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Imaging proton migration from X-rays and neutrons

Andrew Parkin,[a] Suzanne M. Harte,[a] Andrés E. Goeta[b] and Chick C. Wilson*[ac]

[a] *Department of Chemistry, University of Glasgow, Glasgow G12 8QQ, UK.*
E-mail: c.c.wilson@chem.gla.ac.uk; Fax: +44 141 3304419; Tel: +44 141 3306579
[b] *Department of Chemistry, University of Durham, South Road, Durham DH1 3LE, UK*
[c] *ISIS Facility, CLRC Rutherford Appleton Laboratory, Chilton, Didcot, Oxon OX11 0QX, UK*

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The short hydrogen bond in the urea–phosphoric acid system has been studied by multiple-temperature X-ray single crystal diffraction. The hydrogen atom is imaged using difference Fourier methods from these data and also from previous neutron diffraction data. The migration of the hydrogen atom is clearly observed using the X-ray difference Fourier maps. The hydrogen atom positions determined from these maps are more reliable than from X-ray refinements of this atom. A greater apparent shift of the proton is observed from X-ray than from neutron diffraction, as might be expected.

Introduction

Neutron diffraction is without doubt the method of choice for the accurate location of hydrogen atom positions in the structures of crystalline solids, usually giving data that enable refinement not only of the positional coordinates of the atom, but also of the anisotropic displacement parameters. However, neutron time is costly and at a premium—the limited number of available diffractometers world-wide making beam-time a precious resource. Other well-recorded difficulties also manifest themselves, including the length of time for data collection, the size of the crystal and the available neutron flux even at modern advanced sources. Whilst the results frequently justify the effort in obtaining good quality neutron diffraction data (and we note here recent substantial improvements in instrumentation and methods in this area), we have been examining in recent work the extent to which it may also be possible to obtain reliable information on hydrogen positions from X-ray diffraction data.[1] It is clear that given a systematic approach, for example harnessing a multiple-temperature protocol, then consistent trends can be found, particularly in difference Fourier maps, allowing one to image the hydrogen atom behaviour reliably. While the difficulties in subsequently refining the hydrogen atom parameters remain formidable and often intractable (particularly for disordered hydrogen atoms), the semi-quantitative insights produced by these images can yield very useful information. Moreover, this information can also help to decide on appropriate complementary neutron diffraction experiments that will yield a full description of the protons of interest.

The complementarity of X-ray and neutron diffraction is a topic that is frequently discussed (see, for example, Wilson[2]). It is well-known that X-ray diffraction gives information on the distribution of electron density, rather than the position of nuclei as with neutrons. In practice this means that the position of a hydrogen atom found from X-ray diffraction data is shifted towards the atom to which it is bonded. This is true in the cases presented here—when we view a Fourier map in the region of a hydrogen atom we are actually plotting the position of *bonding density*, not that of the proton nucleus. This can be exploited to our advantage in the case of observing temperature-dependent proton migration using both X-ray and neutron diffraction, as described in this paper.

Recent advances in single crystal X-ray diffractometer technology has resulted in a proliferation of image plate and area detector (CCD) based diffractometers. These diffractometers allow rapid data collection with high multiplicity/redundancy compared to older 4-circle machines. Increases in detector sensitivity have allowed routine detection and refinement of hydrogen atom positions, so that unconstrained refinements can often be undertaken. However, in many systems, especially if proton disorder or other anomalous hydrogen atom behaviour is suspected, it can be both more reliable and informative to use a Fourier map approach to investigate what is happening in the system. We use here the example of the observed migration of the proton in the short strong hydrogen bond in urea–phosphoric acid to illustrate this point.

The 1:1 co-crystal of urea and phosphoric acid (UPA) has been extensively studied by crystallographic methods since the first room temperature solution and refinement.[3] The continuing interest in this material is largely due to the existence of a short O···O contact (~2.4 Å) between the two moieties and because it forms a well-defined model system for the study of such short hydrogen bonds. The large, high quality crystals that can be grown also contributed to this interest, with further X-ray studies being undertaken[4,5] before a room temperature single crystal neutron study revealed the position of the hydrogen atom sitting almost exactly centred between the two O atoms.[6] In 1987 Savage *et al.* postulated that the short hydrogen bond should be interpreted as a three-centre, four-electron bond,[7] a description that seems particularly appropriate at room temperature.† Both X-ray[8] and neutron[9] data at low temperature have, by contrast, indicated that a significant degree of asymmetry in the hydrogen atom position is observed on cooling, with as much as 0.10 Å difference between O–H and H···O distances. However, it is worthy of note that this asymmetry is nowhere near as large as in

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† In the case of protons lying midway between two chemical moieties it becomes difficult to decide to which of these moieties the proton actually belongs. In the case presented here, at 350 K there is obviously a degree of bonding between the proton and both O4 and O5, but it is impossible to conclude whether we have a molecular or ionic solid. It is chemically unreasonable to conclude that we have a truly separate H^+ ion and so the logical conclusion to draw is that we have a 3-centre (comprising O5, H1 and O4), 4-electron (comprising the "bonding pair" between O5 and H1, and the "lone pair" on O4) bond.

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medium strength hydrogen bonds and the "covalent" O–H distance is still significantly lengthened in UPA at 15 K (1.14 Å compared with a normal covalent O–H bond length of ~1 Å). This low temperature behaviour is also reproduced in recent plane-wave DFT calculations that have lent strong support for the observed degree of asymmetry.[9] The issue of where the hydrogen atom is located in this hydrogen bond under various conditions was recently studied in detail by multiple-temperature neutron diffraction studies,[10,11] which indicated that the hydrogen atom moved from an asymmetric position at low temperature to an approximately centred position at room temperature and higher, a shift of around 0.04 Å between 150 K and 300 K.[10] This multiple-temperature approach can be of great assistance in constructing reliable models of systems with unusual behaviour[12] and we report here an extension of the previous neutron diffraction work on UPA using multiple-temperature X-ray diffraction.

Experimental

X-Ray data sets were collected at temperatures of 150, 200, 250, 300 and 350 K by a series of ω scans at different ϕ values on a Bruker SMART 6000 CCD diffractometer equipped with an Oxford Cryosystems N_2 low temperature device, using graphite-monochromated MoKα radiation ($\lambda = 0.71073$ Å).[13] Urea–phosphoric acid crystallises in the orthorhombic *Pbca* space group with $Z = 8$. No absorption corrections were carried out. The structures were refined using the previously determined coordinates of Wilson *et al.*[10] at all temperatures using SHELXL-97.[14] Refinement was on F^2 against all independent reflections by full-matrix least squares. At all temperatures all hydrogen atoms except H1 (see Fig. 1) were located from difference Fourier maps and their positions and isotropic atomic displacement parameters freely refined. H1, the hydrogen atom of interest in this work as it displays the proton migration, was very clearly imaged in all data sets and subjected to a number of different refinement strategies.‡A thermal ellipsoid plot of the asymmetric unit of the crystal structure at 150 K is shown in Fig. 1 (with H1 shown with its neutron-determined ADPs for clarity) and refinement data for the two extreme temperature data sets are given in Table 1. All other refinement details are available in the cif files.§

The neutron data used for comparison in this paper are the data collected by Wilson *et al.*[10]

All Fourier maps were produced within the program WinGX.[15]

Results and discussion

Difference Fourier maps were calculated for each of the X-ray and neutron data sets at each temperature, phased from a model produced by removing the hydrogen atom in the short hydrogen bond. A comparison of the X-ray and neutron difference Fourier maps (Fig. 2) shows that a similar effect is observed using both techniques; namely, that the hydrogen atom is observed to migrate with temperature. However, it should be noted that this effect is considerably clearer in the X-ray than in the neutron maps as discussed below. At 150 K the position of the hydrogen in these Fourier map images is significantly closer to the urea moiety (so that the urea is best described as an uronium ion), while at 350 K it is located at the centre of the hydrogen bond and is formally bound to neither moiety. This had been confirmed previously by the neutron refinements.[10,11] As noted, there is a large difference observed in the position of the maximum density in the neutron and X-ray Fourier maps at low temperature. In the X-ray case the asymmetry is far more pronounced, caused by the asphericity effect due to bonding, as mentioned before. Interestingly, the hydrogen atom is almost exactly centred at 300 K from the neutron data, whereas the electron density is not, suggesting that the hydrogen bonding density is not centred until it is above room temperature. At 350 K, since the hydrogen is symmetrically positioned, these bonding effects affect the apparent distance of the hydrogen from both oxygen atoms equally and thus the centred proton is seen by both neutron and X-ray methods. The consequence of this is that there is a larger *apparent* shift in the positions of the density maximum in the X-ray data as the temperature is increased compared to that observed in the neutron structure (~0.1 Å *cf.* ~0.04 Å). Although we know we are observing the centroid of the electron density rather than the true position of the hydrogen atom in the X-ray experiment, we have shown that with care, and an appropriate use of a systematic approach, this fact can be used to our advantage when it comes to observing changes over temperature—the changing nature of the hydrogen bond is actually emphasised more in the X-ray than the neutron images.

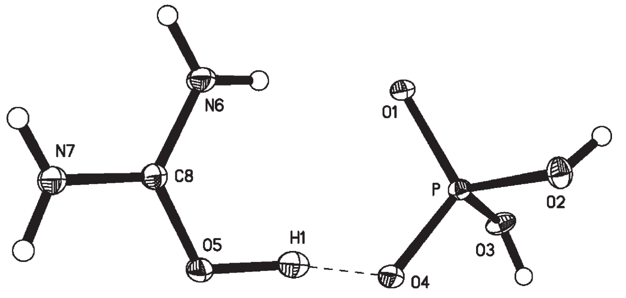

Fig. 1 Thermal ellipsoid plot of the structure of the 1:1 urea–phosphoric acid co-crystal, with the hydrogen bond exhibiting proton migration illustrated. Crystallographic information is taken from the 150 K X-ray structure and thermal ellipsoids are shown at the 30% probability level.

It is worth noting that the standard refinement of the hydrogen atom parameters from the X-ray data was by no means routine and the results are less consistent than those viewed

Table 1 Refinement data for the two extreme temperature X-ray structures of urea–phosphoric acid ($CH_7N_2O_5P$, molecular weight 158.06).[a]

	150 K	350 K
a/Å	7.4613(3)	7.4904(6)
b/Å	8.9753(4)	9.0176(7)
c/Å	17.5018(9)	17.7254(16)
U/Å^3	1172.05(9)	1197.27(17)
μ/mm^{-1}	0.428	0.419
N_{total}	7798	7970
N_{unique}	1784	1825
R_{int}	0.0157	0.0192
$N_{\text{parameters}}$	106	106
R_1 ($I > 2\sigma I$)	0.0274	0.0348
wR_2 (all data)	0.0807	0.1017

[a] Additional information on these and all other data sets is available in the cif files, available as Electronic supplementary information

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‡ Allowing the hydrogen atom to refine freely resulted in unrealistic coordinates and values for U_{iso} when compared to the neutron values, due to the inability to refine the hydrogen atom anisotropically using the X-ray data. Likewise, constrained and restrained refinements with the O5–H1 bond length being fixed or tethered does not agree with the observed neutron values. The difference Fourier maps calculated for the X-ray peaks always lay in the plane defined by C8, O4 and O5. The final course of action for the refinements fixed the coordinates and ADPs of H1 to the neutron-determined values and did not allow them to refine.

§ CCDC reference numbers 231379–231383. See http://www.rsc.org/suppdata/nj/b3/b315515c/ for crystallographic data in .cif or other electronic format.

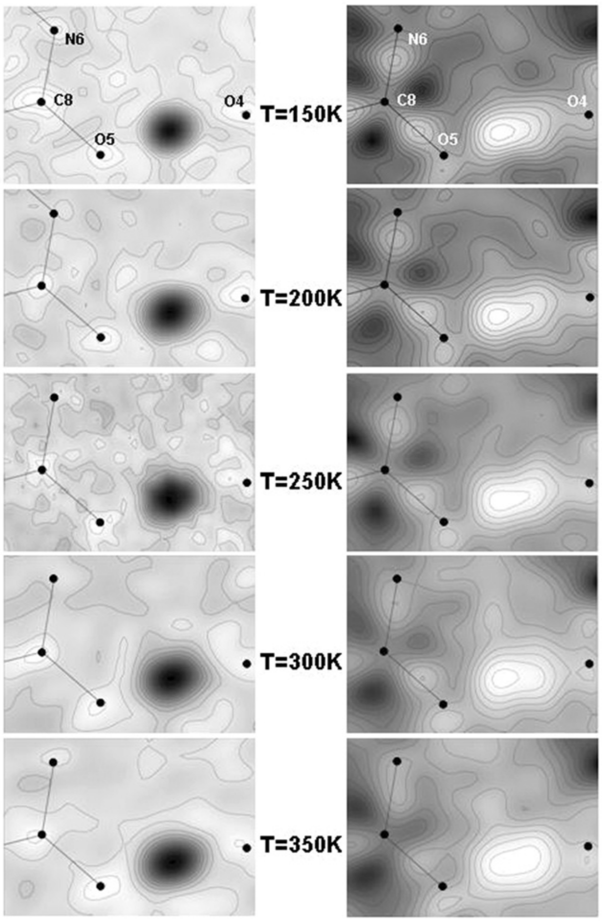

Fig. 2 Difference Fourier maps ($F_o - F_c$) obtained at temperatures of 150, 200, 250, 300 and 350 K from both neutron (left) and X-ray (right) diffraction data. The maps were calculated on a plane through atoms C8, O4 and O5, with contours plotted at consistent intervals throughout the neutron and X-ray maps. Note that hydrogen peaks are negative in neutron diffraction. The atoms are labelled on the 150 K map.

directly from our Fourier images (Fig. 3). The migration of the hydrogen atom from being closer to O5 at low temperature to approximately centred above room temperature is seen in the neutron and X-ray Fourier cases—note the enhanced appearance of this migration in the electron density (X-ray Fourier in Fig. 2). By contrast, the X-ray refined positions are less consistent and indeed locate the hydrogen atom closer to O4 at high temperature, in contradiction to the neutron results and Fourier images, which is clearly not correct. This can be explained easily, as the X-ray refined positions attempt to model the distinctly anisotropic shape of the electron peak with an inappropriate isotropic thermal parameter, thereby unrealistically shifting the coordinates of the atom away from the true position of the atom. The compelling conclusion from this work is that the Fourier images give a clearer and more realistic picture of the hydrogen behaviour in non-standard hydrogen bonds in the X-ray case than a refinement of the atomic position.

Further interest is shown by the neutron data indicating that the hydrogen atom is approximately centred at 300 K, whereas the hydrogen still lies more closely associated with atom O5 according to the X-ray Fourier. The physical migration of the hydrogen atom only appears to be matched by the migration of the hydrogen bonding density to the centre of the two oxygen atoms at 350 K.

Concluding remarks

Although the problem of hydrogen atom placement using X-ray diffraction is generally regarded as solved, this work

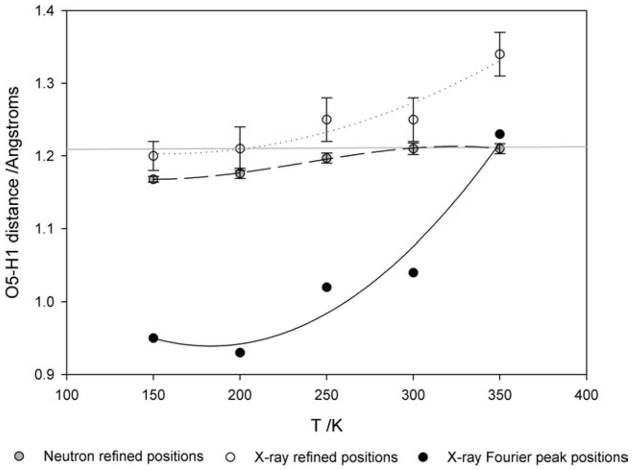

Fig. 3 Graph showing the effect of the technique used on the observed/refined hydrogen atom position. The midpoint of the two oxygen atoms O4 and O5 is indicated by a straight line; from the neutron refinement the OHO angle is around 170° (Wilson *et al.*[10]). Standard uncertainties on the refined bond lengths are given; it is, however, difficult to estimate the standard uncertainties on the position of the Fourier peak, so none are shown. Fitting lines shown are guides to the eye. Neutron data reflect the true position of the hydrogen nucleus. When the position of the hydrogen atom is refined using the X-ray data it should reflect the position of the electron density maximum. However, the broad indistinct potential minimum observed for this atom leads to difficulty in its refinement. This is reflected in unrealistic isotropic thermal parameters and displacement of its position to an unreasonable location compared to the true position of the electron density maximum as indicated by the Fourier map. Given the difficulty in refining this atom isotropically, any anisotropic or higher level modelling based on the X-ray data is clearly precluded.

on a well-known system illustrates that modern equipment is now capable of providing data of such high quality on a routine basis that it becomes possible to map out at least qualitatively the behaviour of protons engaging in unusual behaviour. This information can be used to guide neutron diffraction experiments and in combination with the latter to enhance the information available about the hydrogen atom behaviour and provide a complete description of the system. For the absolute refinement of H atom positions, displacement parameters and occupancies, neutron diffraction remains clearly the method of choice, but our work here has shown once again that X-ray diffraction is an extremely powerful diagnostic tool, even of hydrogen atom behaviour. In the particular case of UPA, the nature of the strong hydrogen bond of interest has in fact allowed us to extract enhanced information from the X-ray pattern. In a very real sense here, neutron diffraction is probing the structure, while X-ray diffraction is probing the bonding and thus the chemistry. Multi-temperature data collection as described here is likely to become the norm in the next few years with standard data collection times becoming sufficiently short to allow structural scientists to use the method to study structural and chemical evolution in a systematic way.

Acknowledgements

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