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Opinion

Reverse Vaccinology: Novel Genome-Based Approach Towards Vaccine Design Against Dangerous Microorganisms

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Development of vaccines has been a turning point in preclusion of several hazardous diseases such as polio, smallpox, anthrax, meningitidis, measles and diphtheria, particularly in those countries having very high mortality for such maladies. The traditional approach for vaccine production against pathogens includes culturing them in laboratory; however, this is not possible for highly infectious pathogens due to their extreme hazards. A novel approach for designing efficient vaccines against such pathogens is reverse vaccinology (RV). RV facilitates identifying potential targets (e.g., outer membrane proteins, surface antigens and surface-associated lipoproteins) for vaccine production, by using the whole genome sequence of a microbial pathogen [1]. Epitopes, being antigenic determinants of protein antigens on the surface of organisms, have an integral role in stimulating immune response against microbes; accordingly, T and B cell epitope correct prediction by various immunoinformatic tools has been a fundamental matter supporting development of highly specific (i.e., epitope-based) vaccines via RV [2-6]. The first pathogen against which the vaccine was prepared using RV was serogroup B *Neisseria meningitides*, The failure of traditional vaccine development process against such pathogen has been owing to the similarity of its proteins to humans plus the hypervariability character of the pathogen. These issues have been resolved by RV, using genome-based approaches such as pan-genome (defined as the global gene repertoire pertaining to a species) and in silico analysis. RV has been also utilized for development of vaccines against several pernicious pathogens including but not limited to *Listeria monocytogenes, Plasmodium falciparum, Bacillus anthracis, Streptococcus mutans, Streptococcus pneumoniae, Streptococcus agalactiae, Staphylococcus aureus, Chlamydia pneumonia, Leptospira interrogans* and pathogenic *Escherichia coli* [7-13]. Overall, the only necessity of this technique for designing successful vaccine candidates is the availability of the whole genome sequence of a large number of microbial isolates in order to screen for homology and to predict epitopes and surface proteins.

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