. N., van Gennip, H. G., Bouma, A., van Rijn, P. A. and Moormann, R. J.: Classical swine fever virus Erns deletion mutants, trans-complementation and potential use as non-transmissible, modified, live-attenuated marker vaccines. *J. Virol.* 74:2973-2980, 2000.
 66. Bouma, A., De Smit, A. J., De Jong, M. C., De Kluijver, E. P. and Moormann, R. J.: Determination of the onset of the herd-immunity induced by the E2 sub-unit vaccine against classical swine fever virus. *Vaccine*. 18:1374-1381, 2000.
 67. Voigt, H., Merant, C., Wienhold, D., Braun, A., Hutet, E., Le Potier, M. F., Saalmüller, A., Pfaff, E. and Büttner, M.: Efficient priming against classical swine fever with a safe glycoprotein E2 expressing Orf virus recombinant (ORFV VrV-E2). *Vaccine*. 25:5915-5926, 2007.
 68. Zhang, F., Yu, M., Weiland, E., Morrissy, C., Zhang, N., Westbury, H. and Wang, L. F.: Characterization of epitopes for neutralizing monoclonal antibodies to classical swine fever virus E2 and Erns using phage-displayed random peptide library. *Arch. Virol.* 151:37-54, 2006.
 69. de Smit, A. J., Bouma, A., Terpstra, C. and van Oirschot, J. T.: Transmission of classical swine fever virus by artificial insemination. *Vet. Microbiol.* 67:239-249, 1999.
 70. Dewulf, J., Laevens, H., Koenen, F., Mintiens, K. and de Kruif, A.: An E2 sub-unit marker vaccine does not prevent horizontal or vertical transmission of classical swine fever virus. *Vaccine*. 20:86-91, 2001.
 71. Dong, X. N. and Chen, Y. H.: Spying the neutralizing epitopes on E2 N-terminal by candidate epitope-vaccines against classical swine fever virus. *Vaccine*. 24:4029-4034, 2006.
 72. Freitas, T. R., Gaspar, L. P., Caldas, L. A., Silva, J. L. and Rebello, M. A.: Inactivation of classical swine fever virus, association of hydrostatic pressure and ultraviolet irradiation. *J. Virol. Methods*. 108:205-211, 2003.
 73. König, M., Lengsfeld, T., Pauly, T., Stark, R. and Thiel, H. J.: Classical swine fever virus, independent induction of protective immunity by two structural glycoproteins. *J. Virol.* 69:6479-6486, 1995.
 74. Hammond, J. M., McCoy, R. J., Jansen, E. S., Morrissy, C. J., Hodgson, A. L. and Johnson, M. A.: Vaccination with a single dose of a recombinant porcine adenovirus expressing the classical swine fever virus gp55 (E2) gene protects pigs against classical swine fever. *Vaccine*. 18:1040-1050, 2000.
 75. Sun, Y., Li, H. Y., Zhang, X. J., Chang, T. M., He, F. and Wang, X. P.: Comparison of the protective efficacy of recombinant adenoviruses against classical swine fever. *Immunol. Letters*. 135:43-49, 2011.
 76. van Rijn, P. A., van Gennip, H. G. and Moormann, R. J.: An experimental marker vaccine and accompanying serological diagnostic test both based on envelope glycoprotein E2 of classical swine fever virus (CSFV). *Vaccine*. 17:433-440, 1999.
 77. Yu, X., Tu, C., Li, H., Hu, R., Chen, C. and Li, Z.: DNA-mediated protection against classical swine fever virus. *Vaccine*. 19:1520-1525, 2001.
 78. van Gennip, H. G., van Rijn, P. A., Widjoatmodjo, M. N., de Smit, A. J. and Moormann, R. J.: Chimeric classical swine fever viruses containing envelope protein Erns or E2 of bovine viral diarrhoea virus protect pigs against challenge with CSFV and induce a distinguishable antibody response. *Vaccine*. 19:447-459, 2000.
 79. Dong, X. N., Chen, Y., Wu, Y. and Chen, Y. H.: Candidate multipptide-vaccine against classical swine fever virus induced potent immunity with serological marker. *Vaccine*. 23:3630-3633, 2005.
 80. Sánchez, O., Barrera, M., Rodríguez, M. P., Frías, M. T., Figueroa, N. E. and Naranjo, P.: Classical swine fever virus E2 glycoprotein antigen produced in adenovirally transduced PK-15 cells

- confers complete protection in pigs upon viral challenge. *Vaccine*. 26:988-997, 2008.
81. Freitas, T. R., Caldas, L. A. and Rebello, M. A.: Prostaglandin A1 inhibits replication of classical swine fever virus. *Mem. Inst. Oswaldo. Cruz*. 93:815-818, 1998.
82. Freitas, T. R., Caldas, L. A. and Rebello, M. A.: Effect of prostaglandin A1 in porcine cells persistently infected with classical swine fever virus. *J. Basic. Microbiol.* 43:468-72, 2003.
83. Tyborowska, J., Zdunek, E. and Szewczyk, B.: Effect of N-glycosylation inhibition on the synthesis and processing of classical swine fever virus glycoproteins. *Acta. Biochim. Pol.* 54:813-819, 2007.
84. Krol, E., Wandzik, I., Szeja, W., Gryniewicz, G. and Szewczyk, B.: In vitro antiviral activity of some uridine derivatives of 2-deoxy sugars against classical swine fever virus. *Antiviral. Res.* 86:154-162, 2010.
85. Zhou, B., Liu, K., Wei, J. C., Mao, X. and Chen, P. Y.: Inhibition of replication of classical swine fever virus in a stable cell line by the viral capsid and *Staphylococcus aureus* nuclease fusion protein. *J. Virol. Methods*. 167:79-83, 2010.
86. Jun, H. R., Pham, C. D., Lim, S. I., Lee, S. C., Kim, Y. S. and Park, S.: An RNA-hydrolyzing recombinant antibody exhibits an antiviral activity against classical swine fever virus. *Biochem. Biophys. Res. Commun.* 395:484-489, 2010.
87. Xu, X., Guo, H., Xiao, C., Zha, Y., Shi, Z. and Xia, X.: In vitro inhibition of classical swine fever virus replication by siRNAs targeting Npro and NS5B genes. *Antiviral. Res.* 78:188-193, 2008.