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Mucosal vaccination of conserved sM2, HA2 and cholera toxin subunit A1 (CTA1) fusion protein with poly gamma-glutamate/chitosan nanoparticles (PC NPs) induces protection against divergent influenza subtypes

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To develop a safe and effective mucosal vaccine against influenza A viruses, gene construct of the highly conserved matrix protein-2 (sM2) and fusion peptide of hemagglutinin (HA2) were successfully joined to the well-known mucosal adjuvant cholera toxin subunit A1 (CTA1). It is possible that the intranasal administration of the recombinant fusion protein sM2HA2 or the recombinant fusion protein resulting from joining gene constructs encoding sM2HA2 and CTA1-conjugated sM2HA2 (sM2HA2CTA1) using poly-γ-glutamic acid (γ-PGA)-chitosan nanoparticles (PC NPs), which are safe, natural materials that are able to target the mucosal membrane as a mucosal adjuvant, could induce a high degree of systemic immunity (IgG and IgA) at the site of inoculation as well as at remote locations. The mucosal administration of sM2HA2CTA1/PC NPs may also significantly increase the levels of sM2- or HA2-specific cell-mediated immunity because increased release of both IFN-γ and IL-4 was observed.In challenge tests in BALB/c mice with 10 MLD50 of A/EM/Korea/W149/06(H5N1), A/Puerto Rico/8/34(H1N1), A/Aquatic bird /Korea/W81/2005(H5N2), A/Aquatic bird/Korea/W44/2005(H7N3) or A/Chicken/Korea/116/2004(H9N2) viruses, the recombinant sM2HA2CTA1/PC NPs provided better protection against lethal challenges compared with sM2HA2 and sM2HA2CTA1 without PC NPs. Thus, sM2HA2CTA1/PC NPs may be a promising mucosal vaccine candidate against pandemic influenza.

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Genome molecular analysis of circulating human influenza A virus isolates in Iran

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Background: Influenza is one of the most important emerging and reemerging infectious diseases that cause significant mortality and morbidity in communities (epidemic) and worldwide (pandemic) and has been posing a threat to economy and public health. The aim of this study is to determine phylogenecity and heterogenecity of the antigenic variations in circulating influenza A/H1N1 and A/H3N2 virus isolates during 2014-2016 in Iran andcompare them with the vaccine strains that were recommended by WHO for the same period. Moreover, determination of drug resistance and influenza significant potential for manipulation are other aims of the current study.

Methods: Clinical samples are collected from 200 individuals in Iran who are diagnosed with influenza illness between 2014 and 2016. Typing and sub-typing of the isolates are performed using multiplex RT-PCR and phylogenetic analysis is carried out for hemagglutinin, neuraminidase and matrix genes of the A/H1N1 and A/H3N2 isolates.

Results: Forty out of 200 samples are positive for influenza A virus and no influenza B virus is detected until now. This study is in progress for more results.

Conclusion: The synchronized seasonal patterns and high genetic diversity of influenza A viruses make possible to capture the evolutionary dynamic and epidemiological rules governing antigenic drift and reassortment and may serve as a "warning" system that recapitulates the global epidemic. Our findings demonstrate that the A/H3N2 is the predominant sub-type of human influenza virus among the patients studied in Iran during 2014-2015. Our research is continued for viruses isolated in Iran between 2015 and 2016.

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