

vaccines currently available reside in the upper right quadrant and have been developed using well-established technologies.

Modern preventive vaccines required for more difficult infectious organisms can build on expanding new technologies and immunological knowledge. Good examples are the several recombinant and conjugate vaccines already licensed, and several vaccines developed using genomics (reverse vaccinology) that are in development. Reverse vaccinology represents a revolution in vaccinology and a milestone in biotechnology. It illustrates how a complex biological problem such as vaccine design can be solved by addressing and integrating in silico predictions and high-throughput in vitro experimental analysis for the identification of optimal vaccine antigen formulations. Beyond the pioneering work with MenB, we see the development and maturation of the technique, as it has been adapted to other biological systems with their inherent difficulties (such as GBS). We also see how newly emerging bioinformatic and immunoinformatic technologies can be integrated with functional genomics approaches to hone down the targets (Fig. 1). With many more antigens discovered for each pathogen, it is now possible to select antigens that respond to validated principles, such as antibody-mediated protection, and with limited or absent antigenic variability.

An important minority of the vaccines described in this book reside in the middle or left quadrant of Figure 3. These are the vaccines for which today's technologies have not yet succeeded, and developing these vaccines requires bridging scientific gaps such as learning to develop vaccines based on T cell-mediated protection. Today, development of these vaccines is being addressed using innovative immunostimulatory molecules and adjuvants, replicating or nonreplicating viral vectors, prime-boost regimens, etc. An alternative approach could be to bring them to the "comfort zone" of the upper right quadrant of Figure 3 by learning how to engineer immunologically silent conserved epitopes into immunodominant epitopes. A good example of this is HIV, where antibodies such as B₁₂ that recognize the conserved CD4-binding site could be able to protect from infection if this epitope were immunodominant.

In conclusion, the majority of the new vaccines addressed in this book are within the reach of today's technologies. Rather, the question is therefore whether or when they will be developed. Unfortunately, technical feasibility is only one of the hurdles in vaccine development. Even more important is often whether there is a market that can justify the huge investment that is necessary to bring vaccines to licensure. Many of the vaccines described in this book are at the "discovery" stage. However, the clinical development phase, during which a discovery is transformed into a potential product, is a long and expensive process. New vaccines today are developed by a few global vaccine manufacturers that can only afford to invest in vaccines that have a high probability of success in the market. In addition, the half dozen largest vaccine manufacturers have the traditional knowledge and the necessary investment to carry out clinical vaccine testing and manufacturing process development of candidate vaccine products. Many of the failures in vaccine development are due to the poor understanding and underestimation of the complexity of this phase.

Thanks to the impressive progress in biotechnology, the vaccine field is embarking on a new post-genomic era: harnessing genome data, and using genomics, proteomics, and immunology techniques in a new interdisciplinary realm of inquiry (Fig. 1). Vaccines targeting hypertension, drug addiction, and

cigarette smoking are examples of how vaccines are being evaluated to target diseases that are not traditionally tackled by vaccination. Vaccines today are usually given to prevent diseases that parents and pediatricians have never seen, and in their minds, they are no longer immediate lifesavers but tools that improve the quality and duration of life.

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