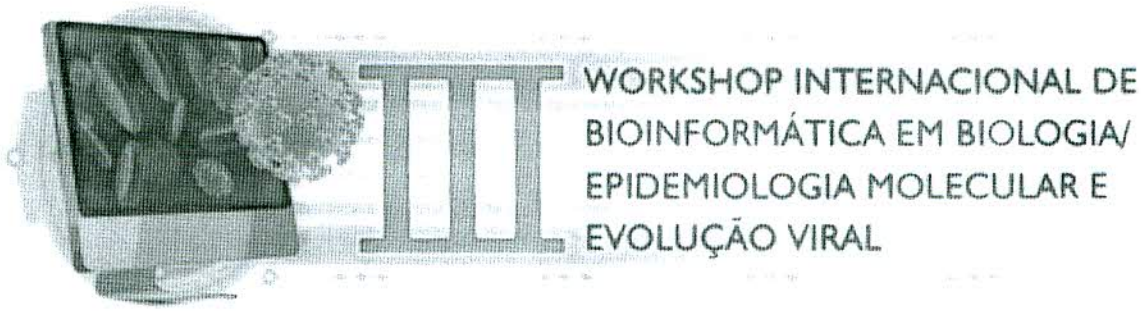

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ABSTRACT BOOK

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THE ROLE OF SOUTH AMERICA IN THE GLOBAL DISSEMINATION DYNAMICS OF INFLUENZA A(H3N2)

The limited influenza A(H3N2) genetic data available from the Southern Hemisphere (particularly from Africa and Latin America), imposes an obstacle for the accurate reconstruction of its dynamics and global dissemination. Our objective was to assess the role of South America in the global dissemination of influenza A(H3N2) during 1999-2012 years. A total of 153 sequences of the HA1 portion of the hemagglutinin gene (HA) of influenza A(H3N2) viruses collected in temperate (Southeast, South) and tropical (Northeast) Brazilian regions between 1999 and 2012 were newly generated and combined with sequences available from other South American countries, Australia, Hong Kong, United Kingdom and the United States (US). Bayesian phylogeographic reconstruction of worldwide influenza A(H3N2) dissemination dynamics showed that South American countries are tightly connected each other and to the US, as well as, maintains limited viral exchanges with other geographical regions. Within South America, we found intensive bidirectional viral exchange between tropical and temperate regions, and also migration between the different temperate regions in South America. These findings suggest that Brazil and other South American countries occupy a peripheral position in the global dissemination of influenza A(H3N2) virus and reveal a complex network of viral dissemination between different South America regions.

Abstract 24

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EVOLUTION OF NOVEL INFLUENZA A VIRUSES OF HUMAN ORIGIN IN SWINE IN BRAZIL

Although Brazil has one of the largest pig populations in the world (~ 41 million pigs), very few and scattered information about influenza A virus (IAV) infection in pigs prior 2009 is available. Previous reports have identified the influenza infection in pigs caused by H1N1 and H3N2 IAVs, but no further characterization of the virus such as viral isolation or genome sequence was performed. Since the recognition of 2009 H1N1 pandemic (H1N1pdm09) virus in pig farms in Southern Brazil in 2009, the influenza surveillance efforts in pigs have increased. As a result, a human-like H1N2 influenza virus was detected in both domestic pigs and captive wild boars in 2011. From 2009 to 2012, a total of 1881 nasal swabs and 1871 sera collected from nursery and growing pigs, and 89 lung tissue samples collected from suckling, nursery and fattening pigs from 131 pig farms located in the southern, midwest and southeast regions of Brazil were submitted to ELISA test, HI assay, RT-qPCR, virus isolation and genomic sequencing. Swine from all tested farms had antibodies to IAV. Seventy-five percent (75.2%) of sera tested by

ELISA were positive for IAV antibodies. The HI analysis revealed specific antibodies for H1N1pdm09, H1N2 and H3N2 in sera from pigs from 33 out of 48 farms. Influenza A virus was detected by RT-qPCR in 59 (3.13%) of 1881 nasal swabs. Moreover, 58 (65.16%) out of 89 lung samples with pneumonia, originated from 44 pig farms, were positive to IAV by RT-qPCR. Forty-one IAVs were isolated. Whole genome sequencing was performed for 16 IAVs, revealing five H1N2, four H3N2 and seven H1N1pdm09 IAVs. The phylogenetic relationships of each analyzed gene segments were inferred with the maximum likelihood (ML) method. The sequence analysis showed that subtypes H3N2 and H1N2 are most closely related to human seasonal H3N2 and H1N2 viruses that circulated in humans in the 1990s and early 2000s, respectively. All of these viruses had MP segments of H1N1pdm09 origin, and all other internal genes that could be sequenced were also of H1N1pdm09 origin. These novel reassortant viruses have not been detected in swine in any other countries to date and appear to be specific to Brazil. Viral diversity has further increased in Brazil via reassortment between co-circulating viruses, including H1N1pdm09. These findings highlight the importance of human-to-swine transmission in the evolution of influenza virus diversity in swine in Brazil.

Abstract 25

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HUMAN IMMUNODEFICIENCY VIRUS: ANTIRETROVIRAL RESISTANCE MUTATIONS AMONG INDIVIDUALS FROM MATOGROSSO DO SUL

The AIDS (acquired immunodeficiency syndrome) epidemic caused by human immunodeficiency virus (HIV) is a global public health problem. Universal access to antiretroviral drugs in Brazil (1996) resulted in increased survival and a significant decrease in hospitalizations related to HIV/AIDS. However, there are many obstacles to effective therapy, including severe adverse effects, limited-entry of viral replication in the drug reservoir, intrinsic host characteristics, treatment adherence, co-infection with other pathogens, and the emergence of resistant viral isolates. This project aims to identify the genetic variability of circulating subtypes, early identifying key mutations presentin protease-polymerase/reverse transcriptase regions of HIV-1 genome, relating them to the antiretroviral therapy (ART) resistance profiles in individuals infected with HIV-1. For this, the extraction will be performed using whole blood samples, targeting HIV proviral DNA, followed by nested PCR of polymerase region. Then, Sanger sequencing will be performed, followed by subtyping identification of mutations associated with drug resistance and transmission networks. It will be constructed phylogenetic tree with evolutionary history inferred by Neighbor Joining method. The evolutionary distances will be calculated usingTamura-Neimethod and evolutionary analyses will be carried out in the MEGA program version 6. The resistance profiles will be analyzed according to the guidelines of the World Health Organization (WHO), using the latest update of "Stanford Surveillance Drug Resistance Mutations Calibrated Population Resistance Tool" (CPR), available from Stanford University (USA) at the website