CHAPTER I

INTRODUCTION

Following the discovery of X-ray by Röntgen in 1895, a good deal of time had been devoted in establishing its fundamental properties and up to 1912, crystallography was in general confined to descriptive morphological crystallography. However, since the inception of classical diffraction experiments by Laue, Friedrich and Knipping\(^1\), the subject "The crystal structure analysis by X-ray diffraction" started making rapid strides, and in recent years, aided with computing facilities, the veil of mystery of many complex structures is being uncovered. The accomplishment of penicillin\(^2\) (Bunn and others, 1952) and vitamin B\(_{12}\)\(^3\) (Hodgkin et. al., 1957) structures are illuminating citations. The detailed refinement of relatively simpler structures on the other hand is equally being emphasized. There is no straight forward method to solve the structure except in very few cases, and particularly in organic compounds (containing only C, N and O) considerable difficulty is encountered. Each crystal affords a problem of its own.

The solution of crystal structure by means of X-ray is ultimately to know the diffracting matter (electrons of the atoms or rather atomic positions) in the unit cell. At each point in the crystal there is certain electron density \(\rho(x,y,z)\) which is a function of coordinates \((x,y,z)\) of the atoms. Since the crystal structure is essentially a repeating pattern in three dimensions, therefore, the density function \(\rho(x,y,z)\) can...
be expressed as the sum of suitable Fourier series. W. H. Bragg
(1915) was first to realise that each X-ray reflection must
correspond to one of the component sinusoidal distributions of
density in the medium. Ewald (1921) showed the importance of
the series by expressing it for periodic density distribution
in an infinite crystal in terms of reciprocal lattice vectors.
Epstein and Ehrenfest used a triple Fourier series to represent
the density of diffracting matter in a crystal which is expressed
as
\[ f(x, y, z) = \frac{1}{V} \sum_{h} \sum_{k} \sum_{l} F(hkl) \exp[-2\pi i (hx + ky + lz)] \]
where \( V \) is volume of unit cell, \( hkl \) is Miller's indices,
\( F(hkl) \) is structure factor of the plane \( (hkl) \) and the structure
factor is given as
\[ F(hkl) = \sum_{j} f_{0j} \exp[-B_{j} \frac{\sin \theta}{\lambda}] \exp 2\pi i(hx_{j} + ky_{j} + lz_{j}) \]
where \( f_{0j} \) is the scattering factor of the \( j \)th atom at rest.
\( B_{j} \) is isotropic temperature factor of \( j \)th atom and \( x_{j}, y_{j} \) and
\( z_{j} \) are the corresponding coordinates. The main obstacle in
summing the series is the complex nature of \( F(hkl) \) which involves
amplitudes as well as phases. The magnitude of the structure
amplitudes can be measured experimentally, but the knowledge
about the relative phases is lost in recording the spectra.
This lack of information about the phases prohibits the direct
determination of the structure by Fourier series. The deter-
mination of these phases thus constitute the central problem
in the Fourier method of crystal structure analysis.

To overcome the phase problem various methods have been
devised. Trial and error is one of them in which a reasonable
trial structure is postulated and if a satisfactory agreement
between observed and calculated structure amplitudes is obtained
then the calculated phases with observed amplitudes are used to sum up the Fourier series.

An attempt to evade the difficulty of phase determination was made by Patterson, A. L. (1934, 1935) in which squares of the moduli of Fourier coefficients are used instead of structure factors. Thus the resulting synthesis gives map which gives information about the interatomic vectors rather than the atomic positions. However, it has been proved to be of immense importance as a starting point for deriving the trial structure. One of the important properties of three dimensional Patterson map realised by Harker, is the occurrence of peaks between the symmetry related atoms. He introduced the method

of calculating certain planes (Harker sections) or lines (Harker lines) which give very useful information leading to the determination of phases.

The Patterson method is of particular use in case of heavy atom compounds. The heavy atom-heavy atom peak is easily located and then the coordinates of other atoms are derived by Fourier synthesis using the phases based upon the calculations of heavy atom position alone. Since heavy atom contribution dominates most of the phases of the reflexions, it proves quite effective in most of the cases.

Another powerful method of determining phases is the use of isomorphous replacement. The general principle is that if it is possible to substitute successively two different heavy atoms in a molecule without disturbing the overall crystal structure, then the phase relationship can be determined from a difference
effect. For example, a most simple case is when heavy atom happens to occupy a centre of symmetry. Let these atoms be $A_1$ and $A_2$ and the remainder of molecule be $O$. Now if these structures are isomorphous, the contribution of $O$ remains constant and we get

$$F_{A_1}O - F_{A_2}O = F_{A_1} - F_{A_2} = \Delta F$$

here $\Delta F$ represents the difference in scattering power of the two heavy atoms and this is sufficient to determine the signs of the two structure factors if their magnitudes can be accurately measured. The use of the method has been made in case of Phthalocyanines, camphor derivatives and sucrose derivatives.

Recently direct methods of determining phases are being developed. Harker and Kasper (1948) devised certain inequality relations between structure factors thereby predicting the signs of some of the structure amplitudes, on the basis of mathematical physical aspects that the electron density is no where a negative quantity in the crystal and that the electrons can, to a close approximation, be considered to be distributed spherically around the atoms. The use in its extended form was made by Gillis (1948 a, b) to determine the signs for oxalic acid structure. D. Sayre (1952) gave a new set of relationships which exists among the structure factors of crystal containing atoms of approximately equal diffracting power such as C, N and O atoms.

The Fourier transform method is making its important place in crystal structure analysis. The Fourier transform of a group of atoms is a function which represents the amplitude.
and the phase of the radiation scattered by the group of atoms in a particular direction. The process of crystal structure determination is essentially the fitting of the reciprocal lattice on the Fourier transform of the contents of the unit cell so that the modulus of the transform at each reciprocal lattice point is equal to the structure amplitude of the corresponding X-ray reflexion.

Once the approximate coordinates of the atoms in a unit cell are obtained, the next task is to refine these parameters. Various methods are available for refining the structure such as Fourier synthesis, difference synthesis and least squares etc. In the Fourier synthesis the maxima in the electron density map will occur away from the assumed position in the direction of true one. The new atomic positions are used to recalculate the phases and the process is repeated till no further change of phases occur in structure amplitudes. In difference synthesis, difference between observed and calculated structure factors with proper phases are used as Fourier coefficients and the resulting map indicates the incorrect positioning of atoms if they lie on steep gradients. The least squares method is based on the minimization of a weighted sum of squares of discrepancies between observed and calculated factors.

This rapidly growing field is difficult to review adequately, but some of the better established and more important methods have been summarized.

Considerable work has been done on the structure of amino acids but there \( \delta \)-keto analogs have so far received a
little attention. These acids are of considerable biochemical interest as intermediates in the bio-synthesis and degradation of amino acids. They are formed during the course of enzymatic oxidative deamination and transamination and capable of enolization, may exist theoretically in cis and trans enol form which has been demonstrated experimentally in several cases (Meister, et al. 1964, Anderson and Hasford. The structure determination of these compounds is difficult owing to the unstable nature of many of them.

Recently structures of sodium salts of some L-keto acids have been determined (Tavale, Pant and Biswas, 1961, 63, 64) by two dimensional data and, therefore, though their results cannot be authenticated, shows an interesting persistent lengthening of C\textsubscript{1}-C\textsubscript{2} bond and enolization in case of sodium 2 oxo-butyrate. This aroused an interest to examine whether these observations represent merely an error or they are real structural features. These prompted us to carry out structure determination work on similar compounds as accurately as possible to provide reliable structural information which might throw light on their chemical behaviour.

The work has been incorporated in four parts, describing the crystal and molecular structures of sodium 2 oxo-valerate, sodium 2-oxo caproate, sodium 2-oxo heptylate and sodium pyruvate respectively. Each part comprises three chapters describing "Crystal data and experimental details", "Trial structure and its refinement" and "Results and discussion" respectively.
REFERENCES


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