

1. INTRODUCTION

protein-engineering studies to improve its properties for the biotechnology industry. The production of cephalosporins could benefit in a similar way from knowing the structure of cephalosporin acylase (CA), since the properties of this enzyme are not optimal for use in production plants. Therefore, the crystal structure determination of CA could provide a basis for improving the substrate specificity of CA by subsequent protein-engineering techniques. Fortunately, a first CA structure has been solved recently (Kim *et al.*, 2000), with many other structures expected to be solved essentially simultaneously. Clearly, crystallography can be not only a major player in the design and optimization of therapeutic drugs, but also in their manufacture.

1.3.5. Vaccines, immunology and crystallography

Vaccines are probably the most effective way of preventing disease. An impressive number of vaccines have been developed and many more are under development (National Institute of Allergy and Infectious Diseases, 1998). Smallpox has been eradicated thanks to a vaccine, and polio is being targeted for eradication in a worldwide effort, again using vaccination strategies. To the best of our knowledge, crystal structures of viruses, viral capsids or viral proteins have not been used in developing the currently available vaccines. However, there are projects underway that may change this.

For instance, the crystal structure of rhinovirus has resulted in the development of compounds that have potential as antiviral agents, since they stabilize the viral capsid and block, or at least delay, the uncoating step in viral cell entry (Fox *et al.*, 1986). These rhinovirus capsid-stabilizing compounds are, in a different project, being used to stabilize poliovirus particles against heat-induced denaturation in vaccines (Grant *et al.*, 1994). This approach may be applicable to other cases, although it has not yet resulted in commercially available vaccine-plus-stabilizer cocktails. However, it is fascinating to see how a drug-design project may be able to assist vaccine development in a rather unexpected manner.

Three-dimensional structural information about viruses is also being used to aid in the development of vaccines. Knowledge of the architecture of and biological functions of coat proteins has been used to select loops at viral surfaces that can be replaced with antigenic loops from other pathogens for vaccine-engineering purposes (*e.g.* Burke *et al.*, 1988; Kohara *et al.*, 1988; Martin *et al.*, 1988; Murray *et al.*, 1998; Arnold *et al.*, 1994; Resnick *et al.*, 1995; Smith *et al.*, 1998; Arnold & Arnold, 1999; Zhang, Geisler *et al.*, 1999). The design of human rhinovirus (HRV) and poliovirus chimeras has been aided by knowing the atomic structure of the viruses (Hogle *et al.*, 1985; Rossmann *et al.*, 1985; Arnold & Rossmann, 1988; Arnold & Rossmann, 1990) and detailed features of the neutralizing immunogenic sites on the virion surfaces (Sherry & Rueckert, 1985; Sherry *et al.*, 1986). In this way, one can imagine that in cases where the atomic structures of antigenic loops in 'donor' immunogens are known as well as the structure of the 'recipient' loop in the virus capsid protein, optimal loop transplantation might become possible. It is not yet known how to engineer precisely the desired three-dimensional structures and properties into macromolecules. However, libraries of macromolecules or viruses constructed using combinatorial mutagenesis can be searched to increase the likelihood of including structures with desired architecture and properties such as immunogenicity. With appropriate selection methods, the rare constructs with desired properties can be

identified and 'fished out'. Research of this type has yielded some potentially immunogenic presentations of sequences transplanted on the surface of HRV (reviewed in Arnold & Arnold, 1999). For reasons not quite fully understood, presenting multiple copies of antigens to the immune system leads to an enhanced immune response (Malik & Perham, 1997). It is conceivable that, eventually, it might even be possible for conformational epitopes consisting of multiple 'donor' loops to be grafted onto 'recipient capsids' while maintaining the integrity of the original structure. Certainly, such feats are difficult to achieve with present-day protein-engineering skills, but recent successes in protein design offer hope that this will be feasible in the not too distant future (Gordon *et al.*, 1999).

Immense efforts have been made by numerous crystallographers to unravel the structures of molecules involved in the unbelievably complex, powerful and fascinating immune system. Many of the human proteins studied are listed in Table 1.3.4.5 with, as specific highlights, the structures of immunoglobulins (Poljak *et al.*, 1973), major histocompatibility complex (MHC) molecules (Bjorkman *et al.*, 1987; Brown *et al.*, 1993; Fremont *et al.*, 1992; Bjorkman & Burmeister, 1994), T-cell receptors (TCR) and MHC:TCR complexes (Garboczi *et al.*, 1996; Garcia *et al.*, 1996), an array of cytokines and chemokines, and immune cell-specific kinases such as Ick (Zhu *et al.*, 1999). This knowledge is being converted into practical applications, for instance by humanising non-human antibodies with desirable properties (Reichmann *et al.*, 1988) and by creating immunotoxins.

The interactions between chemokines and receptors, and the complicated signalling pathways within each immune cell, make it next to impossible to predict the effect of small compounds interfering with a specific protein-protein interaction in the immune system (Deller & Jones, 2000). However, great encouragement has been obtained from the discovery of the remarkable manner by which the immunosuppressor FK506 functions: this small molecule brings two proteins, FKBP12 and calcineurin, together, thereby preventing T-cell activation by calcineurin. The structure of this remarkable ternary complex is known (Kissinger *et al.*, 1995). Such discoveries of unusual modes of action of therapeutic compounds are the foundation for new concepts such as 'chemical dimerizers' to activate signalling events in cells such as apoptosis (Clackson *et al.*, 1998).

In spite of the gargantuan task ahead aimed at unravelling the cell-to-cell communication in immune action, it is unavoidable that the next decades will bring us unprecedented insight into the many carefully controlled processes of the immune system. In turn, it is expected that this will lead to new therapeutics for manipulating a truly wonderful defence system in order to assist vaccines, to decrease graft rejection processes in organ transplants and to control auto-immune diseases that are likely to be playing a major role in cruelly debilitating diseases such as rheumatoid arthritis and type I diabetes.

1.3.6. Outlook and dreams

At the beginning of the 1990s, Max Perutz inspired many researchers with a passion for structure and a heart for the suffering of mankind with a fascinating book entitled *Protein Structure – New Approaches to Disease and Therapy* (Perutz, 1992). The explosion of medicinal macromolecular crystallography since then has been truly remarkable. What should we expect for the next decades?

In the realm of safe predictions we can expect the following: