Vaccinomics: The Newest, the Safest; But…

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Bioinformatics is an interdisciplinary field bringing together the concept of biology, mathematics, statistics and computer science for quantitative utilization, classification, modeling, querying and analysis of biological data. The goal of vaccinomics is to utilize immunological knowledge to design a vaccine that targets the antigenic parts of infectious agents that enables the virus to be killed through specific immune response by the use of bioinformatics (immuno-informatics). Viruses are one of the smallest of all biological entities that are capable of infecting all forms of life including bacteria, animals and plants. Viral genome is very complex containing either DNA or RNA. DNA viruses are said to be more stable than RNA viruses. Immune systems are of two types: innate and adaptive. What differentiate the former from the latter is the ability of the latter to produce immune response with specificity and memory. Innate immune system relies on physical barriers whereas the adaptive is of cell-mediated chemical responses.

Vaccines relates to adaptive immunity being specific in dealing with the pathogen. Vaccines have been critical weapons that improve immunity to a particular disease. These are biological preparations containing an agent resembles a disease-causing microorganism and is often made from attenuated or killed forms of the microbe, its toxins or any of its surface proteins. These microbial particles when injected would be able to stimulate the body's immune system to recognize the agent as foreign, destroy it, and "remember" it, so that the immune system can more easily recognize and destroy any of these microorganisms that it later encounters. RNA viruses such as influenza is capable of mutating rapidly; posing a grave consequence of yearly vaccination to cope with ever changing population of newer strains. The success of a vaccine is dependent on the nature of the virus, its genomic content, and understanding its antigenic properties.

The reverse vaccinology which is part of the vaccinomics, uses bioinformatics techniques to screen the entire genomes of pathogens to determine genes that could lead to good epitopes, the peptides in an antigen to which the antibodies actually bind, and proteins that are surface situated.

Since the 1980s, many immunoinformatics methods have been developed and used to predict T-cell and B-cell immune epitopes. One of the most vital steps in analyzing an invading pathogen for possible vaccine targets is identifying the epitope regions. Despite the inherent prospects in vaccinomics over the traditional vaccine design, there are few major drawback such as: unpredictability and complex nature of the immune system, pleomorphism in MHC class I molecules. The use of mathematics, modelling and statistics pose a compounded limitations to scientists from other disciplines. Unlike the traditional vaccines; i*n silico* design of vaccine design approach targets only proteins instead of other bimolecular targets. Although bioinformatics offer potent, cost-effective and time saving vaccine; vaccine failure is still possible due to genetic diversities in low- and middle-income countries of the world.

Finally, the current success in the fight against COVID-19 should be improved upon by addressing the highlighted limitations for safer delivery of personalized vaccines by the continuous usage of vaccinomics in order to cope with ever dynamic viral and human genomics. The future must address the persistent issue of selecting suitable animal model for testing vaccine candidates.

This publication is timely, especially in this period of COVID-19 vaccine controversies; we look forward to a promising future for collaboration in great deal between the wet and dry laboratories.

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