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Molecular characterization of influenza viruses circulating in Cuba April 2009 to August 2010

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Influenza is a respiratory disease with high epidemic behavior; the main etiologic agents are influenza viruses A and B. The virus influenza A are primarily responsible for annual epidemics and the only causing pandemics. Fighting these viral agents is based mainly in the use of vaccines and drugs that inhibit viral proteins M2 and NA. Currently, the use of antiviral drugs has been limited by the emergency and circulation of influenza virus variants resistant to adamantane worldwide. The neuraminidase inhibitors have been the drug of choice available for the treatment and prophylaxis of influenza virus before the availability of influenza vaccine. The aim of this work was the molecular characterization of influenza virus circulating in Cuba in the period April 2009-August 2010. Phylogenetic analysis of seasonal influenza viruses and pandemic virus showed that both viruses were genetically similar to the strains included in the vaccine recommended by 'WHO'. Molecular characterization of these agents circulating in Cuba showed the necessity of systematic monitoring of these Cuban genetic variants. In the present work we identified genetic variants of influenza A resistant to oseltamivir. It was detected for the first time in Cuba the circulation of influenza A (H1N1) viruses with resistant markers to the antiviral drugs available.

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Epidemiologic pattern and diseasome exploration for physical performance: A new horizon for genetic and environmental cross-talk in health and disease

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Both genetic and environmental factors contribute to human diseases. Most common diseases are influenced by a large number of genetic and environmental factors, most of which individually have only a modest effect on the disease. Though genetic contributions are relatively well characterized for some monogenetic diseases, there has been no effort at curating the extensive list of environmental etiological factors. However, considering the interaction between the factors, a network of association and clustering would explain the influencing factors on health and disease. In this study we evaluated association of factors on physical performance. From a comprehensive search of the MeSH annotation of MEDLINE articles, NIH Genetic Association Database (GAD) and OMIM database, genetic and environmental etiological factors associated with physical performance were identified. Clustering of both genetic and environmental etiological factors puts genes in the context of environment in a quantitative manner. After extraction of genetic factors, associated diseases with those genes were searched. Finally a matrix of association was formed. The degree of associations was determined by pooling the published data and the network of "etiome" was constructed by Gephi. A 22 by 22 gene-gene interaction showed ACE gene with the highest centrality. Also 600 cells gene-disease matrix were illustrated including the degree of associations and 95% CIs. The diseasome of physical performance demonstrated interesting clusters of diseases and risk factors with an average degree of 7.4 and average clustering coefficient of 0.60. The network principally included two main clusters around diabetes and neoplastic diseases, while diabetes had the highest strength and centrality. The diseasome helps a better understanding of genetic and environmental factors attributed to physical performance in order to find effective treatments for linked factors. Diabetes and ACE gene polymorphism should take a paramount attention in this regard.

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