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RESEARCH ADVANCES IN AFRICAN SWINE FEVER VIRUS (minireview)

Hu Jianhe

Professor

Henan Institute of Science and Technology (Henan, China)

ORCID: 0000-0002-6768-0851

xxjianhe@126.com

Rebenko Halyna

PhD in Veterinary Sciences, Associated Professor

Sumy National Agrarian University (Sumy, Ukraine)

ORCID: 0000-0002-1884-4901

rebenko.halina@gmail.com

Zhang Jingjing

Veterinary Medicine Student of the Joint Master's Degree Program

Henan Institute of Science and Technology of China

and Sumy National Agrarian University of Ukraine

African swine fever remains one of most economically threatened diseases that has been hurting to the swine industry in Ukraine since 2014 and in China since 2018. African swine fever is an acute, highly lethal infectious disease caused by African swine fever virus, which has occurred and spread in many countries around the world, causing a catastrophic blow to the swine industry in the affected countries. ASFV is characterized of large genome, encoding 150-200 proteins, including variety of immunoregulatory proteins, which can resist immunity. African swine fever virus mainly enters pigs through the respiratory and digestive tract. The target cells infected are mainly mononuclear-macrophages, and the receptor is still unclear. Research on the development of diagnostic techniques and tests related to African swine fever are continuing and their proper using is crucial. There are many studies on African swine fever virus vaccines, including inactivated vaccines, attenuated vaccines, subunit vaccines and genetic vaccines. But so far these vaccines have not been able to protect domestic pigs from African swine fever virus infection. The article mainly reviews the researches of ASF virus, epidemiology, pathogenesis, diagnostic techniques and attempts to vaccine`s develop, that provides theoretical basis for the prevention and control of ASF.

***Key words**: African swine fever; African swine fever virus; vaccine; porcine infectious disease.*

Introduction

Recently, all farmers and stakeholders in the swine industry are threatened by the most dangerous transboundary disease with high economic losses - African swine fever (ASF). As can be known from OIE's through their Early Warning System, 25 Countries/Territories notified outbreaks: 11 in Europe (Bulgaria, Belgium, Hungary, Latvia, Moldova, Poland, Romania, Russia, Serbia, Slovakia and Ukraine); 10 in Asia (China (People's Republic of), Indonesia, Korea (Democratic People's Republic of), Korea (Republic of), Laos, Myanmar, Philippines, Russia, Timor-Leste and Vietnam) and 4 in Africa (Cote D'Ivoire, Kenya, South Africa and Zimbabwe) [report N33 December 2019].

The pork industry in Ukraine remains vulnerable to ASF outbreaks mostly because of low biosecurity measures in individual farms (households and smallholder farms) (Rebenko H., Tytova T., 2018). Due the outbreaks of ASF the number of pigs that are holded in small-scale pork production farms decreased by 1 million heads: from 3.6 million in 2015 year to 2.6 million in 2019 year (Yurchenko O, 2019).

According to Chinese Government statistics the 26% year-on-year decline in the national pig herd (in the middle of 2019) are registered. China has around 50% of the global pig herd and accounts for around 50% of global pig meat consumption. That is why the appearance of ASF in China will have a significant impact on global agricultural markets (Nathan Pitts, Tim Whitnall, 2019).

For effective control of disease spreading it seems important to review latest information about African swine fever and to improve understanding of the disease dynamics in affected regions.

The **aims** of the research are the gathering and processing of information about African swine fever, their current presence, distribution and threaten. As well as considering the measures of the disease control.

Materials and methods. Investigations were based on the literature systematization, collection of the official information from reports and analytical processing of data.

African swine fever (ASF) is an acute, heat, highly contagious, ultra-high lethal disease caused by African swine fever virus (ASFV). Once the disease occurs, no medicine can cure, and the mortality rate can reach 100%. It belongs to the World Organization for Animal Health (OIE) Class A disease (Shuang Su, Xuefeng Lv, Meng Li, 2011). ASFV is the only member of the African swine fever virus family and the African swine fever virus genus. It is a double-stranded DNA arbovirus that can proliferate in the blunt-edge carp. It has some characteristics of iridescent virus and poxvirus. There are 1 serotype and 22 genotypes. ASFV is a large (greater than 200 nm), enveloped, icosahedral double-stranded DNA virus with a linear genome. Different strains have different sizes of genomes, generally between 170 kbp and 193 kbp, encoding 150~200 proteins with repeats at the end of the genome (Tulman, E. R., Delhon, G. A., Ku, B. K. & Rock, D. L., 2009, Dixon, L. K., Chapman, D. A., Netherton, C. L. & Upton, 2013, Alonso, C. et al., 2018)

ASF is widely spread and has a wide distribution of time and space. The outbreaks since 2007 year were Czech, Polish, Ukraine, Georgia, Armenia, Azerbaijan, Belarus, Lithuania, Latvia, Estonia, Moldova, Romania, Côte d'Ivoire, South Africa, Mali, Burundi, etc. Studies have shown that the ASF epidemic in the Caucasus and Russia has a high prevalence, and its epidemic trend is long-term and unfavorable (Penrith M L, Guberti V, Depner K, et al., 2011, Cwynar, P., Stojkov, J., Wlazlak, K., 2019). On August 3, 2018, the ASF epidemic in Shenyang, Liaoning, China, was confirmed by the National Reference Laboratory (Qinghua Wang, Weijie Ren, Jingyue Bao, et al., 2018).

Because the ASFV virulent strain genome can encode a variety of proteins to interfere with the host's natural immune system, so as to inhibiting and evading the host's immune response, creating favorable conditions for its own proliferation and spread, there is no effective vaccine for ASF prevention and treatment (Perez-Nunez, D. et al., 2015). Therefore, the development of vaccines is of great significance in controlling the disease. In addition, pathogenicity and pathogenesis research as an important part of animal virus research is the theoretical basis for studying animal diseases. This paper closely follows the new development trend of ASF international epidemic situation, and summarizes the research situation of ASFV from pathogens, epidemiology, pathogenic mechanism, diagnostic technology and vaccine, and provides theoretical basis for the prevention and control of ASF.

Etiology. ASFV is the only member of the African swine fever virus family and the African swine fever virus genus, and has similarities with certain features of the iridescent virus family and the poxvirus family. ASFV is a single-molecular linear double-stranded DNA virus, encapsulated by a capsule, icosahedral symmetrical, with a diameter of only 175-215 nm. There is a hole in the capsid center of the virus particle, making its structure a special six hexagon prism (Dixon L.K., Abrams C.C., Chapman D.G., et all, 2008). The ASFV genome is 170-190 kb in length and has 151 open reading frame ORFs encoding a total of about 150-200 proteins. The mature particles of the virus contain more than 50 major proteins, which play an important role in the infection process (Jia, N., Ou, Y., Pejsak, Z., Zhang, Y. & Zhang, J., 2017). Among them, P72 accounts for 1/3 of the total protein volume of virions, has a conserved protein sequence, and has good antigenicity. It can produce high titer anti-P72 antibody after infection, and is usually used for serological diagnosis of African swine fever. According to the nucleic acid sequence of the C terminal of the P72 gene, African swine fever can be divided into 24 genotypes (Achenbach, J. E. et al., 2017). The genome of the African swine fever virus is susceptible to variability, and the genetic processes are diverse, making it difficult to induce the production of neutralizing antibodies, so the serotype is not yet classified. By using restriction endonuclease digestion analysis, it was found that ASFV from America and Europe is the same genotype, while the isolated African strain has multiple genotypes, indicating that there were significant genotype differences between strains from different regions. The first strain to determine the full sequence of the genome is a non-toxic Spanish strain of BA71V, often used as the subject of laboratory study (Rodríguez, J. M., Moreno, L. T., Alejo, A., Lacasta, A., Rodríguez, F. and Salas M.L., 2015). At present, the whole ASFV gene sequences of 11 strains have been determined. One of them is virus (ASFV/Kyiv/2016/131) isolated from the spleen of a domestic pig in Ukraine with a lethal case of African swine fever. Using only long-read Nanopore sequences, we assembled a full-length genome of 191,911 base pairs in a single contig. (Kovalenko G., Ducluzeau, A-L, Ishchenko, L., Sushko, M et al., 2019)

ASFV is highly resistant to the external environment and can withstand a fairly wide pH (pH 4~13). It lasts for half a year in blood, feces and tissues. It lasts for up to 3 months in infected raw or undercooked pork products and can survive for several

years in frozen meat (Junwei Wang, Zhiliang Wang, 2010). The virus can be inactivated at 60°C for 20 minutes and can be inactivated a lipid solvent and a partial disinfectant (p-phenyl phenol disinfectant).

Epidemiology. European wild boars, warthogs, jungle pigs, giant forest pigs, sick pigs, rehabilitated domestic pigs and African soft palate are long-term sources of ASFV infection (Jori, F.; Bastos, A.D., 2009). Blome, S.; Gabriel, C.; Beer, M., 2013). Once the disease is established as endemic in an area, animals that survive for over a month are able to recover from the infection and even remain sub-clinically infected. But the role of survivor animals in the maintenance of the disease is still unclear.

The whole blood, tissues, secretions and excretions of the affected pigs and dead pigs contain viruses. Studies have shown that oral administration of the virus (dosage of10^5 HAD50/mL) or nasal (dose of $10^{2.9}$ HAD50/mL) can cause infection in pigs; the acute infection period does not exceed 7 to 13 days, and the latent infection only appear in Europe before. Some pigs infected with attenuated strains; wild boar infections lasted for 21 days (Guinat, C. et al., 2016).

Africa's Ornithodoros soft palate not only carries ASFV for a long time, but also transmits pathogens vertically to offspring (XiaoJun Yang, Ze Chen, Jingze Liu, 2008). The ability of the ASFV to survive within particular ecosystems is defined by the biology of its wild host populations and also the features of livestock production systems, which influence host and vector species densities and interrelationships (Costard, S.; Mur, L.; Lubroth, J.; Sanchez-Vizcaino, J.M.; Pfeiffer, D.U., 2013).

ASFV mainly has three methods of spreading: direct contact propagation, indirect contact propagation and vector tick transmission. Direct contact spread involves domestic pigs and wild boars. Whether it is a domestic pig or a wild boar, once it is in the same line as a healthy pig after illness, it will cause infection in the herd. Wild boar plays an important role in ASFV transmission. The body of the wild boar that died of the disease and the soil in which the corpse rots are important factors in the spread of ASFV (Jori, F.; Bastos, A.D., 2009). However, wild boars in different countries have played a different role in ASFV transmission. For example, when studying the ASFV epidemic in Sardinia, Italian scientists believed that wild boars did not play a big role in the spread of ASFV. They believed that as long as the swine epidemic is extinguished, the wild boar epidemic will be purified (Mur, L. et al., 2016).

Indirect contact transmission: one is to feed waste containing infectious meat; the other is through illegal trade channels to purchase infected pigs, contaminated litter or feces, swill, etc. Contaminated vehicles, equipment, and clothing may also cause ASFV transmission when environmental pollution is severe. The spread of ASFV may cause by vaccination and drug treatment, such as poor disinfection or replacement of contaminated needles. Fresh grass and seeds contaminated by wild boar excreta can also cause spread of infection. African soft palate infects ASFV mainly by sucking infected pigs blood. For some virus isolates with high-propagation rate, almost 100% of susceptible sputum can replicate and maintain high titers at 4 weeks after the blood is saturated, and the virus in the sputum can also be transmitted horizontal and vertical propagation by male and female mating, spawning, etc (Beltrán-Alcrudo, D.; Guberti, V.; De Simone, L.; De Castro, J.; Rozstalnyy, A.; Dietze, K.; Wainwright, S.; Slingenbergh, J., 2009; Costard, S.; Mur, L.; Lubroth, J.; Sanchez-Vizcaino, J.M.; Pfeiffer, D.U., 2013).

In the affected areas, other blood-sucking insects, such as mosquitoes and flies, can also mechanically spread ASFV. The flies can spread ASFV after inhaling the blood of infected pigs for 24 hours, and can carry ASFV with high blood titer for more than 48 h. Blood louse can also carry viruses. In 1921, Montgomery managed to infect white rats, guinea pigs, rabbits, cats, dogs, goats, sheep, cattle, horses, pigeons and other animals are all unsuccessful. However, in 1956, Velho reported that pigs were killed by ASFV after the 26th generation of the rabbits. This indicates that the virus is only susceptible to pigs and does not cause infection to other animals (Guinat, C. et al., 2016).

Some researchers consider that African swine fever has high morbidity in naïve pig populations and can result in very high mortality (Costard, S.; Mur, L.; Lubroth, J.; Sanchez-Vizcaino, J.M.; Pfeiffer, D.U., 2013). But other researchers concern that defining ASF as “a highly contagious disease” can be delusive because it leads to false expectations and then underestimation of the problem (Guberti, V., 2018).

Pathogenic mechanism. ASFV enters pigs mainly through the respiratory tract and digestive tract. After the virus infects the body, it first proliferates in the tonsil, and then invades the whole body with blood and lymphatic system, triggers viremia, and replicates in vascular endothelial cells and macrophages. Invasion of blood vessels and lymphatics vessels causes pathological changes such as serous exudation, hemorrhage, thrombosis and necrosis in the corresponding organ tissues. pigs that died of diseases often show symptoms such as systemic organ and organ hemorrhage, impaired immune system, and decreased lymphocytes (Sanchez, E. G. et al., 2012). The interaction between ASFV and different hosts determines the pathogenicity of the virus to different hosts. For domestic pigs, the pathogenicity of different strains to domestic pigs is different. After the body is infected with the virus, there are different clinical symptoms such as acute death to subclinical infection (Malogolovkin, A. et al., 2015). For wild pigs, it shows different characteristics from domestic pigs. wild boars often show no obvious symptoms after infection with ASFV and only accompanied by hypoviremia. In endemic areas, most adult wild boar sera show ASFV-positive and persistent infection, but the amount of detoxification is low or not detoxification (Pietschmann, J. et al., 2016). For ticks, it mainly infects ASFV by ingestion the blood of poisoned pigs. The phagocytic cells in the intestinal epithelial cells of ticks are the initial sites of virus replication. Subsequently, virus replication occurs in undifferentiated intestinal cells, after 2~3 weeks, the virus spread to other tissues. The study found that susceptible ticks after 4 weeks of blood fullness, virus replication occurred in the body, and maintains a high virus titer, through the bite can spread the virus from the ticks’ body to susceptible pigs (Luka, P. D. et al., 2016; Burrage, T. G., 2013; Bernard, J. et al., 2016).

The main target cell of ASFV infection are porcine mononuclear-macrophages. Therefore, mononuclear-macrophages are the first place to detect the virus, followed by dendritic cells, endothelial cells, megakaryocytes, platelets, neutrophils and hepatocytes, can also detect ASFV (Munoz-Moreno, R., Galindo, I., Cuesta-Geijo, M. A., Barrado-Gil, L. & Alonso, C., 2015). Studies have found that there are many viral binding sites on the surface of ASFV susceptible cells, and the invasion process of the virus requires cell surface receptor mediated, in which cellular lipid cholesterol participates in the process of ASFV infection (Cuesta-Geijo, M. A. et al., 2016). After ASFV enters the cell, the virus core is transported around the nucleus. First, the enzymes and protein factors encapsulated in the virion are used for transcription and translation of early mRNA, and the required DNA polymerase and other materials are provided for virus replication. After 6 hours of infection, ASFV begins to replicate in the cytoplasm, and its replication in a manner is very similar to that of poxvirus (Hernaez, B., Guerra, M., Salas, M. L. & Andres, G. 2016). After 3~4h of ASFV infection, the replication of virus DNA is beginning in nucleus, it produces a replicative intermediate. After that, it moves to the cytoplasm, forming large intermediates that mature in the cytoplasm's "viral factory" (Dixon, L. K., Chapman, D. A., Netherton, C. L. & Upton, C., 2013). The infection process of ASFV involves the rearrangement of vimentin. The microtubule-dependent vimentin aggregates in a star shape at the viral assembly site and then localizes to the center of the microtubule tissue. When the viral DNA replication begins to star structure into a cage structure. Structure that blocks the transfer of viral components into the cytoplasm and aggregates late viral structural proteins into viral assembly sites (Netherton, C. L. & Wileman, T. E., 2013). The formation of ASFV virions occurs in the "virus processing plant" area around the nucleus, where P54 plays a very important role in viral infection, especially when viral proteins are transformed into viral envelope precursors via the endoplasmic reticulum membrane (Rodriguez, J. M., Garcia-Escudero, R., Salas, M. L. & Andres, G., 2004). Mature virions are arranged along microtubules after being formed in the "virus processing plant". The virions are transported to the cell membrane by conventional kinesin in the tubulin system and released them from the cells by budding (Galindo, I. et al., 2015).

Vaccine research. In view of the huge impact of ASFV on the pig industry, the national economy and food safety, vaccine development has become the subject of research by many scientists, including inactivated vaccines, attenuated vaccines, genetically engineered vaccines, subunit vaccines and nucleic acid vaccines (Rock D L., 2017). (Table 1.).

Table 1. The review of attempts to develop of vaccine for African swine fever prevention

N	Type	Conclusions from the research results	Authors
1	***Inactivated vaccine research***	The inactivated vaccine was developed after the first discovery of the African swine fever virus, but have not been effective. Inactivated vaccines are difficult to stimulate the innate immune system to induce high levels of cellular immunity due to their inherent defects. Although some of them can stimulate antibodies produced by pigs, it is difficult to detect the presence of neutralizing antibodies. With the deepening of ASF research, the results showed that the use of the new adjuvant Polygen TM or Emulsigen-D could not resist ASFV attacks.	Blome, S., Gabriel, C. & Beer, M. (2014).
2	***Subunit vaccine***	The ASF subunit vaccine uses a baculovirus as an expression vector to express a protective antigen of an African swine fever virus with a neutralizing epitope in a prokaryotic or eukaryotic cell, and then binds the obtained protein or polypeptide to an antigen presenting cell in order to induce higher anti-ASFV neutralizing antibodies. There are many kinds of structural proteins encoded by ASFV. Three important antigenic proteins P72, P54 and P30 have been found to have protective effects. Antibodies that produce P72 and P54 prevent viral adsorption, and antibodies to P30 prevent viral endocytosis. Recombinant proteins expressed in P30, P72 and P54 only delay clinical symptoms and reduce viremia levels, providing only 50% protection against effective protection. ASFV has complex structural proteins and immune evasion mechanisms, and it is difficult to obtain good immunoprotective effects against neutralizing antibodies produced by the above three antigens.	Gomez-Puertas, P. et al., (1996). Shengqiang Ge, Xiaodong Wu, Zhicheng Zhang et al., (2016). Ming Ren, Xiaoyu Guo, Jing Wu, et al., (2018).

3	***Viral live vector vaccine and live attenuated vaccine***	At present, the viral live vector vaccine is mainly expressed in the induction of immune response. Related studies have used rabies virus, poxvirus or adenovirus as vectors to express ASFV protective antigen gene in order to obtain better cellular immunity and cytotoxic T lymphocyte (CTL) responses. In order to obtain an ideal immune response, a "cocktail" type of mixed immunization was used, but these studies did not carry out a challenge protection test, and the protective effect needs to be further verified to ensure the feasibility of the vaccine development method. Live attenuated vaccines (LAV) can be divided into three categories according to the source of the strain: passage attenuated strains, natural attenuated strains and recombinant attenuated strains. During the epidemic of ASF in Spain and Portugal, side effects such as pneumonia, abortion and death occurred after immunization of animals with attenuated passages. Subsequently, Krug et al. subcultured the isolate ASFV-G in Vero cells, and the virus virulence was completely lost when transmitted it to the 110th generation, but it was not effectively protected by inoculation into domestic pigs. Immunization of animals with natural attenuated strains can induce cross-immunoprotection of different isolates of ASFV type I, but at the same time have incalculable side effects, and there are many potential safety problems.	Lopera-Madrid, J. et al., (2017). Arias, M. et al., (2017). Krug, P. W. et al., (2015).
4	***Nucleic acid vaccine***	Also known as DNA vaccine, the development technology is not very mature. Argilaguet et al. cloned the P72, P30 and P54 genes of ASFV into eukaryotic expression vectors to prepare DNA vaccines for ASF, but DNA vaccines do not provide protection against infection after immunization of pigs. Fusion of the single-chain variable region gene of the specific antibody expressing ASFV P30 and P54 genes and porcine leukocyte antigen II in eukaryotic expression vectors allows some animals to obtain immunoprotection. Recent studies have found that ASFV genomic DNA plasmid expression libraries provide 60% protection and require multiple DNA vaccines constructed with ASFV antigens for higher immunoprotection. In this regard, we should look for more and improve the protection level of nucleic acid vaccines.	Argilaguet, J. M. et al., (2012). Sunwoo, S-Y., Pérez-Núñez, D., Morozov, I. et al. (2019)
5	***Vaccine based on ASFV receptor and protective antigen***	Receptors and key antigens that currently mediate ASFV invasion of cells are still unclear. The cell challenge protection test has found that CD163 is a receptor of ASFV, and the expression level of CD163 is positively correlated with the degree of ASFV infection, but transgenic pigs with CD163 gene knockout by CRISPR/Cas9 do not show effective resistance to ASFV. Prove that CD163 is not a receptor of ASFV. Studies have shown that p12 protein may be a key antigen that mediates viral invasion, but in ASFV infection cells experiment, the addition of excess p12 antibody did not effectively block viral binding and infection, suggesting that p12 is not the only antigen that mediates viral adsorption. Studies have shown that p32, p72 and p54 also play important roles in the process of virus adsorption, p72 and p54 promote the binding of viruses and macrophages, while p32 contributes to virus internalization. What are the receptors for ASFV and need to be further explored.	Gallardo, C. et al., (2009). Popescu, L. et al. (2017).
6	***Vaccine for oral immunization***	Oral immunization of wild boar with a non-hemadsorbing, attenuated ASF virus of genotype II isolated in Latvia in 2017 (Lv17/WB/Rie1) conferred 92% protection against challenge with a virulent ASF virus isolate (Arm07). This is the first report of a promising vaccine against ASF virus in wild boar by oral administration. Further studies should assess the safety of repeated administration and overdose, characterize long-term shedding and verify the genetic stability of the vaccine virus to confirm if Lv17/WB/Rie1 could be used for free-ranging wild boar in ASF control programs.	Barasona, J., Gallardo, C., et al. (2019).

There were many attempts to develop the vaccine that can provide protection against ASF virus, but protection was not 100%. The vaccine development and production has failed, mainly because ASFV has a complete anti-host vaccine response mechanism. The ASFV genome encodes a variety of proteins that interfere with the host's natural immune system, thereby inhibiting and evading the immune response, creating powerful conditions for its own proliferation and spread. In order to develop a vaccine that stimulates an effective anti-ASFV T-cell response Netherton, C. with collegs investigated which of the >150 viral proteins are recognized by the cellular immune response. The proteins capable of inducing ASFV-specific cellular and humoral immune responses in pigs were identified. Pools of viral vectors expressing these genes did not protect animals from severe disease, but did reduce viremia in a proportion of pigs following ASFV challenge (Netherton, C., et al., 2019).

Diagnosis. The symptoms and lesions of African swine fever and classical swine fever are very similar, and the mortality rate of the disease is close to 100%, and the economic loss is huge, so there needs to be a rapid and effective

laboratory differential diagnosis. At present, there are mainly the following main detection methods:

First, PCR and real-time quantitative PCR detection methods for the conserved region of P72 gene can be used for rapid and effective detection of porcine spleen, blood, lymph nodes and other tissues (Hongli Li, Jinshan Cao, Junwei Wang, et al., 2012, Jianhua Wang, Zhizhen Dong, Dan Zhao et al., 2016).

The second is the ELISA method, which is applicable to the sandwich ELISA detection method for P72 protein in the spleen, blood, lymph nodes and other tissues. It also has whole virus or P72, P54 and other antigen coatings, and ELISA method for detecting serum antibodies. The third is the blood adsorption test. African swine fever virus has blood adsorption characteristics, and the red blood cells can be adsorbed on the infected macrophages to form a characteristic garland(Yunhao L., et al., 2014). The fourth is the direct immunofluorescence test, which is used to check pathogens in spleen, lymph nodes and other tissue sections. It has direct, rapid and effective characteristics, but only 40% of the subacute and chronic infections are detected because of the long course of disease. Some viruses have formed immune complexes, which are difficult to detect. The fifth the detection method is colloidal gold test paper, which has the advantages of rapidity, sensitivity and specificity, and is especially suitable for rapid clinical diagnosis. Zhang Xinyu et al. purified the ASFV p54 recombinant protein by using colloidal gold and spraying it on the fiberglass pad. The staphylococcal A protein (SPA) and anti-p54 polyclonal antibody were used as detection lines and quality control lines to prepare colloid gold immunochromatographic test strip for detecting of ASFV p54 antibody. The sensitivity of the test strip reached 200 ng/mL (Xinyu Z., Weiyong Z., Shanyuan Z., et al., 2014).

Outlook: ASF is a type of infectious disease with extremely complex pathogenesis and clinical symptoms. If we fail to detect and implement strict control measures at an early stage, they will spread rapidly and continue to spread, causing serious economic losses to society. The viability of ASF in ecosystems is determined by the relationship among the host, density of the vector, and habitat of the wildlife that affect ASF. The characteristics of livestock production system and the habitat of the soft ticks can also be affected.

There are three main characteristics of ASF epidemic:

1.In the spread of ASF, human factors account for a large proportion (such as hidden infections and sub-clinical infections when selling pigs);

2.low biosafety populations are more vulnerable to ASF invasion (the retail pigs are the main ASF attack group);

3.ASF is likely to spread to areas bordering epidemic areas. For these reasons, to better prevent and control the disease, it is necessary to have sufficient knowledge of its epidemiology in order to implement targeted measures.

Early vaccine research has focused on inactivated vaccines and attenuated vaccines. Numerous studies have shown that inactivated vaccines can induce antibodies in the body, but they have little protection. Although the attenuated vaccine has a certain protective effect on homologous strong virulence, due to the high variability of ASFV, its safety is very poor, which often causing diseases, leading to serious spread of pathogens. Spain and Portugal tried to use attenuated vaccines in the early days of ASF's introduction, but they all ended in failure. The use of attenuated vaccines led to large-scale and long-term epidemics, which seriously affected the process of disease control and elimination. In the past 20 years, molecular biology and immunology techniques have also been used to conduct a number of exploratory studies on vaccine and immune problems of ASF. ASFV in the process of adsorption and entry into cells, and P30, P54, P72 and other viral proteins are involved. Therefore, most of the ASF subunit vaccines and recombinant vaccines tend to select these genes, but subunits developed with baculovirus and other expression systems. Vaccines can only delay the onset of clinical symptoms and reduce the level of viremia to a certain extent, but it does not produce sufficient protection.

At present, detection techniques for ASFV mainly include viral nucleic acid detection technology and immunological technology based on viral antigen/antibody reaction. Immunological detection of antibodies can understand the process of ASFV infection, occurrence, and development, but antibodies will only appear after the virus has been infected for a certain period of time. Therefore, antibody detection methods such as ELISA have certain limitations. Molecular biology techniques such as PCR and fluorescence quantitative PCR can detect viral nucleic acid in the early stage of pigs infection with ASFVV, and play an important role in the early detection of ASFV. Among them, the PCR method is simple to operate, high sensitivity, and good reproducibility, and requires certain instruments and reagents, and is suitable for general laboratory use. Fluorescence PCR method combines PCR with fluorescence detection to overcome the shortcomings of conventional PCR, such as easy contamination, electrophoresis after amplification, and viral nucleic acid can be accurately quantified of and the detection sensitivity is higher than the conventional PCR method. In short, ASFV's laboratory testing methods have their own advantages and disadvantages, but the testing results of various methods are required to be accurate, fast and sensitive, so as to take timely, effective prevention and control measures. It is believed that with the continuous development of molecular biology and immunology technology, the ASFV laboratory diagnostic method will be continuously improved, and further provide technical support for the monitoring and comprehensive prevention and control of African swine fever.)

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***Ц. Ху**, професор, Хенанський інститут науки і технологій (Хенань, Китай)*

***Г. Ребенко**, доцент, Сумський національний аграрний університет (Суми, Україна)*

***Ц. Чжан,** студентка магістратури, Сумський національний аграрний університет (Суми, Україна) та Хенанський інститут науки і технологій (Хенань, Китай)*

Нові досягнення у дослідженні вірусу африканської чуми свиней (огляд)

У статті розглянуті публікації останніх років щодо африканської чуми свиней, яка залишається однією з найбільш економічно значущих хвороб, що завдають надзвичайної шкоди свинарству. Епізоотія АЧС в Україні існує з 2014 року, а в Китаї зареєстрована з другої половини 2018 року. АЧС - захворювання, яке на сьогодні зареєстроване в багатьох країнах Європи, і продовжує поширюватися двома шляхами: з дикими кабанами та з інфікованою свининою та продукцією з неї. А, зважаючи на інтенсивну міжнародну торгівлю та рух людей, вже загрожує іншим вільним від вірусу континентам. Вірус африканської чуми свиней характеризується великим геномом, що кодує 150-200 білків, серед яких виявлені різноманітні імунорегуляторні білки, функцією яких є запобігання чи уповільнення імунних реакцій та утворення специфічного імунітету. Основний шлях проникнення вірусу до організму свиней через дихальний та травний тракти, але клітинами-мішенями для вірусу є в основному мононуклеарні макрофаги, а рецепторний механізм досі залишається незрозумілим. Діагностичні методики та тести для виявлення вірусу африканської чуми свиней розроблені, але їх удосконалення та раннє (або своєчасне) застосування є вирішальним. Існує багато досліджень щодо вакцин проти вірусу африканської чуми свиней, включаючи інактивовані вакцини, які навіть за використання сучасних ад'ювантів не змогли вплинути на клітинний імунітет, а незначні рівні віруснейтралізуючих антитіл не захищають тварин від захворювання. Для виготовлення субодиничних вакцин використовували білки P72, P54 та P30, що підвищують рівень віруснейтралізуючих антитіл у імунізованих свиней, проте навіть цей рівень зміг забезпечити лише затримку розвитку серйозних клінічних ознак хвороби, зменшували рівень віремії та давали не більше 50% захисту. Спроби розробити живі аттенуйовані вакцини завершувалися або усвідомленням неефективності імунного захисту або значною кількістю побічних ефектів. Для розробки генно-інженерних вакцин використовували різні віруси-вектори, що повинні були підсилити клітинну імунну відповідь. Але поки що ці вакцини не змогли захистити домашніх свиней від вірусу африканської чуми свиней. Виявлена кореляція між рівнем експресії CD163 в клітинах свиней та інтенсивністю інфекції давала надію, що вилучення CD163 як рецептору для адгезії вірусу АЧС зможе зробити свиней несприйнятливими до хвороби. Проте, виведені трансгенні свині не виявили стійкості до вірусу. Обнадійливі попередні результати отримані при пероральному використанні вакцини з латвійського штаму Lv17/WB/Rie1, але випробування ще не завершені. Таким чином, пошук способів розробити ефективну вакцину триває.

***Ключові слова:** африканська чума свиней; Вірус африканської чуми свиней; вакцинація; інфекційні захворювання свиней.*

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