

The influenza A virus subtypes H1N1, H1N2 and H3N2 ,HDFx: A Novel Immunomodulator and Potential Fighter Against Cytokine Storms in Viral Flu Infections- Carica papaya Linn

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Abstract

The discovery of a new, biologic host-defense protein, “HDFx”, may provide a unique way to ameliorate and prevent the “cytokine storms” and haemorrhages seen in severe influenza infections. The influenza A virus subtypes H1N1, H1N2 and H3N2 are prevalent in pig populations worldwide. All scientific data point towards swine as the key host species for new human influenza pandemics, which have been suggested to evolve in pigs from viral genes of avian, human and porcine origin. Therefore, it is of major importance to record the evolution of swine influenza viruses in pigs, and in particular monitor hallmarks of adaptation to humans. The scope of this paper was to increase the understanding of the genetics of swine influenza virus (SIV), and to investigate the importance of different viral gene markers in association with differences in pathogenicity of two viruses of H1N2 subtype in pigs. The results from this study demonstrate, for the first time, natural reassortment in H1N2 viruses in the pig populations of Sweden. As well as India

Keywords: Ischemic Stroke, Post-Stroke Depression, Cerebral Hemodynamic, Bioelectrical Activity of the Brain, Melitor

Introduction

H1N2 viruses have an avian-like SIV H1N1 haemagglutinin (HA) and a European H3N2 SIV-like neuraminidase (NA). Nucleotide sequence comparison revealed significant differences between the two consecutive H1N2 isolates. To be able to understand the geno-typic differences observed in the genomes of these H1N2s, and to identify the genetic markers responsible for the differences, a re-verse genetic system was developed. Four recombinant SIV H1N2 viruses were constructed that displayed differences in virulence in mice, r1021 (more virulent) and r9706 (less virulent), as well as the same viruses with swapped PB1 segments. Interestingly, the current findings showed that the replacement of the PB1 segment of r9706 by that of r1021 increases the virulence of the virus that replicate with higher titer in mice lungs, while the opposite is true when PB1 r9706 is introduced into r1021. This study demonstrates that differences in virulence of swine influenza virus subtype H1N2 are attributed at least in part to the PB1 segment. The findings pre-

sented in this thesis support the observations concerning the continuous reassortment processes of SIVs in pigs, resulting in repeat-ed and independent emergence of certain HA/NA combinations. This may lead to emergence of new viral variants of severe patho-genicity of pigs. Continuous and efficient surveillance and further detailed genetic and phenotypic analysis can help to identify such novel viral variants, having more potential to cross species barriers and to pose health risks even to humans and to other host species A disturbing trend in antimicrobial-antiviral resistance is the ad-vent of “superbugs” which often complicates the treatment of flu-immunocompromised patients. To this must be added the nu-merous hospitalizations and increased morbidity from contaminat-ed meats, vegetables, seafoods, and dairy products.

Many of the emerging types of avian flus [e.g. H1N1, H2N2, H3N2, A(H10N8)] have a very serious hemorrhagic component to them which complicates effective treatment. Any new, effective