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Review Article

The Importance of Vaccines for Improvement of Human Immune System

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Abstract

In the context of our current knowledge and understanding of key aspects of immune function and microbial interactions with the host, a collection of in-depth reviews in this issue of Immunity summarizes needs, opportunities, and obstacles to the development of new vaccines. Using a systems-level, multiplexed approach to the analysis of the human immune system can complement traditional, highly focused research efforts to accelerate our progress toward this goal and the improvement of human health. The purpose of this Perspective is to provide a broad overview that discusses our current limitations in designing effective novel vaccines for diseases that typically do not typically induce robust resistance in infected individuals.

Keywords: Immune function, Vaccines, Microbial interactions, Ecological niche

INTRODUCTION

Life is a never-ending struggle to occupy and thrive in a particular ecological niche while competing with other organisms. Such competition is frequently between predators and prey, not between free-living species independently seeking adequate resources. If we exclude conflicts between species, the real conflict, especially for humans, is between us as prey and the microbial and/or parasitic world as predators. Past the actual obstructions of skin and mucous layers, our capacity to win in this fight is subject to the legitimate working of our safe framework **(Zhang R et al., 2018).**

Experts in many aspects of the organization and function of the immune system that are relevant to achieving immune resistance to infection, as well as others with a thorough understanding of vaccinology, provide timely reviews of the state of knowledge in their respective fields in this special issue of Immunity. Indeed, these reviews provide impressive information. But simultaneously, they are uncovering in what they say regarding the limits we actually have as for understanding the genuine relates of resistance for diseases including HIV, Mycobacterium. Either Plasmodium or tuberculosis falciparum or our capacity for rational vaccine development against the wide variety of organisms that continue to cause significant morbidity and mortality worldwide **(Dalakouras A et al., 2018).**

From this point of view, I present a less in-depth, more descriptive, and prescriptive view of where we currently stand in our comprehension of how the immune system works in humans and where the community needs to go in order to harness the immune system more effectively for improved human health **(Bouche N et al., 2006).**

In recent years, these accomplishments, particularly those in which immunity was induced that was superior to that which is normally present in the host population, gave some people hope that academic and industrial scientists could quickly develop vaccines that are effective against the many pathogens that continue to be major health issues. However, these expectations were not based on a thorough understanding of the history of vaccinology or the limitations of our current knowledge of human immunity and its capacity to deal with certain infectious agents **(Pratt AJ et al., 2010) (Sakurai K et al., 2010).** The fact of the matter is that nearly all of the effective vaccines that have been developed up to this point work by producing antibodies, which neutralize viruses, toxins, or bacteria. These vaccines are very specific, and our success has been limited mainly to cases in which the most pathogenic strains of a virus or

bacteria can be identified and these few serotypes do not change much over time. This is because these pathogens have a lot of genetic diversity **(Naito Y et al., 2012).** These grants multivalent immunizations to be concocted that cover the range of strains to which obstruction is wanted this is the situation for polio, pneumococcal antibodies, and numerous others. We have developed an early warning system that enables seasonal manufacture of the specific vaccine required for that year, and in fact, protection can be limited if there are multiple circulating strains in a given season. This allows us to successfully combat influenza, which does show significant variation in neutralizing determinants over short time frames **(Jain PK et al., 2018).**

However, diseases in which we do not know how much of what specificity of antibody of what isotype in what tissue site leads to protection or even how to generate such antibodies in adequate titer and to maintain such levels over many years pose a problem for this quantitative antibody paradigm. In cases where the best neutralizing sites are shielded by protein folds or carbohydrates, as is the case with HIV, or when the pathogen varies in the relevant target structures for such antibodies to such an extent that even a multivalent vaccine would not generate adequate coverage of the variants, this is also a problem **(Das PR et al., 2020).**

Our current body of knowledge regarding human immunity has been generated by a number of distinct approaches. As a result of both natural history studies of individuals with various diseases and laboratory analyses of serum and tissues from infected or ill subjects, scientists and physicians in the 19th and early 20th centuries made the first significant contributions to the field. An initial picture of human immunity was provided by the work of Pasteur, von Pirquet, Schick, Portiere and Richet, Bordet, Arthus, von Behring, and Kitasato, among others. This picture included the antibody response to infection or vaccination, the effector activities of antibodies in vitro and in vivo, the nature of allergic and immunopathology states, the existence of responses characterized by mononuclear cell infiltrate **(Abdurakhmonov IY et al., 2016) (Pumplin N et al., 2016).**

RESULTS

During this time period, human immune analysis moved in two different directions. The investigation of the effects of genetic variation on response, particularly with regard to susceptibility to particular infectious diseases in the context of immunodeficiency, was one particularly fruitful avenue **(Koch A set al., 2014).** These studies have provided remarkable insight into which molecular players contribute to human host defense as more and more powerful tools were made available to identify the genetic locus that is responsible for an immunodeficiency that leads to the excessive occurrence of specific infections. The advances emerging from such examinations have been richly summed up in on-going surveys, so I will just specify that the outcomes range from the normal to the unforeseen **(Smagghe G et al., 2019).** New insights into apoptotic pathways and the components of the signal transduction machinery that are downstream of the TCR or involved in the polarization of CD4+ effector T cells have been provided by additional patient-based research.

CONCLUSION

It is important to note that the global, extensively multiplexed, omic-scale analysis of the human immune system that underpins the aforementioned strategy is in no way intended to replace in-depth studies of the immune system's components and fine-grained behavior. The frameworks approach isn't intended to uncover the subtleties of intracellular flagging pathways in unambiguous cells, albeit a portion of its advances, similar to multiplex phosphoflow, can add to such examinations. Even though improved computational methods for identifying cell subpopulations with unique combinations of staining achieved with a large number of known markers can potentially identify such a cell type without the new antibody, it is not optimally set up to discover a new type of cell if such a cell is only revealed by a new surface marker to which an antibody is not available and thus not included in the complex staining panels used for flow analysis. High-resolution descriptions of either the positioning of various inflammatory cells in specific tissue sites or the pathology of the involved tissue may be possible in the future using imaging methods as part of the large panel of assays performed in a systems-level enterprise, but existing technologies are not ideal for addressing how two cell types communicate with one another.

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CONFLICT OF INTEREST

The author declares no conflict of interest.

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