African Swine Fever Virus Genome Detection Using Real Time Q PCR Polymerase Chain Reaction Method- Comparison of two Sample Specimen (Blood and Organs)

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Abstract. The study aims to show the result of CT (threshold cycle) data collected over a three-year study conducted in the molecular biology laboratory of D.S.V.SA Constanta using the Real Time Polymerase Chain Reaction method to demonstrate the pathogenetic effect of African swine fever virus during the replication and vascular changes present in all affected organs.

Keywords: Polymerase Chain Reaction (PCR), African Swine Fever virus

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1. Introduction

African Swine Fever (ASF) is a contagious viral disease of domestic pigs and wild boars. It is a notifiable disease to OIE (World Organization for Animal Health). Since Eustace Montgomery had first studied the virus in 1921 the reports had shown a pattern of significant increase of outbreaks around the globe. The virus is highly pathogenic with 100% mortality in pigs. There is no effective vaccine or treatment for this disease. In Europe many countries have reported the disease as a first occurrence to OIE through WAHIS (World Animal Health Informational System WAHIS) from 2016-2022: Moldova notified the disease in September 2016, Check Republic in June 2017, followed by Romania 2018, Hungary in April 2018, Bulgaria in August 2018, Slovakia in July 2019, and most recently Serbia in January 2020 and Greece in February 2020. Since January 2020, 8 countries have reported ASF as a first occurrence in the country, while 12 countries reported its spread to new zones (Hungary, Italy, Latvia, Moldova, and Romania). This highlights a continuous spread of the disease into new countries, and new zones in countries already affected. In Asia and the Pacific, China notified the presence of the disease for the first time in August 2018, Philippines in July 2019, Korea in September 2019 Indonesia in November 2019 (OIE World Organization for Animal Health[1]

African Swine Fever is a large icosahedral DNA virus which replicates predominantly in the cytoplasm of infected cells. The ASF double - stranded DNA genome varies in length from abought 170 to 193 kbp depending on the isolate and contains between 150-167 open readings frames (ORF)[2] .These are closely spaced and

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