

Functional genomics and reverse vaccinology approach to identify vaccine candidates against influenza virus

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The advent of whole-genome sequencing changed the way to think about vaccine development, enabling the targeting of possible vaccine candidates starting from the genomic information this process is named reverse vaccinology. As the genomic era progressed, reverse vaccinology has evolved with a pan-genome approach and multi-strain genome analysis became fundamental for the design of universal vaccines. The current research describes the applications of genome-based approaches in the development of vaccine against influenza virus using bioinformatics algorithms.

The currently available vaccines against influenza are viral strain specific and, hence, their efficacy is limited when the circulating strain is not the one included in them.

The study involves epitope based broad-spectrum vaccine for human use. The epitopes which are common to the vast majority of influenza virus strains regardless of their antigenic drifts and shifts are been identified for the three most important proteins Hemagglutinin (HA), Neuraminidase (NA) and matrix protein (M1, M2). The epitopes identified were subjected to population coverage analysis as the analysis is quite crucial due to polymorphism of MHC molecule, which display distinct peptide binding specificity. A combination of B- and T-cell epitopes is used to confer protection against viral infection. The vaccine, activating both the humoral and cellular arms of the immune response, induces long-lasting protection against many strains of the influenza virus. Consequently, it is expected to protect against future strains as well.

Biography

Bhawna Rathi has completed her Ph.D. work from SGPGI, Lucknow, India. She has been into research for 9 years. She has 7 international publications and has attended many national and international conferences. She is working as Assistant Professor at Amity University, India.

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