

Analysis and selection of genes encoding the expression of protective antigens of the African swine fever virus for further development of a vaccine based on adeno-associated virus vector

Marina Efimova^{a,b}, Elena Zakirova^c, Vladimir Kuzmin^d, Alexander Aimaletdinov^c, Lenar Garipov^a, Kamil Khaertynov^b, Yuri Davidyuk^c, **Eduard Shuralev^{a,b,e}**, Albert Rizvanov^c & Rustam Ravilov^a

^a Kazan State Academy of Veterinary Medicine named after N.E. Bauman, Kazan, Russian Federation

^b Kazan State Medical Academy – Branch Campus of the FSBEI FPE RMACPE MOH Russia, Kazan, Russian Federation

^c Institute of Fundamental Medicine and Biology, Kazan Federal University, Kazan, Russian Federation

^d Saint-Petersburg State Academy of Veterinary Medicine, St. Petersburg, Russian Federation

^e Institute of Environmental Sciences, Kazan Federal University, Kazan, Russian Federation

Presenting Author Email: eduard.shuralev@mail.ru

Abstract

African swine fever (ASF) is a hazardous, highly contagious disease of domestic and wild Suidae, characterized by rapid spread, high mortality level of infected animals and threat to global food security. The natural focal potential of ASF is due to the spontaneous susceptibility of wild boars (*Sus scrofa*) and transmission of infection by argasid ticks that act as vectors and reservoirs of infection. The development of vaccines is considered to be the most effective measure to prevent and control the spread of ASF virus in the wildlife. Current approaches to the development of an ASF vaccine are focused on vaccines based on viral vectors, in particular, an adeno-associated viral vector. However, the key to the efficacy of such vaccines is the choice of the protective antigens.

The aim of the research was to select the genes encoding the expression of ASF virus protective antigens. The data was retrieved using a systematic review. According to that, the largest number of studies in the world is aimed at developing vaccines based on such antigens as viral proteins P72, p54 and P30, encoded by the genes B646L, E183L and CP204L, respectively. The viral proteins pp60, EP402R, and p10, encoded by the CP530R, EP402R, and K78R genes, respectively, are also promising antigens for vaccine development.

Phylogenetic analysis of the nucleotide sequences of 6 genes and the amino acid sequences of the proteins encoded by them revealed that all ASF virus strains identified in Russia and a number of Eastern European countries belong to genotype II, and the sequence identity values are equal or close to 100%. Summarized data leads to that the multi-antigen vaccine against ASF can become an effective means of anti-epidemic measures to eliminate natural focus of infection in wildlife both in Russia and neighboring countries.

Keywords: African swine fever, wildlife, natural focus of infection, vaccine, phylogenetic analysis