Acta Crystallographica Section C Crystal Structure Communications ISSN 0108-2701

Hydrogen bonding in *C*-methylated nitroanilines: a room-temperature monoclinic polymorph of 4-methyl-3-nitroaniline with Z' = 2

Choudhury M. Zakaria,^a† John N. Low,^b Janet M. S. Skakle,^b Susan A. McWilliam,^b James L. Wardell^b and Christopher Glidewell^a*

^aSchool of Chemistry, University of St Andrews, St Andrews, Fife KY16 9ST, Scotland, and ^bDepartment of Chemistry, University of Aberdeen, Meston Walk, Old Aberdeen AB24 3UE, Scotland Correspondence e-mail: cg@st-andrews.ac.uk

Received 12 July 2001 Accepted 18 July 2001

The title compound, $C_7H_8N_2O_2$, is monoclinic (space group $P2_1/n$) at 295 (2) K with Z' = 2. The two types of molecule form independent C(7) chains, and the structure is related to that of the low-temperature triclinic polymorph, where Z' = 4 in $P\overline{1}$, by a simple displacive transformation.

Comment

When crystallized from ethanol, 4-methyl-3-nitroaniline, (I), is triclinic $P\overline{1}$ at 150 (2) K with Z' = 4 (Cannon *et al.*, 2001). Of the four independent molecules, two form individual chains built from N-H···O hydrogen bonds, while the other two types combine to form molecular ladders. At ambient temperatures, however, this material is monoclinic $P2_1/n$ with Z' = 2. The unit-cell dimensions and the atomic coordinates indicate that the low-temperature triclinic and ambienttemperature monoclinic polymorphs are related by a simple displacive phase transformation.



The molecular dimensions of the two independent mol-

ecules in the monoclinic polymorph (Fig. 1) are very similar

(Table 1) and the C-C bond lengths show a significant

deviation of the aryl rings from regular hexagons; this feature

was also observed in the triclinic polymorph. The two mol-

ecules do, however, differ markedly in the twist of the nitro

difference alone precludes the possibility of any further symmetry.

Each molecule acts as a single donor and single acceptor in $N-H\cdots O$ hydrogen bonds (Table 2); thus, half of the N-H bonds and half of the O atoms do not participate in the hydrogen bonding, so that the sole motif of supramolecular aggregation is the formation of C(7) chains (Bernstein *et al.*, 1995). Molecules of type 1 and 2, containing atoms N11 and N21, respectively, each act as hydrogen-bond donors to





The two independent molecules in (I) showing the atom-labelling scheme. Displacement ellipsoids are drawn at the 30% probability level.





Part of the crystal structure of (I) showing the two independent C(7) chains. For the sake of clarity, H atoms bonded to C atoms have been omitted. Atoms marked with an asterisk (*) or hash (#) are at the symmetry positions (1 + x, y, z) and (-1 + x, y, z), respectively.

another molecule of the same type, so generating by translation two distinct chains, both running parallel to the [100] direction and each containing just one type of molecule (Fig. 2). Four chains of each type run through each unit cell, but there are no N-H···O or C-H···O hydrogen bonds between adjacent chains, nor are there any aromatic π - π stacking interactions.

The unit-cell dimensions of the triclinic and monoclinic polymorphs of (I) are very similar and the triclinic unit cell can be derived from the present monoclinic cell by means of the transformation (010, $\overline{100}$, 001). Subject to this transformation and an origin shift, the atomic coordinates of the two forms indicate that triclinic molecules of types 1 and 2 (Cannon et al., 2001) map into the monoclinic type 2 molecules at (x, y, z) and $(\frac{1}{2} - x, \frac{1}{2} + y, \frac{1}{2} - z)$, respectively, while triclinic molecules 3 and 4 map into the monoclinic type 1 molecules at (-x, -y, -y)-z) and $\left(-\frac{1}{2}+x, \frac{1}{2}-y, \frac{1}{2}+z\right)$, respectively. It is noteworthy that the conformations of the various molecules, as judged by the C-C-N-O torsion angles (Table 1) and particularly by the dihedral angles between the aryl rings and the $C-NO_2$ groups, faithfully follow this mapping. Thus, in the triclinic polymorph, molecules 1 and 2 have nitro-group twists of 31.91 (8) and 28.99 (8) $^{\circ}$, respectively, comparable with the $32.5 (2)^{\circ}$ twist in monoclinic type 2 molecules, while triclinic type 3 and 4 molecules have nitro-group twists of 7.91 (8) and $3.92 (8)^{\circ}$, respectively, compared with a twist of $7.5 (2)^{\circ}$ in monoclinic type 1 molecules. These observations all point to a simple displacive phase transformation between the triclinic and monoclinic polymorphs.

Experimental

A sample of compound (I) was obtained from Aldrich. Crystals suitable for single-crystal X-ray diffraction were grown from a solution in ethanol. The same phase was obtained by recrystallization from CH_2Cl_2 .

Crystal	data
---------	------

$C_7H_8N_2O_2$	$D_x = 1.363 \text{ Mg m}^{-3}$
$M_r = 152.16$	Mo $K\alpha$ radiation
Monoclinic, $P2_1/n$	Cell parameters from 3128
a = 8.2473 (7) Å	reflections
b = 7.5676(7) Å	$\theta = 3.2-27.5^{\circ}$
c = 23.7798 (16) Å	$\mu = 0.10 \text{ mm}^{-1}$
$\beta = 91.717 \ (5)^{\circ}$	T = 295 (2) K
$V = 1483.5 (2) \text{ Å}^3$	Plate, orange
Z = 8	$0.36 \times 0.18 \times 0.08 \text{ mm}$

1517 reflections with $I > 2\sigma(I)$

Intensity decay: negligible

 $R_{\rm int} = 0.105$

 $\theta_{\max} = 27.5^{\circ}$ $h = -10 \rightarrow 10$

 $k = -9 \rightarrow 9$

 $l = -30 \rightarrow 28$

Data collection

Nonius KappaCCD diffractometer φ scans, and ω scans with κ offsets Absorption correction: multi-scan (DENZO-SMN; Otwinowski & Minor, 1997) $T_{min} = 0.951, T_{max} = 0.985$ 11 137 measured reflections 3128 independent reflections

Refinement

Refinement on F^2	H-atom parameters constrained
$R[F^2 > 2\sigma(F^2)] = 0.061$	$w = 1/[\sigma^2(F_o^2) + (0.1003P)^2]$
$wR(F^2) = 0.204$	where $P = (F_o^2 + 2F_c^2)/3$
S = 1.01	$(\Delta/\sigma)_{\rm max} = 0.002$
3128 reflections	$\Delta \rho_{\rm max} = 0.15 \ {\rm e} \ {\rm \AA}^{-3}$
201 parameters	$\Delta \rho_{\rm min} = -0.13 \ {\rm e} \ {\rm \AA}^{-3}$

Compound (I) crystallized in the monoclinic system; space group $P2_1/n$ was uniquely assigned from the systematic absences. H atoms were treated as riding atoms with C–H distances of 0.93 (aromatic) or 0.96 Å (methyl), and an N–H distance of 0.86 Å. The crystal

Table 1

Selected geometric parameters (Å, °).

C11-C12	1.381 (4)	C21-C22	1.380 (4)
C12-C13	1.371 (4)	C22-C23	1.383 (4)
C13-C14	1.402 (4)	C23-C24	1.402 (3)
C14-C15	1.390 (4)	C24-C25	1.384 (4)
C15-C16	1.364 (4)	C25-C26	1.370 (4)
C16-C11	1.395 (4)	C26-C21	1.399 (3)
C11-N11	1.374 (4)	C21-N21	1.374 (4)
C13-N13	1.471 (4)	C23-N23	1.465 (3)
N13-O11	1.201 (4)	N23-O21	1.219 (3)
N13-O12	1.195 (4)	N23-O22	1.215 (3)
C14-C17	1.497 (4)	C24-C27	1.503 (4)
C12 C12 N12 O11	172 5 (4)	C12 C12 N122 O21	21.5(2)
$C_{12} = C_{13} = N_{13} = O_{11}$	1/2.3 (4)	$C_{22} = C_{23} = N_{23} = O_{21}$	-31.3(3)
C12-C13-N13-012	-8.4 (4)	C22 - C23 - N23 - O22	148.3 (3)

Table 2	
Hydrogen-bonding geometry (Å, °).	

$D - H \cdots A$	D-H	$H \cdots A$	$D \cdots A$	$D - H \cdots A$
N11 $-$ H11 B ···O11 ⁱ	0.86	2.41	3.181 (5)	150
$N21 - H21B \cdot \cdot \cdot O21^{ii}$	0.86	2.45	3.285 (4)	163

Symmetry codes: (i) 1 + x, y, z; (ii) x - 1, y, z.

quality was not high and, as expected, only *ca* 50% of the reflections were labelled 'observed' at ambient temperature.

Data collection: *KappaCCD Server Software* (Nonius, 1997); cell refinement: *DENZO–SMN* (Otwinowski & Minor, 1997); data reduction: *DENZO–SMN*; program(s) used to solve structure: *SHELXS*97 (Sheldrick, 1997); program(s) used to refine structure: *SHELXL*97 (Sheldrick, 1997); molecular graphics: *PLATON* (Spek, 2001); software used to prepare material for publication: *SHELXL*97 (Sheldrick, 1997) and *PRPKAPPA* (Ferguson, 1999).

X-ray data were collected at the EPSRC X-ray Crystallographic Service, University of Southampton. The authors thank the staff for all their help and advice. CMZ thanks the Association of Commonwealth Universities for the award of a Commonwealth Fellowship 2000–2001.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: GG1075). Services for accessing these data are described at the back of the journal.

References

- Bernstein, J., Davis, R. E., Shimoni, L. & Chang, N.-L. (1995). Angew. Chem. Int. Ed. Engl. 34, 1555–1573.
- Cannon, D., Glidewell, C., Low, J. N., Quesada, A. & Wardell, J. L. (2001). Acta Cryst. C57, 216–221.
- Ferguson, G. (1999). PRPKAPPA. University of Guelph, Canada.
- Nonius (1997). *KappaCCD Server Software*. Windows 3.11 Version. Nonius BV, Delft, The Netherlands.
- Otwinowski, Z. & Minor, W. (1997). Methods in Enzymology, Vol. 276, Macromolecular Crystallography, Part A, edited by C. W. Carter & R. M. Sweet, pp. 307–326. London: Academic Press.
- Sheldrick, G. M. (1997). SHELXL97 and SHELXS97. University of Göttingen, Germany.

Spek, A. L. (2001). PLATON. University of Utrecht, The Netherlands.