experiments in mice indicate that this protein has only a few dominant T-helper cell activating sites which, as expected, are restricted by the major histocompatibility system (MHC class II) of the vaccine recipient[4,6]. Moreover, although the CSP-repeat region, which in *P.falciparum* is invariant in different parasite strains, contains one such MHC restricted site, the other important T-cell sites defined thus far are in a molecular region that varies between strains[7].

A similar genetic restriction to a few epitopes probably also holds true for the human T-cell response to the CSP (M.F. Good *et al.*, manuscript in preparation). The findings imply that it may be necessary to use a vaccine formulation incorporating T-cell activating structures derived from other sporozoite molecules than the CSP to achieve the goals indicated above. This is by no means impossible[8] but remains to be investigated.

The second major problem is a related one and also involves T-cell activation. Recent animal experiments suggest that an important part of the protective effect of a sporozoite vaccine is antibody independent[9], probably reflecting a direct T-cell-mediated inhibition of parasite development in the liver[10]. If true for human malaria as well — and there is no

reason to believe that it is not — this also means that one will probably have to search for additional T-cell activating sporozoite molecules to design an efficient subunit vaccine.

Despite the problems discussed above (and others that I have not mentioned here), the reports by Ballou *et al.*[1] and Herrington *et al.*[2] are important steps on the way to the design of vaccines preventing malaria infection. Although the remaining problems are serious, they are not insurmountable. Considering the fact that it took only 3 years from the structural definition and cloning of *P.falciparum* CSP until the clinical trial of the first vaccines, it may well be hoped that the second or third generation of improved sporozoite vaccines will become available in the foreseeable future. □

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Polymer science

Interdiffusion at interfaces

Barton A. Smith

Two pieces of plastic can be welded together by bringing them into contact at an elevated temperature. This process has many practical applications, including the joining of plastic pipes, the moulding of plastic parts from powdered resins, and adhesion in multilayered materials. The strength of the weld results from the interdiffusion of the polymer molecules across the initial interface. The interdiffusion process for polymers differs from that in small-molecule and atomic solid systems, because of the entangled state of the the long polymer chains in the melt. There has recently been considerable controversy over the type of theory which correctly describes polymer–polymer interdiffusion[1]. Proposed theories have differed markedly in their predictions of the way in which the rate of interdiffusion depends upon parameters such as the length of the polymer molecules. Composto *et al.* describe on page 234 of this issue[2] some experiments carefully designed to provide a direct test of these theories.

In the simplest case, the welding of identical materials, the interdiffusion proceeds at the same rate as diffusion of those molecules in the bulk sample, and is characterized by the self-diffusion

coefficient. Self diffusion has been studied extensively over the past decade and is described adequately by the 'reptation' model of polymer motion. The more interesting cases involve the interdiffusion of different polymers, or chemically identical polymers of very different molecular weights. These cases are more complex because the mixing is driven by both entropy and enthalpy, and because both the mixing energy and the mobility of each molecule depend upon the composition of the material, which varies continuously across the interface.

Attempts have been made to predict the mutual diffusion coefficient, D_M, which characterizes the interdiffusion rate, from the tracer or self diffusion coefficients of the individual components. (The tracer diffusion coefficient describes the random brownian motion of individual molecules, in the absence of any composition gradients.) As the general case is too complex to solve analytically, theories have been based on certain simplifying assumptions and boundary conditions. The recent controversy has centred on two assumptions that lead to different forms for the equation predicting D_M.

One theory[3] allows for a flux of

vacancies across the interface and assumes that the osmotic pressure is constant, resulting in D_M being a linear combination of the mobilities of the two components. Thus, D_M is controlled primarily by the mobility of the more rapidly diffusing polymer, in agreement with experimental results. The vacancy flux model has been criticized because it allows a significant density gradient across the interface.

The alternative assumption, that the density is constant, requires the fluxes of the two components to be equal and opposite. The result is that the mobilities of the two components are strongly coupled. A 'slow' theory[4] resulted from the the idea that the tracer diffusion coefficient of the slow component would control D_M. Recent experiments would seem to confirm the vacancy flux theory. For example, Composto *et al.*[2] describe in this issue a series of measurements of both the tracer and mutual diffusion coefficients in the miscible blend of polystyrene and poly(xylenyl ether). They find that D_M scales inversely with the molecular weight of the polystyrene, the faster moving species, and report good quantitative agreement between their data and the predictions of the vacancy flux theory. The 'slow' theory is clearly in error, predicting the interdiffusion to be more than ten times slower than the measured rate in some cases.

Recently it has been realized, however, that the constant-density assumption does not necessarily lead to a 'slow' theory. The resulting mutual diffusion (for each composition) is analogous to that obtained for a dilute or semi-dilute polymer solution: D_M depends strongly upon the mobility of the solvent, which in this case is the more rapidly diffusing polymer. This has also been described as the convective flow of the slow molecules caused by the influx of the rapidly diffusing ones[5]. Jordan *et al.*[6] have recently analysed concentration profiles of the interdiffusion of different molecular-weight polyethylenes. They confirm that the faster component controls D_M, and suggest that the current thinking along the lines of the constant density model may lead to the best description of polymer–polymer interdiffusion. We can look forward to further experiments of this type to guide us to a more detailed theoretical description of the process. □

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