Genome-wide comparison inferred the origin and evolution of B-cell epitopes on the proteins of human influenza A virus

Edgar E. Lara-Ramírez1, Aldo Segura-Cabrera1, Ma. Isabel Salazar2, Mario A. Rodríguez-Pérez1, Xianwu Guo1*

1Centro de Biotecnología Genómica, Instituto Politécnico Nacional, Reynosa, México;

2Departamento de Inmunología, Escuela Nacional de Ciencias Biológicas, Unidad Profesional Lázaro Cárdenas, Instituto Politécnico Nacional, México

Abstract

The novel strain H1N1 caused the outbreak of first pandemic influenza in 21 century. Now it is a common component of current seasonal in- fluenza viruses. The recent transmission and plentiful genome sequences available provided a good opportunity to study the origin and evolution of epitopes on the proteins of human influenza virus. In the present study, the B-cell epitope compositions in the pandemic strains, circulating traditional seasonal strains, swine strains as well as highly virulent avian strain H5N1 were identified with the aid of the Immune Epitope DataBase (IEDB) and were compared at genomic level. A total of 14210 distinct sequences down-loaded from NCBI database were used for analysis. Some epitopes on proteins HA or NA, not conserved in recent seasonal strains, were found in 2009 pandemic strains but existed in the early human strains (1919-1935). The pandemic strain shared higher conserved epitopes with “bird flu” virus H5N1than classic human seasonal strains. The epitopes that could exist at common antigenic regions of HA protein are needed to further identify. The genetic exchanges between human and swine population by transmission was very active but the princepal side of the transmission could be from swine to human. These results provided valuable information on influenza A virus evolution and transmission by means of epitope analysis at genomic level.