

## 4. DIFFUSE SCATTERING AND RELATED TOPICS

if the condensed monomer film is exposed to ultraviolet light (Day & Lando, 1980). It may be possible to carry out the polymerization within a confined space (Rybnikar *et al.*, 1994) or in dilute solution (Liu & Geil, 1993) to form crystals suitable for electron diffraction data collection. In the latter case, whisker formation with the chain axis parallel to the lath plane has been observed. Films can be cast on a water surface by evaporation of an organic solvent from a polymer solution. The film can then be stretched to give a suitably oriented specimen for data collection (Vainshtein & Tatarinova, 1967). In addition, it may just be possible to obtain suitable data from drawn microfibrils to supplement the single-crystal diffraction information from other preparations.

Data collection from these thin microcrystals often employs the selected-area diffraction technique in the electron microscope that is described in detail elsewhere (Dorset, 1995*b*). Using an approximately eucentric goniometric tilting device in the electron microscope, the sampling of three-dimensional reciprocal space is tomographic, *i.e.* the tilts of a nearly planar Ewald sphere surface (owing to the very small electron wavelength) are always referred to a set of reciprocal axes that intersect (0, 0, 0). For any given crystal habit, there is always a missing set of data owing to the physical limitation to the tilt imposed by the finite thickness of the specimen holder within the pole-piece gap of the electron microscope objective lens (Vainshtein, 1964). For this reason, it is desirable to crystallize two orthogonal orientations of the chain packing (using the above-mentioned approaches), if possible, so that all of the reciprocal lattice can be sampled. If electron micrographs are to be used as an additional source of crystallographic phases then 'low-dose' techniques for recording such images should be employed to reduce the deleterious effects of radiation damage caused by the inelastic interactions of the electron beam with the crystalline sample (Tsuji, 1989).

When the diffraction patterns are recorded on photographic film and these are then measured with a densitometer, relative reflection intensities can often be expressed simply as the integrated peak area without need for a Lorentz correction (Dorset, 1995*b*). Only if the diffraction maxima are extensively arced (*e.g.* in patterns from epitaxial films) is such a correction required. That is to say,  $|\Phi_{\text{obs}}| \propto KI_{\text{obs}}^{1/2}$  where  $|\Phi_{\text{obs}}|$  is the observed structure-factor magnitude. Assuming the kinematical approximation holds, the calculated value is

$$\Phi_{\mathbf{h}}^{\text{calc}} = \sum_i f_i \exp 2\pi i(\mathbf{h} \cdot \mathbf{r}_i),$$

where  $f_i$  are the electron scattering factors (Doyle & Turner, 1968), *e.g.* as tabulated in Table 4.3.1.1 in *IT C*. By analogy with X-ray crystallography (see Chapter 2.2), normalized values can be found from

$$|E_{\mathbf{h}}|^2 = I_{\mathbf{h}}^{\text{obs}} / \varepsilon \sum_i f_i^2,$$

with the usual scaling condition that  $\langle E_{\mathbf{h}}^2 \rangle = 1.000$ . [Note, however, that these intensities only describe the chain monomer packing in the 'stem' region of the lamellar microcrystal. Details owing to the surface chain folds are lost (even if they are strictly periodic), because of reasons similar to those described by Cowley (1961) for the electron scattering from elastically bent silicate crystals.]

## 4.5.3.3. Crystal structure analysis

Two approaches to crystal structure analysis are generally employed in polymer electron crystallography. As already mentioned, the procedure adapted from fibre X-ray crystallography relies on the construction of a model (Brise, 1989;

Perez & Chanzy, 1989). Conformational searches (Campbell Smith & Arnott, 1978) simultaneously minimize the fit of observed diffraction data to calculated values (the *R* factor based on structure factors computed *via* known atomic scattering factors) and a nonbonded atom-atom potential function (Tadokoro, 1979). Reviews of structures solved by this approach have been published (Dorset, 1989, 1995*b*).

Recently, direct phasing methods of the kind used in X-ray crystallography (Chapter 2.2 and, applied to electron diffraction, Section 2.5.8) have also been found to be particularly effective for electron crystallographic structure analyses (Dorset, 1995*b*). While the Fourier transform of an electron micrograph would be the most easily imagined direct method, yielding crystallographic phases after image analysis (see Section 2.5.5), this use of micrographs has been of less importance to polymer crystallography than it has been in the study of globular proteins, even though there is at least one notable example where it has been helpful (Isoda *et al.*, 1983*a*) for the determination of a structure from X-ray fibre data. On the other hand, high-resolution images of polymer crystals are of considerable use for the characterization of packing defects (Isoda *et al.*, 1983*b*).

In polymer electron crystallography, the sole reliance on the diffraction intensities for structure analysis has proven, in recent years, to be quite effective. Several direct-methods approaches have been pursued, including the use of probabilistic techniques, either in the symbolic addition procedure, or in more automated procedures involving the tangent formula (see Chapter 2.2). The Sayre (1952) equation has been found to be particularly effective, where the correct structure is identified *via* some figure of merit after algebraic phase values are used to generate multiple solutions (Stanley, 1986). More recently, maximum-entropy and likelihood methods (Gilmore *et al.*, 1993) have also been effective for solving such structures. After the initial atomic model is found, it can be improved by refinement, generally using Fourier techniques. Least-squares refinement can be carried out under most favourable circumstances (Dorset, 1995*a*), but requires the availability of a sufficient number of diffraction data. Even so, the refinement of thermal parameters must be uncoupled from that of the atomic positions. Also, positional shifts must be dampened (if X-ray crystallographic software is used) to prevent finding a false minimum, especially if the kinematical *R* factor is used as a figure of merit.

## 4.5.3.4. Examples of crystal structure analyses

At least four kinds of electron diffraction intensity data sets have been used as tests for direct phase determination *via* the approaches mentioned above.

*Case 1: Zonal data sets – view down the chain axis.* Such data are from the least optimal projection of the polymer packing, because of extensive atomic overlap along the chain axis. Initially, symbolic addition was used to find phase values for *hk0* data sets from six representative polymers, including three complicated saccharide structures (Dorset, 1992). Most of the determinations were strikingly successful. Later, an unknown data set from the polysaccharide chitosan was obtained from Grenoble (Mazeau *et al.*, 1994) and direct phase determination was able to find a correct model (Dorset, 1995*b*). More recently, other polymers have been tested [including one case where an electron micrograph provided many of the starting phase terms (Dorset, 1995*b*)] also comparing favourably with the solution found by energy minimization of a linkage model. For all examples considered so far, the projected symmetry was centrosymmetric.

Later, it was found that a partial phase set provided by symbolic addition could be expanded to the complete zone by the Sayre equation (Dorset *et al.*, 1995). In all of these tests (Dorset, 1995*b*), there were only one or two examples where there were serious deviations from the phase terms found by other methods. Even in these instances, the potential maps could still be used as