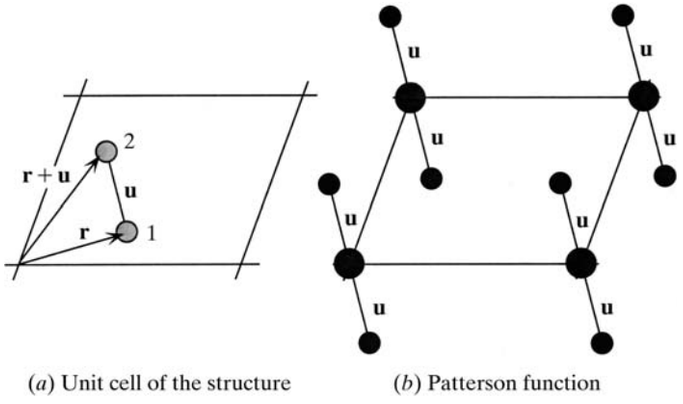

(*a*) Unit cell of the structure (*b*) Patterson function

Fig. 2.1.9.1. (*a*) A two-dimensional unit cell with two atoms. (*b*) The corresponding Patterson function. Reproduced with permission from Drenth (1999). Copyright (1999) Springer-Verlag.

tion, in which the heavy-atom positions are derived from a difference Patterson calculated with coefficients $(|F_{PH}| - |F_P|)^2$, where $|F_{PH}|$ is the structure-factor amplitude of the heavy-atom derivative and $|F_P|$ is that of the native protein (see Part 12). The vectors between the heavy atoms are the most prominent features in such a map.

The number of peaks in a Patterson map increases much faster than the number of atoms. For n atoms in the real unit cell, there are n^2 Patterson peaks, n of them superimposed at the origin, and $n \times (n-1)$ elsewhere in the Patterson cell. Because the atomic electron densities cover a certain region and the width of a Patterson peak at **u** is roughly the sum of the widths of the atoms connected by **u**, overlap of peaks is a real problem in the interpretation of a Patterson map. It can almost only be done for unit cells with a restricted number of atoms unless some extra information is available. For crystals of macromolecules, it is certainly impossible to derive the structure from an interpretation of the Patterson map.

The situation can be improved through sharpening the Patterson peaks by simulating the atoms as point scatterers. This can be achieved by replacing the $|F(\mathbf{h})|^2$ values with modified intensities which, on average, do not decrease with $\sin\theta/\lambda$. For instance, suitable intensities for this purpose are the squared normalized structure-factor amplitudes $|E(\mathbf{h})|^2$ (Section 2.1.4.6), the average of which is 1 at all $\sin\theta/\lambda$. A disadvantage of sharpening to point peaks is the occurrence of diffraction ripples around the sharp peaks, induced by truncation of the Fourier series in equation (2.1.9.1). Therefore, modified intensities corresponding to less sharpened peaks are sometimes used [*IT* B (2001), Chapter 2.3, pp. 236–237]. Diffraction ripples that seriously disturb the Patterson map are generated by the high origin peak, and, particularly for sharpened maps, it is advisable to remove this peak. This implies that $P(\mathbf{u} = 0) = 0$ [equation (2.1.9.1)]. It is easy to verify that this requires coefficients $[|F(\mathbf{h})|^2 - \langle|F(\mathbf{h})|^2\rangle]$ for the $|F(\mathbf{h})|^2$ map and $[|E(\mathbf{h})|^2 - 1]$ for the $|E(\mathbf{h})|^2$ map. Note that the term for $\mathbf{h} = 0$ is omitted and that the average of $|F(\mathbf{h})|^2$ must be taken for the appropriate $\sin\theta/\lambda$ region.

The symmetry in a Patterson map is related to the symmetry in the electron-density map, but it is not necessarily the same. For instance, screw axes in the real cell become non-screw axes in the Patterson cell, because all interatomic vectors start at the origin. It is possible, however, to distinguish between screw axes and non-screw axes by the concentration of peaks in the Patterson map. For instance, the consequence of a twofold symmetry axis along **b** is the presence of a large number of peaks in the $(u0w)$ plane of the Patterson map. For a screw axis with translation $\frac{1}{2}$ along **b**, the peaks lie in the $(u\frac{1}{2}w)$ plane. Such planes are called Harker planes (Harker, 1936). Peaks in Harker planes usually form the start of the interpretation of a Patterson map. Harker lines result from mirror planes, which do not occur in macromolecular crystal structures of biological origin.

Despite the improvements that can be made to the Patterson function, for structures containing atoms of nearly equal weight its complete interpretation can only be achieved for a restricted number of atoms per cell unless some extra information is available. Nowadays, most structure determinations of small compounds are based on direct methods for phase determination. However, these may fail for structures showing strong regularity. In these cases, Patterson interpretation is used as an alternative tool, sometimes in combination with direct methods. It is interesting to see that the value of the Patterson function has shifted from the small-compound field to macromolecular crystallography, where it plays an extremely useful role:

(1) in the isomorphous replacement method, the positions of the very limited number of heavy atoms attached to the macromolecule can be derived from a difference Patterson map, as mentioned earlier in this section;

(2) anomalous scatterers can be located by calculating a Patterson map with coefficients $[|F_{PH}(\mathbf{h})| - |F_{PH}(-\mathbf{h})|]^2$, in which $|F_{PH}(\mathbf{h})|$ is the structure-factor amplitude of the protein containing the anomalous scatterer;

(3) molecular replacement is based on the property that the Patterson map is a map of vectors between atoms in the real structure, combined with the fact that such a vector map is (apart from a rotation) similar for two homologous structures: the unknown and a known model structure.

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