bonded S⋯H contacts of 2·91 Å, in agreement with the smaller van der Waals radius.

There is no simple explanation for the differences in the observed lengths of P–P and P–C bonds in molecules I and II.

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The Crystal Structure of Glucitol–Pyridine

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The crystal structure of a 1:1 glucitol–pyridine complex, $C_6H_{14}O_6.C_5H_5N$, has been determined by the application of the symbolic addition and tangent formulas to diffractometer Cu $K\alpha$ data. The anisotropic refinement terminated at $R=0.04$. The space group is $P2_1$ with two molecules in a unit cell of dimensions $a=4.652$ (3), $b=10.207$ (4), $c=13.439$ (5) Å, $\beta=90.3$ (3)°. The structure consists of layers of hydrogen-bonded glucitol molecules separated by layers of pyridine molecules stacked in a herringbone arrangement. The two layers are linked by O–H⋯N hydrogen bonds of 2.814 Å. The glucitol molecule has a non-planar carbon chain such that the parallel alignment of C(1)–OH to C(3)–OH and C(2)–OH to C(4)–OH is avoided.

Introduction

Glucitol forms a 1:1 solvent complex on crystallization from pyridine, which has been used for purification (Strain, 1934, 1937). A similar derivative has been reported for 2-deoxyglucitol (Wolfrom, Konigsberg, Moody & Goepp, 1946). In addition to the intrinsic interest in the structure of the complex, this compound provides an opportunity to examine the conformation of the glucitol molecule in a crystal-field environment different from that in the crystal structure of D-glucitol itself, which has also been determined (Jeffrey & Park, 1970).

Crystal data

Large, transparent monoclinic crystals of
$$C_6H_{14}O_6.C_5H_5N,$$
m.p. 76°C, which decomposed on exposure to air, were obtained by slowly cooling a saturated solution of D-glucitol in pyridine. They gave the following data:

Space group $P2_1$, from systematic absences $0k0$ absent for k odd

$a=4.652$ (3) Å $V=638.15$ Å³
$b=10.207$ (4) $Z=2$
$c=13.439$ (5) $D_m=1.365$ g.cm⁻³ at 23°C

Table 1. *Fractional atomic coordinates and anisotropic thermal parameters in glucitol-pyridine complex*

Key to atomic numbering is given in Fig.1. The estimated standard deviations given in parentheses refer to the last decimal positions. The temperature factor expression used was

$$\exp[-(\beta_{11}h^2 + \beta_{22}k^2 + \beta_{33}l^2 + 2\beta_{12}hk + 2\beta_{13}hl + 2\beta_{23}kl)].$$

	x	y	z	β_{11}	β_{22}	β_{33}	β_{12}	β_{13}	β_{23}
C(1)	0·7081 (5)	0·3858 (4)	0·1738 (2)	0·0360 (10)	0·0081 (3)	0·0032 (1)	0·0022 (4)	−0·0010 (3)	0·0008 (1)
C(2)	0·6172 (5)	0·5249 (3)	0·1488 (2)	0·0301 (9)	0·0066 (2)	0·0031 (1)	−0·0005 (4)	−0·0008 (3)	−0·0001 (1)
C(3)	0·4552 (4)	0·5333 (3)	0·0491 (2)	0·0226 (8)	0·0046 (2)	0·0032 (1)	−0·0003 (3)	−0·0003 (3)	−0·0000 (1)
C(4)	0·6480 (4)	0·5077 (3)	−0·0411 (2)	0·0239 (9)	0·0047 (2)	0·0029 (1)	0·0000 (3)	−0·0003 (2)	−0·0000 (1)
C(5)	0·4666 (5)	0·4724 (3)	−0·1330 (2)	0·0260 (9)	0·0050 (2)	0·0033 (1)	−0·0004 (3)	−0·0014 (3)	−0·0000 (1)
C(6)	0·6427 (6)	0·4486 (3)	−0·2269 (2)	0·0422 (11)	0·0074 (3)	0·0027 (1)	−0·0008 (5)	−0·0006 (3)	−0·0002 (1)
C(7)	0·1481 (9)	0·3656 (5)	0·4298 (3)	0·0816 (23)	0·0140 (5)	0·0067 (2)	0·0010 (9)	−0·0054 (6)	−0·0008 (3)
C(8)	0·0782 (9)	0·3502 (7)	0·5276 (3)	0·0671 (19)	0·0199 (7)	0·0070 (2)	0·0039 (10)	0·0006 (5)	−0·0008 (3)
C(9)	0·1977 (9)	0·2507 (5)	0·5809 (2)	0·0725 (19)	0·0179 (6)	0·0041 (2)	−0·0076 (9)	−0·0020 (4)	−0·0030 (4)
C(10)	0·3849 (9)	0·1682 (5)	0·5346 (3)	0·0857 (23)	0·0136 (4)	0·0055 (2)	−0·0018 (9)	−0·0020 (5)	−0·0008 (3)
C(11)	0·4420 (9)	0·1893 (5)	0·4351 (3)	0·0775 (21)	0·0146 (5)	0·0059 (2)	−0·0032 (9)	−0·0027 (5)	−0·0002 (3)
N	0·3257 (7)	0·2856 (5)	0·3819 (2)	0·0829 (17)	0·0159 (4)	0·0040 (1)	−0·0102 (8)	0·0014 (4)	−0·0024 (3)
O(1)	0·4718 (4)	0·2983 (3)	0·1792 (1)	0·0548 (10)	0·0059 (2)	0·0028 (1)	−0·0018 (3)	0·0010 (2)	0·0002 (2)
O(2)	0·4398 (4)	0·5685 (3)	0·2279 (1)	0·0566 (10)	0·0067 (2)	0·0027 (1)	0·0019 (3)	0·0012 (2)	−0·0001 (1)
O(3)	0·3337 (3)	0·6615 (3)	0·0406 (1)	0·0254 (6)	0·0053 (1)	0·0034 (1)	0·0011 (2)	−0·0016 (2)	−0·0004 (1)
O(4)	0·8273 (3)	0·6179 (3)	−0·0614 (1)	0·0212 (6)	0·0055 (2)	0·0039 (1)	−0·0011 (2)	−0·0002 (2)	−0·0005 (1)
O(5)	0·2948 (3)	0·3601 (3)	−0·1106 (1)	0·0241 (6)	0·0056 (2)	0·0041 (1)	−0·0005 (2)	−0·0013 (2)	−0·0003 (1)
O(6)	0·8043 (3)	0·3305 (3)	−0·2228 (1)	0·0332 (7)	0·0073 (2)	0·0037 (1)	−0·0001 (3)	0·0002 (2)	−0·0012 (1)
H(C1)	0·828	0·363	0·120						
H(C1')	0·830	0·393	0·234						
H(C2)	0·809	0·574	0·143						
H(C3)	0·299	0·468	0·052						
H(C4)	0·783	0·435	−0·022						
H(C5)	0·345	0·536	−0·143						
H(C6)	0·770	0·524	−0·239						
H(C6')	0·534	0·442	−0·287						
H(C7)	0·044	0·439	0·398						
H(C8)	−0·051	0·435	0·562						
H(C9)	0·143	0·242	0·649						
H(C10)	0·471	0·097	0·575						
H(C11)	0·604	0·141	0·390						
H(O1)	0·424	0·292	0·226						
H(O2)	0·436	0·649	0·227						
H(O3)	0·163	0·655	0·017						
H(O4)	0·740	0·671	−0·061						
H(O5)	0·388	0·307	−0·095						
H(O6)	0·947	0·346	−0·179						

with a thin film of Krylon plastic spray to retard decomposition. The $\theta/2\theta$ scanning mode and variable scan-width was used with Cu $K\alpha$ radiation ($\lambda = 1\cdot5418$ Å); 1161 reflections were measured, of which 37 were less than three standard deviations above background. Absorption corrections were applied in the reduction to structure amplitudes, using an IBM 1130 program (Craven, 1963) based on the procedure of Busing & Levy (1957).

Structure determination and refinement

The phases of 204 largest normalized structure amplitudes were obtained by application of the symbolic addition and tangent formula (Karle & Hauptman, 1956; Karle & Karle, 1966). An IBM 7090 version of the Hall (1968) program was used. The $|E|$ values and starting phases for the tangent refinement were 106,

$3\cdot47$, π; $\underline{105}$, $3\cdot07$, π; $\overline{1}14$, $2\cdot25$, π; $\overline{1}06$, $2\cdot92$, 0; $\overline{3}54$, $2\cdot90$, π; $\overline{2}31$, $2\cdot83$, $\pi/2$, of which the first three were arbitrarily assigned.

A three-dimensional E map with 201 terms showed twelve peaks which were consistent with the carbon and oxygen atoms of a stereochemically reasonable model for the glucitol molecule. A more complete Fourier synthesis revealed the pyridine molecule. The carbon and oxygen parameters were refined by a block-diagonal least-squares calculation on an IBM.1130 computer (Shiono, 1968) to an R value of $0\cdot05$. The hydrogen atoms were located on difference syntheses at R values of $0\cdot10$ and $0\cdot07$. All parameters except the thermal parameters of the hydrogen atoms were refined by full-matrix least squares on an IBM 7090 computer (Shiono, 1966) to a final R of $0\cdot042$. The H thermal parameters used were those of the atoms to which they are attached. The function minimized was
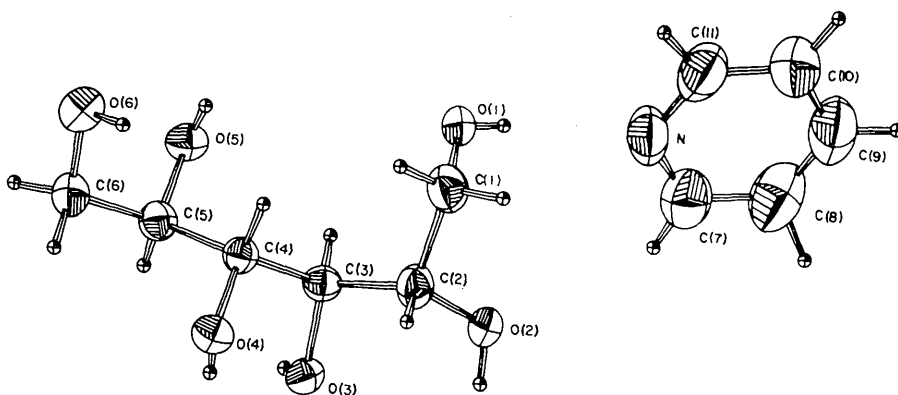

Fig. 1. *ORTEP* plot of one asymmetric unit of the glucitol–pyridine complex, showing atomic notation and thermal ellipsoids.
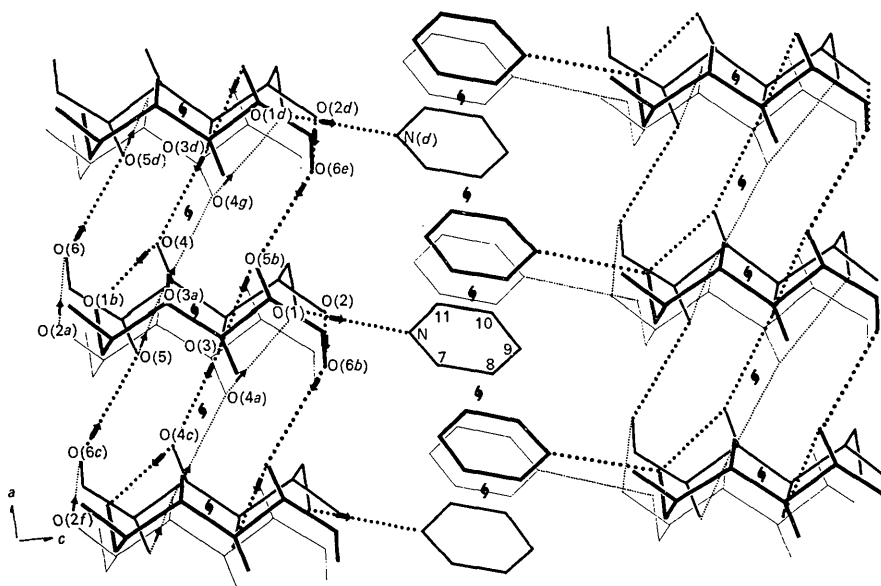

Fig. 2. View of the crystal structure of glucitol–pyridine down the b axis. Dotted lines are hydrogen-bonds; arrows indicate donor direction.
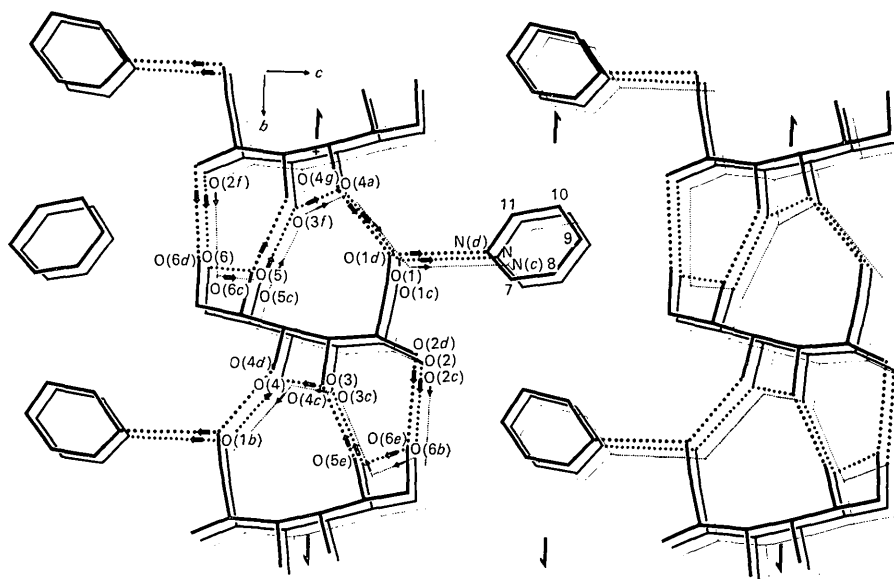
Fig. 3. View of the crystal structure of glucitol–pyridine down the a axis. Dotted lines are hydrogen-bonds; arrows indicate donor direction.

$\omega_i(|F_o| - |KF_c|)^2$ where $\omega_i = |F_o|^{-2}$ for $|F_o| \geq |4F_{min}|$

and

$|4F_{min}|^{-2}$ for $|F_o| < |4F_{min}|$: $|F_{min}|$ was 9·64.

The final parameters are given in Table 1 and the corresponding structure factors in Table 2. The atomic notation is shown in Fig. 1. The atomic scattering factors were those by Cromer & Waber (1965) for C, N and O and by Stewart, Davidson & Simpson (1965) for H.

Discussion

The crystal structure is illustrated in Figs. 2 and 3. It consists of layers of glucitol molecules separated by layers of pyridine molecules, the packing of which shows a marked similarity to that in the structure of the $C_6H_5N.ICl$ complex (Hassel & Rømming, 1956, 1957), and in the hydrochloride, $C_6H_5N.HCl$ (Rérat, 1962). The other pyridine complex structure which has been studied, $C_6H_5N.BF_3$, shows no obvious similarity in packing (Zvonkova, 1956). The layers are parallel to (001) and one molecule thick. The glucitol molecules are hydrogen-bonded within their layers with a parallel alignment of the molecules, which is characteristic of the crystal structures of the alditols. The pyridine molecules are aligned so that their rings are stacked parallel in columns in the a direction and alternately inclined in a herringbone arrangement in the b direction. The closest approaches between pyridine atoms are $H(C7)\cdots H(C10)$, 2·79 Å, and $C(8)\cdots C(11)$, 3·60 Å. Other shortest van der Waals separations in the structure are between the glucitol and pyridine atoms and are $O(6)\cdots C(9) = 3·32$, $O(2)\cdots C(10) = 3·44$, $O(6)\cdots C(8) = 3·60$ Å.

The glucitol and pyridine layers are associated by a O–H$\cdots$N hydrogen bond of 2·814 Å to form a very simple type of hydrogen-bonded complex consisting of alternate layers of the two species of molecules. As in the case of the glucose–urea (cf. Snyder, Rosenstein, Kim & Jeffrey, 1970), the stability of the crystalline complex implies the formation of a system of intermolecular hydrogen bonds and van der Waals interactions with a lattice energy greater than that of the separate structures of like molecules. It is a general rule in the alditol crystal structures, that the number of intermolecular hydrogen bonds per molecule is equal to the number of hydroxyl groups, since each oxygen atom is involved in two hydrogen bonds, one as donor and one as acceptor. In this structure, each oxygen atom forms a donor and acts as an acceptor except O(2)H, which forms only a donor bond to O(6) on an adjacent molecule. This is compensated by the bond from O(1)H to the pyridine nitrogen atom. Therefore, instead of six O–H$\cdots$O bonds per molecule, as in D-glucitol for example, there are in the complex, five O–H$\cdots$O and one O–H$\cdots$N bonds. The O$\cdots$O hydrogen bond distances have values (between 2·744 and 2·906 Å Table 3) which extend over a wider range about a greater mean value than in the alditols, and are presumably correspondingly weaker. These hydrogen bonds form finite chains, which start with O(2), linking six glucitol molecules in the donor–acceptor sequence, and terminate at the pyridine nitrogen atom, i.e. O(2) → O(6) → O(5) → O(3) → O(4) → O(1) → N. In the alditols, the hydrogen bonding generally forms infinite chains or closed loops. The pyridine molecules in the layers pack in a herringbone arrangement similar to that in benzene (Cox, Cruickshank & Smith, 1958) and other small aromatic molecules. That this

normal type of van der Waals packing can be accommodated between the layers of hydrogen-bonded glucitol molecules so as to permit the formation of O-H···N bonds would seem to be the most simple geometrical explanation for the particular stability of this 1:1 complex.

The glucitol molecule has a non-planar carbon-chain conformation, derived from the planar zigzag extended chain arrangement by a rotation of 120° about C(2)–C(3) as shown below:
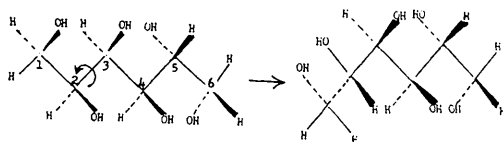
The equations for the two planes containing the carbon atoms are given in Table 4, and the detailed conformation angles about the C–C bonds are given in Fig. 4. This conformation is consistent with the observation that the carbon-chain conformations in the crystal structures of pentitols and hexitols are those which avoid the parallel alignment of C(n)–O and C(n+2)–O bonds, i.e. C(1)–O and C(3)–O, C(2)–O and C(4)–O in this case. Planar zigzag carbon chains are therefore found in DL-arabinitol (Hunter & Rosenstein, 1968), D-mannitol (Berman, Jeffrey & Rosenstein, 1968; Kim, Jeffrey & Rosenstein, 1968), galactitol (Berman & Rosenstein, 1968), and non-planar chains in D-glucitol (Jeffrey & Park, 1970), ribitol (Kim, Jeffrey & Rosenstein, 1969) and xylitol (Kim & Jeffrey, 1969). This general relationship between configuration and conformation in the polyols is discussed in detail by Jeffrey & Kim (1970).

The interatomic distances and angles are given in Table 5. In the glucitol molecule, the mean C–C and C–O distances are 1·530 and 1·425 Å. The spread of ±0·011 and ±0·006 Å, respectively, about these mean values is not significant. The C–C–C and C–C–O angles are 110·8 to 114·0° with a mean of 112·6°, and

Table 3. *Hydrogen bond distances and angles in glucitol-pyridine*

i	j	k	l	D_{jk}	$\angle ijk$	$\angle lkj$
C(1)	O(1) →	N	C(7)	2·814 Å	105·6°	126·5°
		N	C(11)			117·0
C(2)	O(2) →	O(6b)	C(6b)	2·906	119·9	124·9
C(3)	O(3) →	O(4c)	C(4c)	2·755	103·2	122·1
C(4)	O(4) →	O(1b)	C(1b)	2·794	109·7	140·3
C(5)	O(5) →	O(3a)	C(3a)	2·822	107·7	112·9
C(6)	O(6) →	O(5d)	C(5d)	2·744	111·5	115·9

Symmetry code

	x	y	z
a	$1-x$	$-\frac{1}{2}+y$	$-z$
b	$1-x$	$\frac{1}{2}+y$	$-z$
c	$-1+x$	y	z
d	$1+x$	y	z
e	$-1+x$	y	$1+z$
f	$1-x$	$-\frac{1}{2}+y$	$1-z$

→: direction of O-H···O bond

Table 4. *Least-squares planes in glucitol-pyridine*

Equation for plane: $Ax + By + Cz = D$, where x,y,z are in Å.

	Atoms in plane		Distance from the best plane		Constant	
Glucitol		C(1)	−1·527 Å		$A =$	0·1098
	C(2)		−0·125		$B =$	0·9798
	C(3)		0·101		$C =$	−0·1675
	C(4)		0·146		$D =$	5·3549
	C(5)		−0·092			
	C(6)		−0·030			
	O(2)		0·042			
Glucitol	C(1)		0·000		$A =$	−0·0987
	C(2)		0·000		$B =$	0·2010
		C(3)	−1·215		$C =$	0·9751
	O(1)		0·000		$D =$	2·7437
		O(2)	1·206			
Pyridine	C(7)		0·009		$A =$	0·7630
	C(8)		−0·004		$B =$	0·5942
	C(9)		−0·003		$C =$	0·2505
	C(10)		0·005		$D =$	4·1809
	C(11)		0·000			
	N		−0·007			

106·9 to 112·9° with a mean of 110·1° respectively. These results are in agreement with those observed in the other polyols.

In the pyridine molecule the C–C mean bond length is 1·367 Å, with a spread of −0·008 to +0·015 Å. This distance is 0·02 to 0·03 Å shorter than has been reported in pyridine oxide hydrochloride (Tsoucaris, 1961), pyridine hydrochloride (Rérat, 1962) and pyridinium dicyanomethylide (Bugg & Sass, 1965). The C–N bonds are 1·329 and 1·330 Å, and the C–N–C angle of 116·5° is the smallest within the ring. The ring is planar within ±0·009 Å. The C–H distances varied from 0·88 to 1·16 Å and the O–H distances from 0·68 to 0·89 Å. The angles involving hydrogen atoms, (*i.e.* X–Y–H) varied from 103 to 125°. Those associated with the pyridine ring grouped around 120°, while the remaining were closer to 110°. No other significance was associated with these variations.

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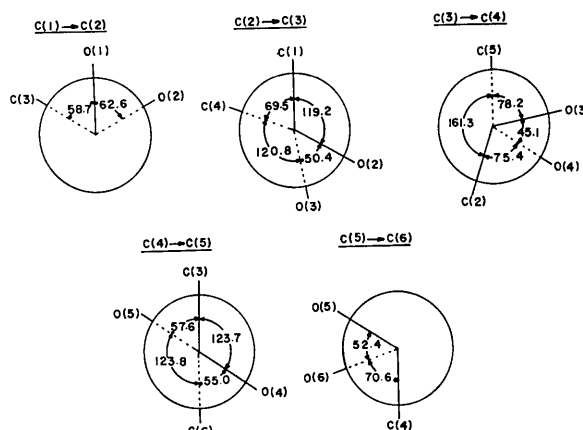BERMAN, H. M. & ROSENSTEIN, R. D. (1968). *Acta Cryst.* B24, 435.

Fig. 4. Conformation angles about the C–C bonds in the glucitol molecule of the glucitol–pyridine complex.

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Table 5. *Intramolecular distances and angles in glucitol–pyridine*

The estimated standard deviations given in parentheses refer to the last decimal positions of respective values. The mean values are calculated from

$$ l = \sum_i \left(\frac{l_i}{\sigma_i^2}\right) \Big/ \sum_i \left(\frac{1}{\sigma_i^2}\right), \quad \sigma_{\text{mean}} = \left(\frac{\sum_i (l-l_i)^2}{N-1}\right)^{\frac{1}{2}} $$

i	j	D_{ij}	$D_{ij}*$	i	j	k	ijk
C(1)	C(2)	1·519 (4) Å	1·520 Å	C(1)	C(2)	C(3)	112·3 (2)°
C(2)	C(3)	1·536 (4)	1·537	C(2)	C(3)	C(4)	113·2 (2)
C(3)	C(4)	1·534 (4)	1·536	C(3)	C(4)	C(5)	110·8 (2)
C(4)	C(5)	1·535 (4)	1·535	C(4)	C(5)	C(6)	114·0 (2)
C(5)	C(6)	1·528 (4)	1·530	O(1)	C(1)	C(2)	112·6 (2)
C(1)	O(1)	1·419 (4)	1·420	C(1)	C(2)	O(2)	106·9 (2)
C(2)	O(2)	1·420 (3)	1·421	O(2)	C(2)	C(3)	110·5 (2)
C(3)	O(3)	1·429 (3)	1·431	C(2)	C(3)	O(3)	108·3 (2)
C(4)	O(4)	1·427 (3)	1·429	O(3)	C(3)	C(4)	108·9 (2)
C(5)	O(5)	1·430 (3)	1·432	C(3)	C(4)	O(4)	111·2 (2)
C(6)	O(6)	1·421 (3)	1·422	O(4)	C(4)	C(5)	110·5 (2)
C(7)	C(8)	1·364 (7)	1·364	C(4)	C(5)	O(5)	108·9 (2)
C(8)	C(9)	1·359 (6)	1·360	O(5)	C(5)	C(6)	110·4 (2)
C(9)	C(10)	1·364 (6)	1·365	C(5)	C(6)	O(6)	112·9 (2)
C(10)	C(11)	1·382 (6)	1·382	C(7)	C(8)	C(9)	119·7 (4)
C(11)	N	1·329 (6)	1·330	C(8)	C(9)	C(10)	118·8 (4)
C(7)	N	1·330 (6)	1·331	C(9)	C(10)	C(11)	118·1 (4)
				C(10)	C(11)	N	123·7 (4)
				C(11)	N	C(7)	116·5 (4)
				N	C(7)	C(8)	123·2 (4)

Glucitol

l_{C-C}	=	1·530 Å	σ_{mean} = 0·007 Å
l_{C-O}	=	1·425	0·005
$\angle_{C-C-C}$	=	112·6°	1·4°
$\angle_{C-C-O}$	=	110·1	1·9

Pyridine

l_{C-C}	=	1·367 Å	0·011 Å
$\angle_{C-C-C}$	=	118·9°	0·8°

* Bond distances corrected for libration.

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The Crystal Structure of the Potassium Methoxide Adduct of 4-Methoxy-5,7- Dinitrobenzfurazan, a Meisenheimer Complex

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The crystal and molecular structure of the potassium methoxide adduct of 4-methoxy-5,7-dinitrobenzfurazan, $K^+[(CH_3O)_2C_6H(NO_2)N_2O]^-$, has been determined by X-ray diffraction techniques. The complex crystallizes as red, monoclinic crystals with $a = 15\cdot152 \pm 0\cdot015$, $b = 9\cdot307 \pm 0\cdot003$, $c = 17\cdot780 \pm 0\cdot010$ Å and $\beta = 106\cdot22 \pm 0\cdot08°$, measured at room temperature. The space group is $P2_1/c$ and with eight molecules per unit cell, $D_c = 1\cdot712$ g.cm^{-3} compared with $D_m = 1\cdot718$ g.cm^{-3}. The structure was solved using the symbolic addition procedure and Fourier syntheses. A refinement by full-matrix least-squares methods converged to a final R of 0·068 for the 4013 observed reflections measured using the stationary-crystal stationary-counter technique with molybdenum radiation. The two methoxyl groups are covalently bonded to the same ring carbon atom with an average C–O distance of $1\cdot415 \pm 0\cdot006$ Å. The sp^3 hybridized carbon atom in the ring produces distortions throughout the entire molecule. The electron withdrawing power of the coplanar furazan ring has a pronounced effect on the benzene ring system.

Introduction

Meisenheimer complexes, the stable intermediates in aromatic nucleophilic substitution reactions, have been of interest (Fendler, Fendler & Griffin, 1969; Crampton & Gold, 1966; Foster & Fyfe, 1966). The question is whether the intermediate formed by the attack of an alkoxide ion on nitroaryl compounds is a covalently bonded species or a charge-transfer complex. The recent crystal structure determinations of 1,1'-dimethoxy-2,4,6-trinitrobenzene potassium dihydrate by Ueda, Sakabe, Tanaka & Furusaki (1968) and the ethoxide adducts of 2,4,6-trinitrophenetole by Destro, Gramaccioli & Simonetta (1968) have confirmed the covalent nature of the intermediate.

The present study was undertaken in 1965 but was not completed until recently. The benzfurazan ring alters the possible resonance structures and the molecular geometry is distinctly different from the two previous studies. A preliminary account of our results has appeared recently (Messmer & Palenik, 1969).

Experimental

Orange-red platelets of the potassium methoxide adduct of 4-methoxy-5,7-dinitrobenzfurazan (KDMDNBF) were kindly supplied by Dr W. P. Norris. Preliminary Weissenberg photographs indicate that the crystals are monoclinic with the systematic absences of $h0l$ for $l = 2n + 1$ and $0k0$ for $k = 2n + 1$, indicating that the space group is $P2_1/c$.

A crystal of dimensions $0\cdot23 \times 0\cdot22 \times 0\cdot10$ mm which was dipped in liquid nitrogen to minimize extinction

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