# ABSTRACT OF THESIS



The structure of a-Glucose-1-Phosphate, the Cori Ester, in the form of its dipotassium salt dihydrate has been determined and the structure compared with those of analogous compounds.

The methods used were based mainly on the three-dimensional vector function, partly using the isomorphous diammonium-Glucose-1-Pho8phate dihydrate. The information derived from the short intramolecular vectors appearing round the origin of the 'sharpened' vector map was found to he particularly valuable. Direct methods of sign determination were also examined and found to be potentially useful.

Refinement was carried out initially hy Fourier methods and finally by the method of Least Squares, all such calculations being done on the D.E.U.C.E. Computer of Glasgow University.

The molecular structure is confirmed as being that found by purely chemical methods. The Glucose-1-Phosphate molecule possesses the long  $(1.59 \text{ Å})$  phosphorous-ester oxygen bond which is found in other sugar phosphate structures and which seems to he characteristic of this class of compound. In addition, the hond from carhon (1) to the ester oxygen is shorter  $(1.37 \text{ Å})$  than average. The angle at this oxygen,  $124^\circ$ , is rather wide.

The crystal structure itself is held together by a comprehensive system of non-covalent bonds linking the cations, the free oxygens of the phosphate group, the hydroxyl groups of the sugar ring, and the water molecules. The completeness of this system explains the comparative hardness of the crystal and its lack of any preferred cleavage.

# THE STRUCTURE OF THE SUGAR PHOSPHATES

# BY X-RAY METHODS.

Thesis presented to the University of Edinburgh

for the degree of Ph.D.

by

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March, I964

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# Acknowledgements

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## INTRODUCTION.

1.

In all living systems, both plant and animal, the phosphate esters of the carbohydrates play roles whose importance is equalled or exceeded only by the proteins and polysaccharides. While one cannot make any rigorous and simple divisions among these esters, as to the relation between structure and biochemical function, it could be said that the pentose esters and the hexose esters dom in general, act as functionally different agents, and the introduction will therefore treat them separately.

The pentose esters occur primarily in a directive role, always combined with heterocyclic residues. They may occur as simple monomers or dimers, as in some co-enzymes, or as long chain polymers, as in deoxyribose nucleic acid (D.N.A.) or ribose nucleic acid  $(R.N.A.)$ . In the former case, the enzyme and co-enzyme will catalyse <sup>a</sup> particular reaction, given the correct substrate, and in the latter case, it is believed that D.N.A. is the "messenger" for complete sets of genettc instructions, while R.N.A. has the more limited task of guiding syntheses of specific proteins, including enzymes. One wellknown exception to the above generalisation is adenosine-5' triphosphate (A.T.P.), <sup>a</sup> pentose ester which is the phosphorylating agent in many biochemical reactions. It is able to transfer one of its two terminal phosphate groups to <sup>a</sup> number of different molecules, without showing any particular specificity.

The /

The structures of only relatively few of these compounds have been fully worked out by X-Ray methods, and <sup>a</sup> summary of the results is given diagrammatically for Cytidine- $3$ -Phosphate (Fig. 1, Ref. 8), Adenosine-5'-Monophosphate (Fig. 2) Ref. 9) and Calcium Thymidylate (Pig. 4» Ref. 11). The structure of Aminoethanol Phosphate (Fig. 3, Ref. <sup>10</sup> ) has been included because of the accuracy to which the phosphate ester group has been refined. Barium-Ribose-5-Phosphate (Ref. 12) has also been solved and refined to moderate accuracy.

The methods used are discussed later, along with those used in the solution of Glucose-l-Phosphate. Part of the reason why so few have been studied lies in the difficulty of obtaining suitable crystals, part in the inherent difficulties of solving many-atom structures of low symmetry. However, it may be noted that the general structure of D.N.A. was deduced largely from models, built up from accurate molecular structures of the few simple related groups which had been studied at that time, such as Adenine, Guanine, Cytosine, and the furanose rings occurring in Ribose and Sucrose. Possibly the least satisfactory part was the phosphate link, whose structure could only be approximated to on geometrical considerations. The hydrogen bonding system, which imparts to these molecules their unique capacity for self-reproduction could not have been more than <sup>a</sup> guess, had it not been that the sub-units of the component nucleotides were known with sufficient accuracy to permit the assessment of distances between heterocyclic rings in the double helix /



Fig 2



Fig <sup>1</sup>



helix, and in particular to show that only certain pairings were possible.  $(Refs. 1, 4, 5, 7, 13)$ .

### Hexose Esters.

The hexose esters, by contrast, are not concerned in any directive function. Polymerised hexose phosphates have only been observed fairly recently in the material forming the cell walls of certain micro-organisms, their role being apparently entirely structural. These have been named the Teichoic acids (Refs. 14, 15).

Fructose 1-6 Diphosphate, Fructose-6-Phosphate, Glucose-l-Phosphate and Glucose-6-Phosphate account for the main part of the observed esters, these being most in evidence in fermentation, respiratory and photosynthetic reactions. In the last of these, simpler glycerophosphates and triose phosphates precede the appearance of the hexoses.

One tentative chain of conversions given (2) includes the sequence:

2 Phosphoglycerin acid  $\rightarrow$  3-Phosphoglyceric acid  $\rightarrow$ Triose Phosphate  $\rightarrow$  Fructose 1-6 DiPhosphate  $\rightarrow$ Glucose-6-Phosphate, Glucose-l-Phoaphate and Fructose-6-Phosphate.

Glucose-l-Phosphate is the immediate precursor of starch.

Possibly even more interesting from the point of view of the difference between Hexose and Pentose esters is the conversion of Glucose-6-Phosphate to Ribose-5-Phosphate, <sup>a</sup> constituent of R.N.A. (Ref. 1. p.191)

The biochemist Lipmann has suggested that in synthetic and /

and degradative reactions, the elements of phospheric acid may be visualised as replacing those of water. The energetics of the various transformations involved are much more favourable than would be the case with the non-phosphorylated sugars. (Ref. 13). Typically, a biochemical process may start with a carbohydrate which is then phosphorylated by A.T.P. or another 'high energy' phosphate, under the catalytic action of the appropriate enzyme, undergoes conversions, such as the chain listed above, and finally gives some product, e.g. glycogen or starch, with loss of the phosphate group.

In this context, it may be worth commenting on the 'high energy phosphate' theory of Lipmann. Briefly, this suggests that certain phosphate bonds act as intermediate energy stores for biochemical reactions. A.T.P. is the best known of these, though far from being the only one. The distinction is made on the basis of the heats of hydrolysis of the phosphate bond (Ref. 2. p. 209) thus:

## Phosphate Heat of Hydrolysis



The difference between the terminal phosphates and that adjacent to the ring in A.T.P., A.D.P. and A.M.P. is most marked.

Glucose-6-Phosphate must be converted to the slightly higher energy Glucose-l-Phosphate prior to the formation of Glycogen /

Glycogen, Starch, Sucrose, or other di- or poly-saccharides, since these are linked through the 1-position. This conversion is catalysed by the enzyme Phosphoglucomutdse, though the exact mechanism is not very clear.

No 'high energy' phosphate has yet been studied by X-Ray investigation, probably because of the difficulty of crystallising these substances.

# The Structure of Di-Potassium Glucose-l-Phosphate Dihydrate.

General: As with all l-substituted sugar derivatives, Glucose-l-Phosphate can exist as two anomers,  $\propto$  and  $\beta$ . The molecule studied was the naturally occurring form, known as the Cori Ester, after its discoverer. It is not formed directly, by straightforward esterification of the 1-hydroxy group, but as follows:

hexokinase Glucose + A.T.P.  $\overbrace{\hspace{2.5cm}}$  Glucose-6-Phosphate + A.D.P. (1) Glucose-6-Phosphate **phosphoglucomutase** Glucose-l-Phosphate (2) 's In (l) equilibrium is far to the right, and in (2) well to the left, with about 95% Glucose-6-Phosphate and 5% Glucose-1-Phosphate at equilibrium.

The Glucose-l-Phosphate so formed may then engage in other reactions, the most important of which is probably the synthesis of starch. This process can be summarised by the simple equation.

Glucose-l-Phosphate  $\overbrace{ }^{ \text{phosphorylase}}$  Starch+Orthophosphoric Acid K The energy required to link the Glucose units comes from the hydrolysis of the phosphate bond, hence, ultimately, from the A.T.P. which phosphorylated the Glucose in the first place. Starch cannot be formed directly from Glucose alone. With the Cori Ester and a different enzyme found in animal systems, Glycogen is formed. The production of Sucrose also requires Glucose-l-Phosphate, thus:

Glucose /

sucrose Glucose-l-Phosphate + Fructose  $\longrightarrow$  Sucrose + Ortho-<br>bhosphorylase phosphoric Acid. phosphoric Acid.

Other disaccharides, some quite unknown in nature, can be syntheaised by reaction of the appropriate sugar with the Cori Ester in the presence of Sucrose Phosphorylase (Ref. 2).

Wolfrom and Fletcher (Ref. 16) describe <sup>a</sup> chemical study of the structure. The high dextrorotation was interpreted as indicating the  $\propto$  - configuration. Synthetic Glucose-l-Phosphate was prepared by treatment of  $\propto$  - Acetobromoglucoae with Silver Orthophosphate. The resulting material, after hydrolysis of the acetate groups and subsequent purification, was found to be identical with the Cori Ester. The fact that Starch and Glycogen are  $\alpha$ -linked and synthesised via the Cori Ester, whereas the  $\beta$  -linked Cellulose is not, might also be evidence for the $\alpha$  -form. None the less, in stereochemical problems, it is difficult to be absolutely certain of conformations deduced by chemical methods alone.

These authors, in passing, point out that Glucose-1 -Phosphoric Acid is stronger than Orthophosphoric Acid, and go on to suggest that it might be more accurate to describe it as <sup>a</sup> glycoside rather than as an ester. This terminology, although probably more correct, does not seem to have been generally accepted.

### Experimental Methods.

Glucose-l-Phosphate is available commercially in <sup>a</sup> very pure state as the Di-Potassium salt Di-hydrate. Crystals were grown of sizes up to  $2 \times 1 \times 1$  mm., occasionally bigger,  $by /$ 

by the slow cooling of an aqueous solution, saturated at  $60^{\circ}$ C, down to about  $25^{\circ}$ C. In carrying out this process, the construction of <sup>a</sup> large, steam-heated water tank, lagged with glass wool, was found to be very useful, as the large quantity of water in it led to much slower cooling than could be obtained by using a wacuum flask. Cooling from about 60°C to about 50°C took some eighteen hours. The crystals were observed to be monoclinic with <sup>a</sup> length-breadth ratio around 2:1. They did not show an easy cleavage in any direction being, in fact, sufficiently hard to be ground into spheres using Bond's sphere grinder (Ref.  $17$ ), or into approximate cylinders by being rolled between sheets of fine emery paper.

A crystal about 0.4mm. in diameter was selected and mounted with the prism axis lying along the axis of rotation. After alignment by means of oscillation photographs, <sup>a</sup> Weissenberg photograph of the zero-layer was taken. In this and all subsequent work, the source of radiation was <sup>a</sup> continuously evacuated, self-rectifying Raymax tube. The data actually used in the determination were collected using Cu -  $K_{\infty}$ radiation, and <sup>a</sup> running voltage and current of 50kV and <sup>20</sup> mA. The camera employed was a 5-cm. radius, vertical travel, normal beam camera (Ref. 18).

Approximate reciprocal lattice dimensions were obtained initially from the h 0 0 and 0 0 1 reflections. Sine  $\Theta$  for each reflection was found by measuring its distance on the film from the sharply defined shadow of <sup>a</sup> knife-edge etrip, which is part of the camera, and which subtends an exactly known angle at /

at the axis of rotation of the crystal. On extrapolating the values so found to sine<sup>2</sup> $\theta = 1$ , reasonably good approximations to a  $*$  and  $\mathbf{r}^*$  were obtained. The cell was monoclinic, and  $\beta^*$ was calculated from the separation of the axial lines on the Weissenberg photograph. These approximate values of  $a^*, b^*$  and  $\beta$ <sup>\*</sup> were then improved in turn, using h 0 1 reflections of high sine  $\theta$  and extrapolating to sine<sup>2</sup> $\theta$  = 1, until consistent values were obtained. Zero layer photographs were obtained about the a and c axes, and values of  $a^*$ ,  $b^*$ ,  $c^*$  and  $\beta^*$  arrived at in the same manner.

The separation of the reflections of ji an(l K<^ <sup>2</sup> radiation at high angles was sufficient to permit measurements of the sine  $\theta$  values to be made on the  $K_{\alpha}$  spots alone. The cell dimensions finally obtained, taking the wavelength of Cu  $K \sim 1$  to be 1.5405 Å were:

> a = 10.440 2 + 0.005 <sup>X</sup>  $b = 9.025 \quad \text{\AA} = 0.005 \quad \text{\AA}$  $c = 7.518 \text{ } \text{\AA} = 0.005 \text{ } \text{\AA}$  $\propto$  =  $\times$  =  $90^{\circ}$  $\beta$  = 110° 24'  $\frac{1}{2}$  6

The cell volume =  $665 \frac{\text{R}^3}{\text{s}}$ .

The density, found by flotation in a solution of iodomethane and chloroform, is 1.85gm/cc, the density of the flotation liquid being found by direct measurement of the weight in <sup>a</sup> density bottle.

On the assumption that there are two structural units per unit cell, the molecular weight of each 3hould be 370.5» The molecular weight of DiPotassium Glucose-l-Phosphate Dihydrate is 372.4» hence there are two units in the cell. The linear absorption /

absorption coefficient,  $\mu$  , is equal to 80 cm.<sup>-1</sup> for Cu K<sub>o</sub> radiation.

The only systematic absences were those occurring in the OkO reflections when  $k = 2n + 1$ , indicating a screw axis parallel to b. The space group is therefore  $P2^1$ .

# Intensity Measurements.

An obvious problem in the measurement of the diffracted intensities was the rather high absorption coefficient. Absorption effects can be minimised either by using very small crystals, or by using <sup>a</sup> short wavelength radiation, absorption coefficients decreasing rapidly with diminishing wavelength.

Lipson and Cochran (Ref. 24) state that, if absorption is to be negligible, the product $\mu^{\dagger}$ , where  $\dagger$  is the mean thickness of the crystal, must be about 0.05. When  $\mu$  = 80cm<sup>-1</sup> this leads to <sup>a</sup> crystal diameter around 0.006 mm, which is too small to be practical. Even with crystals around 0.1 mm diameter, it was found that high angle reflections were extremely weak, unless long exposures, comparable with the filament •life' of <sup>a</sup> continuously evacuated tube, were employed.

Calculation of the absorption coefficient for Mo  $K-\infty$ radiation, of 0.71  $\frac{0}{0}$  wavelength, showed it to be only about 10  $cm<sup>-1</sup>$ . Accordingly, a Molybdenum anode and a zirconium filter were fitted to the X-ray tube. Oscillation photographs were taken, with a fairly *harge crystal*, at a working voltage and current of 70 k V and 7.0mm A. Raising the tube current led to instability. The result diffraction pattern recorded was extremely weak, only <sup>a</sup> few low-angle reflections being discernable. This was not too surprising, since the absorption of X-rays by the Silver Halide crystals in the film, which leads to blackening, also decreases greatly with decreasing wavelengths. Much more serious was the greatly increased background on the film. This fogging is presumably caused by <sup>a</sup> greater ratio of •white' /

'white' to characteristic radiation being emitted from a Molybdenum target, and this method had to be abandoned.

M.J. Buerger has shown that for <sup>a</sup> cylindrical crystal, the optimum ratio of absorption to diffraction is obtained when the crystal diameter =  $2/\mu$ . If  $\mu$  = 80 cm<sup>-1</sup>, one obtains a value of 0.25 mm. Intensity data were therefore obtained from crystals whose cross sections were between 0.2 and 0.5 mm. The absence of an easy cleavage in any particular direction made the use of rather irregularly shaped fragments unavoidable for axes other than the  $b$  -axis, which could be ground to an approximate cylinder. Since the hardness appeared to be anisotropic, the cylinders tended to be elliptical in cross section rather than circular. Spherical, or almost spherical, crystals in the correct size range were obtained but the difficulty of orientating these was much greater than with <sup>a</sup> crystal chip, there being no recognisable edges or faces on them. If it is not possible to get the desired axis vertical with the normal goniometer arcs, it is necessary to demount the crystal, and replace it more nearly at the correct angle. Marking the sphere at the 'north', 'west', and 'east' positions with coloured ink was tried, but the smallness of the crystal necessitated extremely small marks, and these came off too easily in the de-mounting and re-mounting process.

To begin with, only the okl, 1kl, hol, h1l, <sup>h</sup> k <sup>o</sup> and <sup>h</sup> k 1 layers were photographed, and the intensities of the zero-layer reflections measured. The multiple film technique was employed with one Ilford 'Industrial G' and two 'Industrial R' films, the G-film being nearest to the orvstal. Intensities /

Intensities were measured by visual comparison with <sup>a</sup> series of oscillation photographs of different timed exposures, recorded on the same types of film, using the same crystal as for the Weissenberg photographs. Scaling between the 'G' and first and second 'B' films was carried out by measuring the intensities of reflections common to two films. A proportional relationship, I  $(G) = k$ , x I  $(B<sub>1</sub>)$  where I  $(G)$  = intensity as measured on the G - film and I  $(B_1)$  = intensity of the same reflection as measured on the first <sup>B</sup> - film, was assumed. <sup>A</sup> similar relation was assumed for the ratios  $B_1:B_2$  and  $G:B_2$ . The 'best' value of k is found then by the relationship  $k^{\text{I}}_{1} = \sum (I(G))^2 / \sum I(G)$  x  $I(B_1)$ (Ref. 29, p. 335).

The estimated intensities so obtained were corrected for Lorentz and polarisation factors by the method of Cochran (Ref. 19). The resulting squared structure amplitudes were left on <sup>a</sup> relative scale. This was also the method used for all succeeding films.

## The Patterson Function,

Projections of the Patterson function down the three cell axes were calculated (Ref. 20). 'Sharpened' projections, which give greater resolution of the maxima, were also calculated and, in practice, used in preference to the unsharpened projections. Calculations at this stage were carried out using the Beevers-Lipson strip method, along with an electromechanical analogue machine.

Reproductions of the revised a-axis, the b-axis, and the c-axis projections are given in figures  $5a$ ,  $5b$ , and  $5c$ , in that order. The most obvious features were the heavy 'ridge' of vectors along the a-axis of the b-axis projection, i.e. along  $Z = 0$ , and the row of peaks, including one which is exceptionally large, at  $y = \frac{1}{2}$  on the c-axis projection. The last mentioned row of peaks was expected, as Harker has pointed out that certain symmetry elements give rise to an accumulation of vectors on certain lines or planes. In this case, we have the symmetry element  $2^1$ , with the equivalent positions  $(x, y, z)$ and  $(-x, y+\frac{1}{2}, -z)$  which must give rise to a peak for the i 'th atom, position  $(x_j, y_j, z_i)$  in the unit cell, at  $(2x_j, \frac{1}{2}, 2y_i)$ in vector space, i.e. all atoms in the cell give rise to a vector somewhere on the plane  $y = \frac{1}{2}$ . In projections parallel to this plane, the result is an accumulation of peaks on <sup>a</sup> line at  $y = \frac{1}{2}$ . In general, if we have two unrelated atoms A and B, at positions  $(X_{\mathbf{A}}, Y_{A}, Z_{A})$  and  $(X_{\mathbf{B}}, Y_{\mathbf{B}},$  and  $Z_{\mathbf{B}})$ , the twofold screw axis will produce vector peaks at:  $(2 /$ 







 $(2x_A, \frac{1}{2}, 2z_A)$  and  $(2x_B, \frac{1}{2}, 2z_B)$  - ("Harker peaks")

 $(x_A-x_B, y_A-y_B, z_A-z_B)$ and $(x_B-x_A, y_B-y_A, z_B-z_A)$ ("Difference peaks")  $(x_A+x_B, y_A-y_B^{-\frac{1}{2}}, z_A+z_B)$  and  $(x_B+x_A, y_B-y_A^{-\frac{1}{2}}, z_B+z_A)$  ("Sum peaks") In attempting to locate the sugar part of the compound, use was made of the symmetry properties of the pyranose ring. While the complete Glucose-l-Phosphate anion does not possess a centre of symmetry, certain parts of it do. All the ring atoms, plus the oxygen atom attached to  $C_0$ , and the atom  $C_6$ , are related by a centre of symmetry in the middle of the ring. When the space group has a centre of symmetry or <sup>a</sup> centrosymmetric projection, this causes the Patterson function to have <sup>a</sup> fairly large multiple peak at <sup>a</sup> point whose vector separation from the origin is equal to that of the centrosymmetric, or approximately centrosymmetric, units in the cell. Where only a centrosymmetric projection exists, the separation in this projection only can be found. This is the 'centre-centre' peak, and the correct identification of this is sufficient to locate the molecular centre.

Further, when the molecule contains a number of vectors which are parallel to each other, as is the case with the pyranose ring, <sup>a</sup> characteristic pattern of maxima in the vicinity of the Patterson origin, at <sup>a</sup> radius of from 1.5 to 2.5 will be produced. <sup>A</sup> specific orientation of the molecule will give rise to <sup>a</sup> corresponding orientation of this pattern. It is not necessary that the apace group should have <sup>a</sup> centre of symmetry to utilise this fact. (Ref. 21)

If /

If the centre-centre vector and the multiple intramolecular vectors are correctly identified, this is sufficient to locate the position and orientation of the symmetrical or partially symmetrical molecule in the unit cell. The overall strategy in approaching the problem, then, was to find positions for the  $K^+$  and P atoms, these being rather heavier than the others, which gave suitable Harker, 'sum' and 'difference' peaks and to deduce the position and orientation of the Glucose ring from the selected centre-centre and multiple peaks.

Unfortunately, the amount of overlapping of maxima in projection is so considerable that it is not always possible to detect the required peaks. This is especially true when there are atoms in the cell which are somewhat, but not greatly, heavier than the ring atoms. <sup>A</sup> single medium-medium vector will then be of about the same weight as the multiple lightlight vectors. It was also true in this case that the centrecentre vector would only occur as <sup>a</sup> large multiple peak on the b -axis projection, as this is the only projection which is centrosymmetric. On other projections, the vectors giving rise to the 'centre-centre' peak will appear as <sup>a</sup> patch of 'positive ground' stretched in the direction of the b-axis, the degree of diffuseness depending on the angle between the molecular plane and this axis. Finally, if Patterson projections are sharpened, the area around the origin is considerably affected by series termination errors. Since some of the intramolecular vectors are short, about 1.5  $\lambda$ , this means that they will occur in a region containing peaks and troughs not actually attributable to real /

real interatomic vectors. If the Patterson projection is not sharpened, the maxima are so coalesced as to be beyond interpretation.

Initially, only the positions of the medium weight atoms were sought. From the **b** -axis Patterson, it was assumed that these three atoms were collinear, and parallel to 'a'. When what seemed to be a reasonable 'fit' on the Patterson map has been obtained, h o 1 structure factors were calculated and compared with the observed values. <sup>A</sup> considerable amount of time was spent trying to obtain <sup>a</sup> set of positions which gave some agreement between observed and calculated structure factors, but no success was obtained.

In view of the complete lack of progress, it was decided that the three dimensional Patterson function might be more fruitful, and that <sup>a</sup> salt of Glucose-l-Phosphoric Acid which was isomorphous with the Potassium salt would also be usefull Rubidium and Ammonium salts are often isomorphous with the equivalent Potassium salt, and these derivatives of Glucose-l-Phosphoric Acid were therefore prepared. This was done by passing <sup>a</sup> solution of the Di potassium salt through <sup>a</sup> resin ion exchange column in the Hydrogen form, (Amberlite I.R. 120 H), thereby obtaining the free acid, and neutralising with Rubidium Carbonate or Ammonia, as required. One difficulty with this procedure is that the Cori Ester is labile to acid, with <sup>a</sup> consequent risk of self-hydrolysis. Both salts were prepared successfully, though not, perhaps, in <sup>a</sup> very pure state. The ammonium salt did not crystallise, possibly because of impurity. The Rubidium salt, however, crystallised well, and Weissenberg photographs about two axes were obtained. These /

17-

These showed it to possess an orthorhombic cell, the space group being probably  $P2_1^22_1^2$ . Since it was not isomorphous, this derivative was abandoned, while efforts to crystallise the ammonium salt were continued.

Concurrently the general <sup>h</sup> <sup>k</sup> <sup>1</sup> intensities for the dipotassium salt were measured. These were estimated on the earlier okl, 1kl, hol, h1l, hko, and hk1 layer photographs, supplemented by upper-layer normal-beam Weissenberg photographs taken about the c, b, and what appeared to be the a-axis. Scaling was carried out by comparing reflections common to two or more axes. During the scaling process, it became obvious that the "a" axis Weissenbergs, from 2kl onwards, were not consistent with the other films. <sup>A</sup> careful comparison of the intensities with those on the non a-axis films, and calculation of the lengths of the cell diagonals showed that the short <sup>a</sup> - <sup>c</sup> diagonal was similar in length to the a-axis. <sup>A</sup> cell with this diagonal as the longer non-unique axis would have the dimensions

> $a^1 = 10.50 \text{ Å}$  $b = 9.025$   $\lambda$  $c = 7.518$   $\frac{0}{10}$  $\beta^1$  =  $111^{\circ}44'$

the original cell being, as given before:

 $a = 10.44$   $\lambda$  $b = 9.025$   $\AA$  $c = 7.518$   $\frac{8}{10}$  $\beta = 110^{\circ}24'$ 

It is apparent that these two cells have rather similar dimensions. This similarity between the two possible cells also intruded at a later stage in the determination. After re-indexing the films, consistent /

consistent  $r^2$ s were obtained.

To begin with, only the unsharpened three-dimensional Patterson function was calculated. This was decided on firstly because it was assumed that resolution would be sufficiently improved over the two-dimensional case, even without sharpening, and secondly, because of doubts about the accuracy of high sin 9 intensities. These appeared mainly on upper-layer photographs, on which reflections were either elongated or compressed, making them more difficult to estimate. This weighted against the exaggeration of these terms relative to the lower angle reflections.

The calculation was carried out on the Glasgow University D.E.U.C.E. Computed, using Fourier summation programme of J.3. Rollett. Sections were calculated in planes perpendicular to the b-axis at intervals of  $\frac{1}{40}$ th of  $\mathbf{b}$ . Each plane was sampled at intervals of  $\frac{1}{40}$ th of 'a' and  $\frac{1}{30}$ th of c. The sections were contoured and drawn out on glass plates which were then arranged at the correct separation in <sup>a</sup> frame lit from below. This enabled one to get an overall qualitative view of the Patterson function in three dimensions. For more detailed work, each section was examined individually.

The most obvious features of the Patterson were heavy peaks along  $z = 0$  at both  $y = 0$  and  $y = \frac{1}{2}b$ . It was also plain from even <sup>a</sup> superficial inspection that the a-axis projection, which had been calculated by hand, was incompatible with the three dimensional synthesis.

The calculation was checked and it was found that <sup>a</sup> projected/

projected area of  $\frac{1}{2}c$  by  $\frac{1}{4}b$  had been calculated instead of  $\frac{1}{2}c$  by  $\frac{1}{6}$ b. This was rectified, and the corrected version is shown in figure 5a. Both this projection and the three-dimensional synthesis strongly suggested that the pyranose ring was lying with its plane perpendicular to the screw axis, and one of the long diameters parallel to the a-axis. Since the medium weight atoms were also lying in <sup>a</sup> common plane, it followed that the vectors from these atoms to the pyranose ring must also be lying in <sup>a</sup> plane, again perpendicular to the screw axis. This agreed very well with the observation that the only regions of marked vector density apart from  $y = 0$  and  $y = \frac{1}{2}b$  was the plane  $y = \frac{11}{40b}$ . From the foregoing evidence, it was concluded that the medium weight atoms lay almost in <sup>a</sup> plane perpendicular to the screw axis, and that the sugar ring lay in <sup>a</sup> plane parallel to this and separated from it by about  $11/40$ b, some 2.5  $\hat{X}$ . This general picture of the structure proved to be correct.

Some idea of the conformation could be gained from the observation that if the  $\beta$ -Glucose-l-Phosphate molecule is arranged so that the Phosphorus atom is 2.5  $\AA$  from the ring plane. the oxygen atoms of the phosphate group are compelled to approach the ring atoms closely. The  $\lt$  -form, however, is in its most  $ext{ended}$  extended configuration when the phosphorus atom is 2.5 $X$ from the ring plane, thus strongly tending to confirm the chemical evidence for the  $\alpha$  -conformation.

The grouping of the atoms in planes has the marked disadvantage that it leads to <sup>a</sup> heavy concentration of peaks on the Harker section, since both Harker and non-Harker vectors will occur at and near  $y = \frac{1}{2}b$ . From the orientation of the molecule, it /

it was apparent that the 'centre-centre' vector must lie distributed about  $0.5$   $\lambda$ , which is the depth of a pyranose ring, above and below the Barker section. This deduction, while correct, led to <sup>a</sup> mis-identification of certain peaks, that is, some peaks at about  $y = \frac{1}{2}b - 0.5$  *x* were given the role of 'possible centre-centre peaks'. Other possibilities were correspondingly weighted less heavily. In retrospect, this misinterpretation was probably the largest single obstacle requiring to be removed before obtaining <sup>a</sup> refinable trial structure.

Since a structure giving satisfactory Harker, sum, difference, and centre-centre peaks could not be devised, work was temporarily concentrated on the a-axis projection, for which the x-co-ordinates of the atoms were not required. <sup>A</sup> fairly prominent peak at the appropriate y-co-ordinate was selected as the 'centre-centre' peak, and from this and the known molecular orientation, y and <sup>z</sup> parameters for the sugar ring were obtained. The y co-ordinate of one atom can be set arbitrarily at zero, with space group  $P2^1$ , and since  $K_1$ ,  $K_2$  and <sup>P</sup> were believed to be collinear and at the same y-level, all three were placed at  $(x,0,0)$  i.e. at the origin in the a-axis projection. Agreement between calculated and observed structure factors was reasonably satisfactory. Refinement was carried out by means of  $(F_{ob} - F_{caloc})$  Fourier synthesis. In the course of refinement, the entire molecule moved in the direction of an increasing z-co-ordinate, indicating that the originally chosen centre-centre peak was incorrect. Only very small changes in molecular orientation were required. Peaks in the  $(\beta - \beta)$ map /

map were taken as being the water molecules, as there were only two of them, and these were included after the fourth cycle. of 0.31, but would not go below this somewhat high value. Fluctuations in the  $({\bigcirc -} {\bigcirc_{c}})$  map. at this stage, were considerable but gave no indication of what atomic shifts were required, since peaks and hollows occurred in spaces where there were no atoms. The area around  $(x,0,0)$  was at a level of almost zero, and more or less flat, reinforcing the belief that at least the medium weight atoms were correctly placed. Attempts were now made to find <sup>a</sup> structure which would fit the three-dimensional Patterson, retaining the y and <sup>z</sup> co-ordinates found from the a-axis projection. This was done by examining the sections from  $y = \frac{9}{40}$  to  $y = \frac{11}{40}$ , and, on the correct assumption that these sections contained the medium atom  $\longrightarrow$  light atom vectors, and hence would contain three 'images' (Ref. 22) of the sugar ring, separated by the same distances as the heavy atoms, trying to 'fit' three molecules on to the peaks in these sections. The z-parameter of the molecular centre was kept constant, and moves made only in the x-direction. Since the  $a-axis$  is  $10.44$   $A$  long, and the 'heavy' atoms had to be at reasonable distances from each other, a separation of about  $3.58$ between images was required. None of the structures postulated from this procedure gave really convincing vector distributions, and those for which structure factors were calculated showed no correlation with observed values. The structure refined to a value of 'R' (i.e.  $\sum |E_i| / \sum |E_i|$ )

slightly increased number of reflections, about 1,350 instead of 1,200 / The Patterson function was now recalculated with a

1,200, and with sharpening. The sharpening function was obtained by dividing the  $F^2$ 's in the h o l plane into ranges of sin<sup>2</sup> $\theta$  containing nearly equal numbers of reflections and calculating the factor required to bring the average  $F^2$  in each range up to that of the innermost range. This, in effect. converts the real, diffuse atoms into imaginary, point scatterers. The limitation of a finite number of terms being available makes reduction to <sup>a</sup> perfect point impossible, but the volume of each peak is, none the less, greatly reduced. The function  $(1 + 8 \sin^3\theta)$  was found to be a fairly good fit through the factors required, and this was accordingly applied to the data. Although resolution of the peaks was considerably improved, no new interpretation of the Patterson was arrived at.

The Ammonium salt had not yet been crystallised, and aftercconcluding that the methods employed up to this point were not succeeding, it was decided thet <sup>a</sup> completely different approach should be tried.

### Direct Methods.

By 'direct methods' one implies methods by which the phases of structure factors are deduced from mathematical relationships between their amplitudes. In practice, only centrosymmetric apace groups or plane groups way be solved, as the relationships at present known are effective only when applied to structure factors with a phase angle of  $0$  or  $\overline{\mathbf{H}}$ radians; i.e. a sign of  $(+)$  or  $(-)$ . The space group P2, is non-centrosymcetric and possesses only one centrasymmetric projection, hence only the h o 1 structure factors can have their phaser determined, even in principle.

In order to apply direct methods, it is convenient to convert the observed structure factors into unitary structure factors. This is defined as the ratio of observed absolute amplitude to maximum possible amplitude. It is given the symbol 'U' and must be between -1 and +1. The procedure determining U is as follows:

If  $f_j$  is the scattering factor for a particular atomic type at a particular sin  $\Theta$  value, and  $\sum_{j=1}^N f_j$  denotes the sum over all atoms in the cell, then  $n_i$ , the unitary scattering factor of the j'th atom is equal to  $f_j/\sum_{j=1}^N f_j$ .

The quantity  $\epsilon$  is defined as:  $\epsilon = \sum_{j=1}^{\infty} (n_j)^2$ , and can always be calculated from the theoretical scattering curves for each type of atom present.

 $r^2$ , if its value were already known on an absolute scale, could readily be converted to U. Since  $F^2$  is not known absolutely, <sup>U</sup> must be found by <sup>a</sup> statistical method similar to that/

that of Wilson (Ref. 26). He showed that, taken over <sup>a</sup> number of reflections in the same sin  $\Theta$  range, the average  $\left\| \mathbb{P} \right\|^2$  was equal to  $\sum_{j=1}^{\infty} r^2$ , If we designate the average  $\left| \mathbb{F} \right|^2$  in a particular sin  $\Theta$  range as  $\langle I \rangle$ , then by plotting  $\epsilon / \langle I \rangle$ against sin 9, <sup>a</sup> curve is obtained of the square of the correcting ratios required to convert F's to U's. Let this be called  $\phi$ . By multiplying the observed F's on the reciprocal net by  $\sqrt{\Phi}$  for the appropriate sin  $\Theta$  value, U's were obtained. A table of U x 1000is given (Table 1).

The simplest, and, if it works, most useful relationship is the inequality derived by Harker and Kasper. When the only symmetry element is <sup>a</sup> twofold screw axis, this takes the form:

 $\mathbf{1} \ \mathbf{v}_{\text{hkl}} \ \mathbf{1}^2 \leq \frac{1}{2} \ \left\{ \mathbf{1} + \left( \mathbf{1} \right)^k \ \mathbf{v}_{\text{2h},0,21} \right\}$  $(Ref\ 24, p. 37).$ 

This can be used to give <sup>a</sup> sign to <sup>a</sup> structure factor of the type  $h = even$ ,  $k = zero$ ,  $l = even$ . It will be observed that although signs can be given only to 'even-even' reflections in the h o l zone, any one of the general intensities may be involved in the relationship. It is also the case that negative signs may be found if the  $U_{h|k|}$  on the left-hand side has an odd value of k.

As an initial trial, however, only the hol intensities were examined. No pairs of U's of the type  $U_{\mathbf{h}}$ ,  $U_{2h}$  of sufficient magnitude to make the inequality useful were found.

The 'triple product' relationship was therefore investigated. This states that if  $S(h)$  represents the sign of a /

Table 1. 1000U

L



 $\mathbf{H}$ 

<sup>a</sup> structure factor of index (h), or <sup>a</sup> combination of indices represented by  $(h)$ , then:

 $S(h) S(h') S(h + h') \approx + 1$ 

where the symbol ' $\approx$  ' means 'probably equals.

e.g.  $S(201) \times S(301) \times S(502) \approx +1$ .

<sup>A</sup> measure of the probability of this sign relation holding was derived by Cochran and Woolfson, who found:  $(R_6f.24)$ ( ^  $P_+ = \frac{1}{k} + \frac{1}{2}$  tanh (( $\zeta$ / $\zeta$ )  $\frac{1}{k}$  U<sub>h</sub> x U<sub>h</sub>,x U<sub>h + h</sub>/ 4 )

where  $P_+$  is the probability and

$$
\epsilon_3 = \sum_{j=1}^{N} n_j^3; \quad \epsilon = \sum_{j=1}^{N} n_j^2
$$

 $\begin{array}{cc} \begin{array}{ccc} 3 & \frac{1}{3}-1 & 3 \end{array} & \begin{array}{c} \overline{1} & \overline{1} & n_1 \end{array} \\ \begin{array}{ccc} \overline{1} & \overline{1} & n_1 \end{array} & \begin{array}{ccc} \text{if } n_1 & \end{array} & \begin{array}{ccc} \overline{1} & \left( \frac{1}{3} & \overline{1} & \overline{1} \end{array} \right) \\ \begin{array}{ccc} \overline{1} & \overline{1} & 1 \end{array} & \begin{array}{ccc} \overline{1} & \overline{1} & 1 \end{array}$ is approximately constant over reciprocal space, so that P is a function of the product  $\begin{pmatrix} 1 & \mathbb{U}_h \\ 0 & \end{pmatrix}$ ,  $\mathbb{U}_{(h+h')}, \begin{pmatrix} 1 \\ 0 & \end{pmatrix}$ , and can therefore be plotted against the product.

The method of application was as follows: U's were marked on <sup>a</sup> drawing of the reciprocal net, and <sup>a</sup> copy of this made on to a transparent sheet. By moving the origin of the copy to a particular reflection h on the first net, the reflections 'h' and  $'(h+h')'$  were found in pairs superimposed on each other. These were listed systematically, the product  $\sharp$  ( $\mathfrak{v}_{h'}$ )( $\mathfrak{v}_{h+h'}$ )  $\sharp$  calculated,  $F_+$  found from a graph of  $F_+$ versus the triple product, and written alongside the list. Rather arbitrarily, perhaps, it was decided that products with  $P_{+}$  0.90 would be accepted, and with  $P_{+}$   $<$  0.90, rejected.

Some 450 triple products, and  $P_+$  for each, were calculated, and from these, three chains of structure factors, the members of each of which probably had the same sign, were

deduced. This was partly made possible by the assumption that all QGL reflections were positive, this being very likely if all the medium atoms lay on  $z = 0$ . The actual sign for each chain was unknown, and they were given the letters a, b, and c. Eight 3ets of sign permutation were therefore possible. Only seven of these were calculated as the permutation 'all signs positive' would have given <sup>a</sup> large peak of electron density at the origin, and the harker section clearly showed that no atom lay exactly on a screw axis. Consequently, the seven permutations were calculated on Deuce, and the electron density maps plotted.

While no definite conclusions could be drawn from these at the time, comparison with the finally calculated structure factors showed that about  $85%$  of the triple product relationships accepted as being "90% probable" were in fact correct. The three chains amounted in all to 55 reflections, and the most nearly correct permutation had 45 of the <sup>55</sup> signs correct. There are <sup>200</sup> <sup>h</sup> <sup>o</sup> <sup>L</sup> reflections, and <sup>a</sup> Fourier map derived from <sup>55</sup> of the strongest reflections, <sup>45</sup> correctly and <sup>10</sup> Incorrectly signed, might not be expected to give much indication of the correct structure. However, the corresponding electron density map is given (Fig. 5d), along with the final structure.

It will be seen that the regions of highest electron density are very close to the positions of atoms  $K_2$  and P, although K, is only poorly represented. Since it was mainly the heavier atoms which were being sought, even these could have been used to find the remaining atoms by <sup>a</sup> superposition method. Extension of the sign relationships to make use of the general <sup>h</sup> <sup>k</sup> <sup>L</sup> /


<sup>h</sup> k <sup>L</sup> reflections was under consideration, but was not proceeded with as the crystalline Ammonium salt of Glucose-l-Fhosphoric Acid became available at about the same time.

Direct methods, then, even used only to tho extent of the simple relationships which could be applied with <sup>a</sup> desk calculating machine, and to one zone of intensities, did give a crude picture of some of the main features of the structure. In view of this, direct methods, using all the available data, and not merely one layer, might usefully be applied to sugar phosphate structures of about the same complexity as Glucose-1- Fhosphate, as <sup>a</sup> routine procedure, since the rules for their application are quite explicit and require no information ercept that which is normally available, that is, reflected intensities, space group, and the chemical composition.

The experimental difficulties are twofold. Firstly, since relationships may be established between reflections in quite different regions of reciprocal space, the scaling of all reflections must be fairly accurate. Any anistropic factor, such as absorption by an irregularly shaped crystal, can make this difficult. Secondly, the most Intense reflections are very valuable in establishing inequality relationships or increasing the probability,  $P_+$ , of a triple product being positive. They are also the reflections moat subject to extinction, particularly if they are at low angles. The'chain reaction' nature of sign-determination means that all may depend on accurately evaluating two or three intense reflections, and if one or more of these is affected by extinction, then the process is made that much more difficult, or even impossible.

Conversely, of course, the existence and correct measurement of <sup>a</sup> fev large reflections can lead to <sup>a</sup> correct structure with comparatively little effort.

#### Isomorphous Replacement.

While work was proceeding on direct methods, enquiry was made to B.D.H. Ltd. concerning the possible preparation of Ammonium Olucose-l-Pbosphate on a small commercial scale. This was successfully prepared and supplied in <sup>a</sup> very pure state. The material was re-crystallised by the same methods used for the potassium salt, and crystals of <sup>a</sup> size suitable for X-Ray photography selected. It was notable that excellent crystals were easily grown, with no tendency toward formation of <sup>a</sup> syrup. Presumably this was possible because of the high purity of the material. Weissenberg photographs of the h o L, h l L, h 2 L, h 3 L, h k o, h k 1, h k 2, h k 3, and o k L layers were obtained using <sup>a</sup> spherical crystal. Calculation of the cell dimensions showed that these were similar to the dimensions of the Potassium salt, being:

> $a = 10.42 \text{ R}$  $b = 9.09$   $A$  $c = 7.55$   $\frac{8}{11}$  $\beta$  = 110<sup>°</sup>37'

The only systematic absences were among the o k o reflections, in the case  $k = (2n + 1)$ , indicating the space group P2,. At a later stage, photographs were taken with a large crystal and <sup>a</sup> rather long exposure, in order to detect the weakest reflections, and these showed faint <sup>o</sup> <sup>k</sup> <sup>o</sup> reflections at  $k = (2n + 1)$ . These cannot, so far, be explained.

Density measurements agreed with the value calculated on the basis of two molecules of Ammonium Glucoae-l-Fhosphate Dihydrate per unit cell, and an analysis for Nitrogen content gave /

gave <sup>a</sup> percentage corresponding to the formula for <sup>a</sup> di-hydrate. The preceding evidence suggested that the ammonium and potassium salts were chemically analogous and crystallised isomorphously. The absorption co-efficient was calculated to be 24  $\text{cm}^{-1}$ .

Both sharpened and unsharpened Patterson projections down the a, b, and <sup>c</sup> axes were calculated. Examination of the a- and c- axis were not very instructive, probably because of the amount of overlapping. The o-axis projection possessed <sup>a</sup> very noticeable peak, marked H<sub>1</sub> on the overlay (Fig. 6) which fell almost exactly on <sup>a</sup> large peak on the Harker section of the three dimensional Patterson function of the Potassium salt. This was taken to be the Phosphorus-Phosphorus peak. A number of structures based on this assumption were postulated, but none of these were satisfactory, and it was decided that the data should be used in <sup>a</sup> somewhat different manner. It can be shown (Ref. 22) that if two isomorphous structures are available, say 'm' and 'n', then after putting the  $F^2$ 's on the correct relative scale, a Fourier summation with the co-efficients  $(\mathbf{Fm}^2 - \mathbf{Fm}^2)_{h\mathbf{k}\mathbf{l}}$ gives <sup>a</sup> vector map similar to the simple Patterson function, but with all vectors other than those from the replaceable atoms to the remaining atoms and to each other removed, this being called the 'difference Patterson'. The relative weights of the peaks, in this case, would be as follows: if  $Cn =$  cation,  $P =$  Phosphorus,  $C = Oxygen$ ,  $C = Carbon$  then:

Cn  $\longrightarrow$  Cn =  $(18^2 - 7^2)$  = 312  $\text{Cn} \longrightarrow P$  =  $(18 - 7) \times 15 = 165$  $\text{Cn} \longrightarrow 0$  =  $(18 - 7) \times 8 = 88$  $\text{Cn} \longrightarrow \text{C} = (18 - 7) \times 6 = 66$  $It$   $'$ 



It is seen that these are more or less in the ratio 4: 2: 1, with Cn Cn as the heaviest vectors. These would, surely, be easily recognised, and the cation positions immediately ascertained. Concurrently with these calculations, the general <sup>h</sup> <sup>k</sup> <sup>1</sup> intensities were being measured, with the help of Mr. P. Rodgers. In fact, the 'difference Patterson' consisted of what appeared to he <sup>a</sup> random collection of peaks, with no obvious interpretation at all.

Since the h 1 L intensities had already been estimated. a sharpened, generalised Patterson function was computed as <sup>a</sup> prelude to the full three-dimensional calculation. The

The three-dimensional Patterson function is :  $P(U,V,W) = \sum_{h} \sum_{k} \sum_{l} |F_{hkl}|^2 \exp 2 \pi i (hU + kV + IW)$  (1)

If we define the generalised projection as :  $P_K(U,W) = b \int P(U,V,W) \exp (-2 \pi i KV) dV$  (2)

and substitute  $P(U, V, W)$  from (1), noting that :  $\int$  exp  $2 \pi i(k-K)$ VdV = 1 if k=K

 $= 0$  if  $k \neq K$ 

then  $P_K$  reduces to :  $1/A \sum_{h} \sum_{l} |P_{hKl}|^2$  exp  $2\pi i(hU+1W)$ which with a twofeld axis parallel to 'b' becomes :  $\frac{1}{h} \sum_{i=1}^{h} |F_{hK1}|^2$  ess2 $\pi(hU*1W)$ 

When  $K = 0$ , this results in the ordinary projection. When  $K=1$ , however, we obtain a generalised projection which consists of peaks in the same positions as the hOl projection, but modulated by  $exp(-2\pi i V)$ . The Patterson is symmetric, so that the sine term vanishes, leaving the peaks modulated by  $cos 2T V$ .

 $Y = 1$ . If we make the simplifying assumption that the Patterson function consists of <sup>a</sup> set of discrete points, then we can see that the first layer 'generalised' Patterson will be exactly like the projection, except that each point will he multiplied by cos  $2 \pi Y$ , where Y is the co-ordinate of that point in vector  $space /$ 

space.

In the Glucose-l-Phosphate structure, it was already well established that the atoms lay mainly in planes with <sup>a</sup> spacing of  $\frac{1}{4}$ b. Hence the vector peaks would occur mainly at  $Y = 0$ ,  $Y = \frac{1}{4}$  and  $Y = \frac{1}{2}$ . This meant that the peaks in the generalised Patterson would bo multiplied as follows.

- At  $Y = 0$ ; by  $+1$ 
	- $Y = \frac{1}{4}$ ; by 0
	- $Y \frac{1}{2}$ ; by  $-1$  (Harker section).

It may be noted that in the generalised Patterson, negative regions are significant. When drawn out (Fig. 7) it showed only one deeply negative region, and this was not coincident with the peak  $H_1$  on the projection. Hence  $\vec{n}_1$  could not lie on the Harker section and could not be the  $P - P$  vector. This negative peak, however, did iio almost exactly on the short cell diagonal (dotted line, Fig.  $6$ ). The peaks around the origin, which should be the other main significant feature of the generalised Patterson (peaks at Y =  $\frac{1}{4}$  are multiplied by Zero) also indicated an orientation of the pyranose ring which had the 1.5  $\frac{0}{1}$  side of the hexagon lying along the diagnnal, whereas the Potassium salt had it aligned with the a-axis. It appeared from this evidence that the h  $0$  1 and h  $|$  L photographs had been indexed so that the diagonal of the cell chosen for the Potassium derivative had, quite fortuitously, been used as the a-axis of the Ammonium derivative. The reason for the failure of the difference - Patterson was now obvious, as non-corresponding unit cells were being compared. This could have been repeated, with the corrected indices, but since the general h k 1  $\mathbb{F}^2$ 's had  $\text{matrix}$  /



mostly been measured, the three dimensional Patterson function was computed.

In order to emphasise the Phosphorus - Phosphorus and Phosphorus - other atom vectors as much as possible, the sharpening function  $(1 + 8 \sin^5 \theta)$ , mentioned above, was applied twice over to the data, giving a multiplying ratio of 81:1 in the  $\mathbf{r}^2$ 's between sin  $\Theta = 0$  and sin  $\Theta = 1$ . This degree of sharpening is quite considerable, and two unsharpened sections were calculated in order to check for possible undesirable effects. <sup>A</sup> further problem was that, in order to save time, most of the intensities above  $L = 5$  had not been measured, and this would lead to elongation of all the peaks in the <sup>Z</sup> direction. In fact, neither the high sharpening nor the cutting off of the data along one axis had any ill effect. Sharpening improved the resolution very satisfactorily and the sharp termination of data affected only the largest peaks, and then to <sup>a</sup> minor extent.

The expected vector pattern round the origin, showing the pyranose ring orientation, appeared very clearly. Also present were four peaks each at about 1.5  $\frac{8}{3}$  from the origin, and arranged in a manner corresponding to that expected from a tetrahedral group. These were the vectors from the Phosphorus atom to its covalently bonded Oxygens, and were sufficient to determine the orientation of the phosphate unit. Finally, in the sphere around the origin, there was a peak at about  $X = 0$ ,  $Y = 1.4 \, \text{\AA}.$  Z = 0. Since the pyranose ring plane was known to be perpendicular to the b-axis, and only the 1-position is axial, this /

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this vector peak presumably included the  $C_1$  - ester oxygen  $(O_7)$ link, and perhaps also the vector from  $C_G$  to  $O_G$ , this being the only other possibility. The sections in the region of  $Y = \frac{1}{4}b$ showed, as expected, the Phosphorus - Glucose ring vectors. <sup>A</sup> fair approximation to the shape and orientation of most of the anion was therefore now known, and it remained to fix the positions of the cations, of thie anion, and of the water molecules.

A direct comparison of the sections  $Y = 0, 1, 2, 3, 17, 18$ , 19, and  $20 - 1/40$ ths of b showed clearly the reason for lack of success in finding the cations. The centre-centre vector must be present on both Patterson maps. It follows from this that <sup>a</sup> vector present on one but not the other cannot be tlie centracentre vector. The maxima on the Ammonium salt map which had diminished relative to their counterparts on the Potassium salt map must correspond to vectors with the cation at one end. Examination of the sections listed above showed that on the Potassium derivative vector map, certain of the larger peaks must be  $K^+ - K^+$  and  $K^+ - P$  vectors. In the region of  $Y = \frac{1}{2}b$ , these included a number of peaks which had formerly been considered as possible centre-centre vectors. Indeed, they included all the larger peaks, the centre-centre peak being very much smaller than had been supposed. The Harker section of the Ammonium salt gave the position of the Phosphorus atom, and with the nature of the larger vectors now definitely established, <sup>a</sup> heavy atom arrangement was devised which accounted convincingly for them. Structure factors in the h O L layer were calculated for /

for the three atoms  $K_1$ ,  $K_2$  and P alone, and the agreement obtained with the observed magnitudes was satisfactory, in view of the fact that these atoms did not contain an outstandingly large proportion of the electron content of the cell (about 28%), and the somewhat approximate location of them.

Since the positions of the atoms in the pyranose ring and the oxygen atoms of the phosphate group relative to the Phosphorus atom were known, location of this atom was sufficient to place the others. It had already been suggested that the peak  $H_1$  on the b-axis Patterson projection of the Ammonium salt was, in fact, the centre-centre peak, and the position of the Glucose ring determined via the Phosphorus atoms also lead to <sup>a</sup> centre-centre peak at  $H_1$ . The co-ordinates of the freely rotating  $0<sub>6</sub>$  and also of the water molecules,  $0<sub>11</sub>$  and  $0<sub>12</sub>$ , were as yet unknown, In an attempt to obtain these, a three dimensional minimum function (Ref. 22, p. 259) was prepared graphically from the Patterson map of the Ammonium derivative. The origin was displaced to coincide with the Phosphorus-Phosphorus peak, as an "image" of the structure relative to the heaviest atom present must possess the greatest weight. In displacing the origin to the Marker section, it had to be borne in mind that the resulting minimum function would have the space group  $P2_1/m$ , leading to a solution plus its mirror image. It was presumed that the ambiguity could be resolved for the required atoms, if found, on packing considerations. As for the glucose residue, this was assumed to be the D-form, although this could not be proved by the X-Ray methods available.

The /

The minimum function did give <sup>a</sup> rough outline of the sugar ring in the position deduced previously, giving further confirmation of its correctness, but the remaining atoms were not found. An 'idealized' structure was then made up, consisting of the  $K^+$  and P positions, as far as they were known, and <sup>a</sup> perfect cyclohexane ring, set in the correct orientation and with its centre on the position indicated by the assumed centre-centre peak. Certain ring addenda,  $0^2$ ,  $0^3$ ,  $0^4$  and  $0^6$ were placed on the assumption that  $C_1$  must be the nearest ring atom to the Phosphorus, and that the Glucose ring was similar to that of pure Glucose. The positions of the Oxygen atoms of the Phosphate group were deduced from the <sup>P</sup> - <sup>0</sup> vectors around the origin. Structure factors of the type <sup>h</sup> <sup>0</sup> <sup>L</sup> with sin  $\Theta \leqslant 0.85$  were calculated for these atomic positions, and agreement was good enough to proceed with an electron density difference map of the b-axis projection. This showed that some small changes in atomic parameters were required, and also three distinct peaks which were taken to be  $0<sub>6</sub>$ ,  $0<sub>11</sub>$ , and  $0<sub>12</sub>$ . The insertion of oxygen atoms on these positions, and recalculation of structure factors, this time up to sin  $\theta = 1.0$ , gave an R - value  $(R = \sum |E_i| - |E_i| + \sum |E_i|)$  of about 0.42. Further difference maps and small shifts reduced this to 0.29, unobserved reflections being inserted as  $F_{ob} = 0$ .

At this stage, <sup>a</sup> model was built of the structure, as it was so far known.  $0<sub>6</sub>$  and the water molecules,  $0<sub>11</sub>$  and  $0<sub>12</sub>$ , were tentatively allocated Y-co-ordinates on spatial considerations, i.e. that  $0<sub>6</sub>$  should be about 1.4 - 1.5  $\lambda$  from C<sub>6</sub>, and that /

that all should be at least 2.6 - 2.9  $\frac{0}{0}$  from non-bonded neighbours. Structure factors for the <sup>h</sup> k <sup>0</sup> zone were computed, and after three difference-Fourier cycles, <sup>R</sup> was approximately 0.25.

It was obvious, however, that the amount of atomic overlap in all three projections was considerable, and although refinement by projections alone could have been continued there appeared to be some advantage in three-dimensional refinement. Consequently, some 1,400 general <sup>h</sup> k <sup>L</sup> structure factors were computed for the co-ordinates deduced from projections. The R-value was 0.35- <sup>A</sup> three-dimensional electron density map was computed, and the maximum for each atomic position found by interpolation using the method of A..D. Booth (Ref. 25). The co-ordinates obtained were only very slightly different, although the heights of the maxima were rather variable, indicating possibly incorrectly located atomic positions. The fact that an F(obs) Fourier strongly tends to return atomic positions similar to those put in is well known, the main indication of wrong position being reduced electron density. One of the water molecules,  $0_{12}$ , was particularly in doubt. The h k 0 reflections were re-calculated for the atoms other than  $O_{12}$ , and a difference map computed. The latter indicated a position for  $0_{12}$  whose Y-co-ordinate was increased by some  $0.45$   $\lambda$ . This substantial shift was made, and the  $h$   $k$   $O$  reflections re-calculated, with a marked improvement in agreement. A further  $(\rho_e - \rho_c)$  map showed that a slight tilt of the entire sugar ring was required. This was very small /

small, too small to be apparent on the Patterson function, but it meant that the line  $C_2$  -  $C_5$  no longer lay exactly perpendicular to the screw axis, which helped to explain the fact that in the Patterson function, the centre-centre peak was much more diffuse than had been anticipated. Not clearly indicated by the Fourier maps was <sup>a</sup> shift of one of the phosphate oxygens,  $0_{10}$ ; this was deduced from an examination of the angles in the phosphate group. A shift of about 0.3  $\frac{0}{0}$  was required. Making all these alterations gave an  $($  h  $k$  O  $)$  disagreement index of about 0.16, with unobserved reflections set equal to  $\frac{1}{\sqrt{2}}$  X minimum observed.

Concurrently with refinement of the c-axis projection, the b-axis projection was also being refined, though none of the atomic shifts required was as large as those outlined above. Calculation of the three-dimensional structure factors was carried out, using the revised co-ordinates, and gave <sup>a</sup> disagreement factor of 0.27. In order to confirm the arrangement of the phosphate group, structure factors were calculated without the phosphate-oxygens, and an electrondensity difference map computed. This only led to <sup>a</sup> very slight change in the positions, but indicated clearly that the faotor which allows for thermal vibration of the Phosphorus atom must be very small, i.e. the vibration of the Phosphorus atom is of small amplitude. On re-calculating the general structure factors, with the improvements in positional and vibrational parameters deduced from this map, a slight improvement in agreement was obtained, and with an R-value of 0.24, refinement by the method of least squares was started.

#### Least Squares.

In the refinement of <sup>a</sup> crystal structure, the aim is essentially to vary the parameters of the atoms in the unit cell until the calculated structure factors give the best agreement possible with the observed values, under the prevailing experimental conditions. In doing this, an attempt is made to minimise the sum  $\sum ||F_{\circ}|-|F_{\circ}||$ , or some similar function. The observed F's, however, are subject to <sup>a</sup> range of errors, as are all experimental measurements, and the refinement process therefore consists of getting the best fit of calculated and observed data, the latter being subject to error.

The principle of least squares states that the most probably correct set of parameters is obtained when the sum of the squares of the deviations between calculated and observed values is minimised, after allowing for the reliability, or  $'$ weight' of each observation (Ref.  $34$ ) i.e. by minimising R' =  $\mathbb{V}(1 \text{ Fo } 1 - 1 \text{ Fo } 1)^2$ , where W is a weighting function for each reflection. If the trial structure is sufficiently close to the correct one, we can, as Hughes first pointed out, set up <sup>a</sup> number of linear equations, thus:

$$
\sum_{i}^{n} \frac{\partial F}{\partial P_{i}} \cdot S_{P_{i}} = F_{o} - F_{c} = \delta F
$$

There is one such equation for each F, and P<sub>1</sub>, P<sub>2</sub>, P<sub>3</sub>...Pn are the variable parameters which must be optimised.

For /

For any individual reflection  $F_1$ , we may expand this and write:

 $\frac{\partial F}{\partial p}$ ,  $\delta p_i + \frac{\partial F}{\partial p_a} \delta p_a + \frac{\partial F}{\partial p_a} \delta p_a - \frac{\partial F}{\partial p_a} \delta p_a - \delta F_i = 0$ 

It is shown in Reference <sup>29</sup> that the optimum parameters may be obtained by solving the 'normal equations'. These are formed with respect to any one of the unknowns by multiplying each of the original equations by the coefficient of the unknown in this equation, and summing the resulting equations. If there are 'n' variables, this leads to a set of 'n' equations, thus:

 $\sum_{k=1}^{\infty} \left(\frac{2k}{2k}\right)^2 (b^k + \sum_{k=1}^{\infty} \left(\frac{6k}{2k}\right) \left(\frac{2k^2}{2k}\right) (b^2 + \cdots + \sum_{k=1}^{\infty} \left(\frac{6k}{2k}\right) \left(\frac{2k^2}{2k}\right) (b^2 - \sum_{k=1}^{\infty} \left(\frac{6k^2}{2k}\right) (b^2 - \sum_{k=1}^{\infty} \left(\frac{6k^2}{2k}\right) (b^2 - \sum_{k=1}^{\infty} \left(\frac{6k^2}{2k}\right) (b^2$ 

# $\sum_{r=1}^{n} \left(\frac{\partial F_r}{\partial r} \right) \left(\frac{\partial F_r}{\partial r}\right) \left(\frac{\partial F_r}{\partial r}\right)$

# $\sum_{i=1}^{n-1} \left(\frac{2k}{9E}\right) \left(\frac{2k}{9E}\right) 2k + \sum_{i=1}^{n-1} \left(\frac{2k}{9E}\right) \left(\frac{2k}{9E}\right) 2k^2 + \sum_{i=1}^{n-1} \left(\frac{2k}{9E}\right) 2k^2 = \sum_{i=1}^{n-1} \left(\frac{2k}{9E}\right) 2k!$

which is effectively an <sup>n</sup> <sup>x</sup> <sup>n</sup> square matrix on the left and <sup>a</sup> column vector on the right. These normal equations are now to be solved for the 'n' required parameters.

This is complicated by two main factors. Firstly, the coefficients vary with each change of parameter, which means that the solution can only be arrived at by successive approximations. Secondly, the number of equations is very large. In the present case of <sup>a</sup> twenty-atom structure with three positional and six vibrational parameters per atom, plus one overall scale factor, there are <sup>181</sup> equations to be solved per cycle of refinement. This can be circumvented by making use of the fact that the principal diagonal consists of the sums of squares, which are large and positive, whereas the off-diagonal terms are the sums of products, which are as likely to be negative as positive and therefore may be quite small, on average. Refinement of the structure can therefore proceed on the diagonal terms only, since they will tend to outweigh the others. When this approximation is made, the parameter shifts become equal to:

$$
\S_{P_i} = \frac{\sum w \left( \frac{\delta F_i}{\delta P_i} \right) \S_{F_i}}{\sum w \left( \frac{\delta F_i}{\delta P_i} \right)^2}
$$

Since it is no longer necessary to compute the offdiagonal terms in the first place, this approximation leads to <sup>a</sup> reduction /

reduction also in the effort required to set up the normal equations, and not only in solving them.

Unfortunately, although off-diagonal terms are much smaller on average, <sup>a</sup> few may be of comparable magnitude to the diagonal terms, which leads in turn to <sup>a</sup> slower convergence on the correct solution. This, however, ia unavoidable in the absence of equipment capable of solving such large seta of simultaneous equations.

The three-dimensional least-squares refinement of Glucose-l-Phosphate was carried out on the D.E.U.C.E. Computer, using the programme of J.S. Rollett (Ref. 38). The weighting system was as follows:

$$
|F_n| \le 32
$$
;  $\sqrt{w} = |F_n|/32$   
 $|F_n| > 32$ ;  $\sqrt{w} = 32/|F_n|$ 

The reason for choosing this weighting is that the root-mean square 'F' is about  $24 - 30$ , and this weighting system would give greatest weight to reflections of about average, or slightly greater than average, intensity. The influence of the weighting system on convergence is hard to determine, but it seemed reasonable that reflections in this intensity region should be the most accurate, and hence of greatest weight. The decrease in <sup>R</sup> per cycle was very small, and after five cycles using the 1»350 general reflections it was 0.21. <sup>A</sup> further cycle suggested that this was about the lowest value for the data available, and that <sup>a</sup> plot of <sup>R</sup> versus parameter would have <sup>a</sup> rather flat minimum. It was apparent from the fact that the discrepancies were /

were more marked at lower sin © values that the probable cause of error was mainly anisotropic absorption, which could only be partially compensated by the facility for anisotropic refinement of the thermal vibration parameters. In addition, for <sup>a</sup> few strong reflections, extinction was almost certainly present e.g.



Two cycles of refinement were therefore oarried out on more limited data, about <sup>960</sup> reflections, which had been measured using an almost cylindrical crystal and corrected for absorption by assuming an exactly cylindrical form. The R-value was then reduced to 18.6%, after scaling the  $F_{ob}$  against  $F_{calc}$  in ten equal ranges of  $sin^2\theta$ . The parameters obtained are given below, those for thermal vibration being the mean values, as the anisotropic components are more probably related to





The bond lengths are given diagramatically below :

 $\colon$ 



 $\uparrow\uparrow\uparrow$ 

Using the approximate formula of Cruickshank (Ref. 30) for

standard deviations of co-ordinates:

$$
\mathcal{L}(x) = \frac{R}{s} \left( \frac{N}{4\rho} \right)^{\frac{1}{2}}
$$

where:

<sup>R</sup> <sup>=</sup> Residual

- $S = r.m.s.$  value of (2 sin  $\Theta/\lambda$ ) for the planes considered.
- <sup>P</sup> <sup>=</sup> difference between number of reflections observed and number of variable parameters.
- $N$  = number of atoms of the type being\_examined required to give the same amount of scattering at  $\overline{S}$  as that of the entire aaymmetrie unit.

i.e. 
$$
\sum_i f_i^2 = N f_x^2
$$

one obtains, for each chemical type:

 $K = 0.008$   $\lambda$  $P$   $6 = 0.009$   $\frac{9}{4}$  $0 \t 6 = 0.024 \t 2$ c  $6 = 0.034$   $8$ 

Using the expression for bond-length deviations:

$$
G = 0.034
$$
\nUsing the expression for bond-length deviations:  
\n
$$
\angle^{2}(\ell) = [ \angle^{2}(x_{1}) + \angle^{2}(x_{2}) ] \cos^{2} \times + [ \angle^{2}(y_{1}) + \angle^{2}(y_{2}) ] \cos^{2} \beta
$$
\n
$$
+ [ \angle^{2}(z_{1}) + \angle^{2}(z_{2}) ] \cos^{2} \delta
$$

where  $\lambda$  = bond length

and  

$$
\cos \alpha = \left(\frac{x_1 - x_2}{8}\right)
$$
,  $\cos \beta = \left(\frac{y_1 - y_2}{4}\right)$ ,  $\cos \gamma = \left(\frac{z_1 - z_2}{8}\right)$ 

errors are obtained for each type of bond which do not vary significantly from the following averages:



Intramolecular /

Intramolecular bond angles are as follows, to the nearest degree:



## Discussion of the Structure.

In the molecular structure, the average C - C bond length is 1.55  $\frac{0}{1}$ , the average C - O length is 1.44  $\frac{0}{1}$ , and average P - 0 = 1.53  $\lambda$ . The bond C<sub>1</sub>- 0<sub>7</sub> is shorter than average by almost twice the <sup>C</sup> - <sup>0</sup> standard deviation, and may therefore be significant. Both McDonald with  $\alpha$  - Glucose (Ref. 34) and McGeachin with the similar $\propto$  - Rhamnose (Ref. 36) observed a shortening of the bond from  $C_1$  to its hydroxyl group, though in the case of Glucose, this has been queried by Killean, Perrier and Young (Ref. 35)• A. Miller (Ref. 37) found no such shortening of the axial C - OH bond in Myo-Inositol. No shortening of the  $0$  - ring carbon bond occurs in Cytidine -  $3'$ -Phosphate, and any such bond shortening must therefore be associated /

associated with the presence of <sup>a</sup> ring oxygen atom adjacent to point of attachment and possibly only in the case of an axial substituent.

The bond  $P - O_{\overline{f}}$  is twice the  $(P - O)$  standard deviation longer than average, which may also be significant. This lengthening of the  $P$   $\rightarrow$  bridge oxygen bond has been found in the phosphate esters mentioned earlier and Cruickshank (Ref. 3a) discusses theoretical reasons for the extension of bonds of this type. P -  $0_{10}$  is just less than twice the S.D. shorter than average. A similar shortening of one of the free  $P - 0$  bonds (& was also observed in Cytidine - 3' - Phosphate and in Dibenzyl- $(39)$  (1) Phosphoric acid, though not in A.M.P., Calcium Thymidylate, or (10) <sup>2</sup> - Aminoethanol Phosphate. <sup>v</sup> The <sup>P</sup> - <sup>0</sup> - <sup>R</sup> angle in Glucose - 1 - Phosphate is  $124^\circ$ , which does not differ greatly from the 121° of Cytidine-3'-Phosphate and Dibenzyl-Phosphoric acid. In the other structures studied so far, the corresponding angle is between 115 and  $119^\circ$ . It is seen then, that  $\propto$  -Glucose-l-Phosphate, Cytidine-3'-Phosphate, and Dibenzyl Phosphoric acid all possess one free  $P - 0$  bond which is shorter than the others. and a rather wide  $P - 0 - R$  angle. There is no obvious reason for this; the feature which these molecules have in common, but which is absent in the other phosphate esters examined, is that the phosphate group is esterified directly to <sup>a</sup> ring system, and not on to <sup>a</sup> side chain. Since only six structures are being compared, however, it is quite possible that this correlation could /

could arise by chance. The rings to which the phosphate group is attached are, for one thing, all different; one furanose, one pyranose, and one aromatic.

Discussion of such variations ultimately must depend on the accuracy of the structure, or, at least, the trust one places in the calculated standard deviations, and on the establishment of a 'normal' value for the quantity being considered. The normal values of the  $C - C$  and  $C - O$  bond lengths have been very well established from the large number of structures containing these bonds which have been independently studied. The situation with respect to the free  $P - 0$  bonds in organic phosphates is rather different, for while these can be written down formally as:

$$
R \longrightarrow 0 \longrightarrow 0
$$

which would make one expect one short bond, the observed values certainly do not give consistent support to this expectation.

The crystal structure and atomic numbering is given in Appendix  $(4)$ . It can be pictured as a scaffolding consisting of <sup>a</sup> chain formed by the following atoms:

$$
K_2 - 0_3 (2.77 \t{8}) \t P - 0_9 (1.53 \t{8})
$$
  
\n
$$
0_3 - 0_{10} (2.65 \t{8}) \t 0_9 - K_2' (2.69 \t{8})
$$
  
\n
$$
0_{10} - P (1.48 \t{8})
$$

/ where  $K_2$  is the symmetry related counterpart of  $K_2$ . This chain runs /

rune parallel to the b-axis and can continue indefinitely. The bond  $P - 0<sub>g</sub>$  is one of the longer free  $P - 0$  bonds and may be partially charged, providing an electrostatio attraction between  $0^{\circ}$  and  $K_2$ . The Glucose ring is held in this frame by the links  $0_6 - K_2$  (2.61 X)<br>  $0_4 - 0_9$  (2.63 X)  $0_4 - 0_9$  (2.63 )  $^{0}3 - ^{0}10$  (2.65 A) and possibly  $0_3 - K_2$  (2.77  $\lambda$ ).

The other cation  $K_1$ , is surrounded by a 'shell' of oxygen atoms at the following distances:



 $(0<sub>2</sub>$ ' and  $0<sub>1</sub>$ ' are in the unit cell adjacent to that containing  $\mathbf{K}_1$ ).

It is apparent, then, that the units forming the crystal are fairly tightly bonded together, as might be expected from the observed hardness and lack of any easy oleavage. The forces involved appear to be <sup>a</sup> combination of ionic and 'hydrogen-bond' types, additional evidence for the latter being found in the infra-red absorption spectrum of the solid, ground up in an organic liquid, which shows considerable absorption in the  $3000$  cm<sup>-1</sup> region usually associated with the hydrogen bond.

#### Methods Employed.

It is noticeable in the descriptions of the structure determinations of the phosphate esters mentioned in the foregoing sections that in all cases but one <sup>a</sup> useful trial structure was obtained by means of some vector method or methods. The exception is the structure of Barium Ribose-5'-Phosphate, found by means of the 'heavy atom' method. It also seems to bs the case that the presence of <sup>a</sup> medium or heavy cation is more of <sup>a</sup> hindrance than <sup>a</sup> help, being large enough to enhance absorption problems considerably without aiding the solution of the structure by very much. Certainly, in work of this class of compound, careful choice should be made of <sup>a</sup> suitable derivative. This choice, of course, will be limited by the number of derivatives which can be prepared in <sup>a</sup> crystalline form. The experiences outlined in the appropriate references (8, 9, 10) and in the examination of Ammonium Glucose-l-Phoephate show that if vector superposition methods are employed the necessarily present Phosphorus atom should be quite heavy enough to lead to <sup>a</sup> good trial structure. This is not because Phosphorus is particularly heavy  $(Z = 15)$  - in fact, it is far too light to use, say, the direct 'heavy atom' method, but because the  $P - P$  vectors are just about heavy enough to be recognizable on a vector map unambiguously, and, even more important, the phosphate must be covalently bound to the sugar residue. This means that in <sup>a</sup> superposition map, or even in the Patterson itself, although the symmetry is higher than that of the structure, it becomes easier to trace <sup>a</sup> chain of permissible other-atom positions, each atom being about 1.5  $\beta$ 

from the next.

A. good deal of very useful information can also be got from the volume around the origin of a vector map, though this does not seem to have been utilised except in the work on Clucose-l-Phosphate.

51.

It has already been explained how <sup>a</sup> light-atom molecule will give rise to <sup>a</sup> distinct pattern around the origin if it contains <sup>a</sup> number of parallel vectors capable of reinforcing each other. This is the situation which applies in the case of the pyranose ring, and also in the pyrimidine and purine groups, when present. The usefulness of this area of vector map, however, is not restricted to groups with parallel vectors. Any small unit of known shape, some of whose vectors may be expected to be distinguishable from the background can be orientated from the vector distribution around the origin. This occurs with the P - 0 vectors of the tetrahedral  $P - O_4$  group.

Location of the actual position of <sup>a</sup> molecule in theunit cell could be done either by using <sup>a</sup> superposition map, derived from the  $P - P$  vector or vectors, in which case a prior knowledge of the possible orientations of the units involved would be of considerable assistance in detecting the correct structure among the inevitable unwanted 'chance' coincidences, or by means of <sup>a</sup> centre-centre type of vector if one is possible. In the latter case it is necessary to remember that this will only exist in projection, since the sugars are optically active and cannot crystallise in <sup>a</sup> centrosymmetric space group. Further to this, atomic groups which are not centro-symmetric /

ccntrosymmetric may possess centrosymmetric projections. In the case of Glucose-1-Phosphate, the -  $PO_A$  group is orientated with one of its  $\overline{4}$  axes parallel to the b-axis, leading to a phosphate 'centre-centre' peak located at the same X, Z, co-ordinates as the <sup>P</sup> - <sup>P</sup> Harker vector, making this, in projection, <sup>a</sup> heavier peak even than single <sup>K</sup> - <sup>K</sup> or <sup>K</sup> - <sup>P</sup> vectors.

For light-atom derivatives of sugar phosphates, sharpening is rather advantageous, though disapproved by at least one authority (Ref. 22, p. 266). The enhancement of P—P and ?—> other atom peaks is considerable, without excessive series termination effects appearing. This is also (၅) commented on by Kraut and Jensen in their work of Adenosine - $5'$  - Monophosphate. The  $IFI^2$ 's of Di-Ammonium Glucose-1-Phosphate Dihydrate were subjected to <sup>a</sup> sharpening ratio of  $(1 + 8 \sin^5\theta)^2$ , and both the Glucose ring intramolecular vectors and the phosphate group vectors appeared quite clearly, although they are close to the origin, where series termination errors should be worst. By contrast, the Patterson function of Di-Potassium Glucose-l-Phosphate Dihydrate, both unsharpened and slightly sharpened, gave <sup>a</sup> relatively poorer, though recognisable, pyranose vector pattern and no identifiable -  $P0^{}_4$ pattern. This was despite the fact that it contained more coefficients, about <sup>1550</sup> for the Potassium salt as opposed to about <sup>700</sup> for the Ammonium salt.

The superiority of three dimensional over twodimensional vector methods is already well known, and the extra labour/

labour of measuring the larger number of reflections required is very little compared to the advantages to be gained. The advent of fast computing equipment over the last few years has made the calculation involved in preparing, say an unsharpened, slightly sharpened, and strongly sharpened version of the same Patterson the least of the problems to be faced in <sup>a</sup> structure determination.

In the course of refinement, both electron density difference maps and the method of Least-Squares were used. It had been hoped that the latter would give a more rapid refinement, than was possible by Fourier methods, especially in the closing stages when shifts were small, and might be more accurately determined by this method than by examination of an electron density map. In practice, convergence proved to be extremely slow. It is possible that this was caused by the omission of the off-diagonal terms in the normal equations.

N

#### Crystallisation of Sugar Phosphates.

The first step in any structure determination is the obtaining of suitable crystals. Glucose-1-Phosphate presented no serious difficulty here. Attempts were also made to crystallise some other phosphates, if possible. Fructose 1-6 Diphosphate, which is of considerable importance in photosynthesis, is fairly readily available, and experiments were made with this substance. The commercial Barium, Calcium and Magnesium salts are all amorphous, powder photographs of each of these showing no evidence of crystallinity. The Potassium, Rubidium, Ammonium, Copper, and Zinc salts were all prepared from the Barium salt by reaction in solution with the appropriate inorganic sulphate. The copper and zinc derivatives were not sufficiently soluble to achieve the concentration necessary for satisfactory crystal growth, while the other derivatives were rather hygroscopic, forming glassy solids on dehydration. It is also probable that crystallisation was hindered by excessive impurity in the starting materials, the purity of many biochemicals being rather variable.

Reference was found to the use of Cyclohexylammonium (40) and Cyclohexylamine (41) salts for the purification of certain sugar phosphates. Cyclohexylammonium salts were hardly likely to be suitable for X-ray structure determinations on account of the multiplicity of puckered rings which must necessarily be present. Cyclohexylamine was therefore considered more promising.

The Cyclohexylamine salt of Fructose 1-6-Diphosphate was prepared by passing <sup>a</sup> solution of the soluble Calcium salt through a cation exchange column in the Hydrogen form and neutralising the free Fructose-1-6 Diphosphoric Acid with Cyclohexylamine /

Cyclohexylamine. The resulting solution was filtered and dried in <sup>a</sup> vacuum desiccator with Sodium Hydroxide as desiccant. The resulting powder was recognised as consisting of fine needles when observed under the microscope. <sup>A</sup> powder photograph also showed it to be crystalline. The powder was then redissolved and dried out again more gently, at <sup>a</sup> lesser degree of vacuum and using anhydrous Calcium Chloride as desiccant. This led to <sup>a</sup> number of clusters of very fine needles, radiating from various growth points. No single crystal of <sup>a</sup> size suitable for X-ray photography was obtained, but an oscillation photograph of <sup>a</sup> bundle of parallel needles showed that the crystals possessed <sup>a</sup> symmetry axis parallel to the needle axis, with <sup>a</sup> cell translation in this direction of about  $6.0 \t3.$  The most probable interfering reaction in the method of preparation was hydrolysis of the phosphate on the ion exchange column, which would have led to <sup>a</sup> mixture of Cyclohexylamine Qrthophosphate and Fructose. Fructose, however, crystallises in almost cubic crystals, with unit cell dimensions of 8.06  $\frac{0}{1}$ , 10.06  $\frac{0}{1}$  and 9.12  $\lambda$  (Reference 42); while Cyclohexylamine Orthophosphate, which was prepared as <sup>a</sup> check, crystallised in flat, mica-like plates. The Cyclohexylamine salt of Fructose-6-Monophosphate has also been prepared, though time has not permitted <sup>a</sup> full examination of methods of crystallising it.

Looking both at the experiments on Fructose  $1-6$ Diphosphate and the description in Reference <sup>41</sup> to the crystallisation of Deoxyribose - <sup>1</sup> - phosphate, it seems that organic /

organic bases can be usefully employed to form crystalline derivatives of sugar phosphates which can not be crystallised with <sup>a</sup> metallic cation. While this will complicate the structure by the increased number of atoms present, the range of possible derivatives, one or more of which may be crystalline, is greatly increased.

### A C K N O W L E D G E M E N T S.

The candidate would like to express his sincere gratitude to Br. C.A. Beevers for his advice and reassurance which were at all times invaluable.

Thanks are also due to former members of this laboratory, and in particular to Dr. A. Miller and Drs. H. Krabbendam for their assistance on computing.

Finally, grateful acknowledgement is made to the D.S.I.R. for receipt of <sup>a</sup> maintenance grant over the period i960 - 1963.

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#### APPENDIX (i)

Sections of the three-dimensional Patterson function of Mpotaasium Glucose-l-Phosphate Bihydrate, taken at right angles to the  $b$ -axis. The appropriate  $y$ -level is indicated at the top of each section.



M



 $\boldsymbol{Z}$ 



 $\mathsf{Z}$ 

 $\bullet$ 





 $\mathsf{z}$ 



 $\lambda$ 

 $\mathsf Z$ 



 $\mathsf Z$ 



Z



 $\boldsymbol{Z}$ 

## APPENDIX (2)

Sections of the Patterson function of Di-ammonium

Olucose-l-Phosphate Dihydrate, set out as in Appendix (l).



 $\boldsymbol{Z}$ 





 $\overline{z}$ 













## APPENDIX (3).

Pinal structure viewed along the a-axie.



# APPENDIX (4).

Final structure viewed along the screw axis.



#### TABLE (2)

Observed and calculated structure factors for Di potassium Glucose-1-Phosphate, listed as: l, <sup>a</sup> K 10  $F(\text{calc})$  10F (obs) 1000 cos  $\lt 1000 \text{ sin }\lt 1000$  sin  $\lt 1000$ 



a<br>a<br>c



 $\widetilde{\mathcal{A}}$ 

 $\mathcal{A}$ 





 $\sim 10^{11}$ 




















 $\hat{\mathcal{L}}$ 

 $\langle \zeta_0 \rangle$ 



 $\frac{1}{2}$ 



## **TABLE** (3)

Relative  $r^2$ 's of Di ammonium Glucose-1-Phosphate

L, K  $\mathbf{H} \quad \mathbf{r}^2$ etc.

listed as



 $\frac{1}{\sqrt{2}}$ 

 $\hat{\boldsymbol{\theta}}$ 



a.<br>K

t.

 $\acute{\epsilon}$ 

 $\tilde{E}$ 

 $\widetilde{\mathcal{C}}$ 



 $\bar{\rho}_L$