electronic reprint

Acta Crystallographica Section E
Structure Reports
Online
ISSN 1600-5368
Editors: **W. Clegg and D. G. Watson**

[(1-Methylcytosine)$_2$H]I, an asymmetric base pair

Jens Müller and Eva Freisinger

Acta Crystallographica Section E
Structure Reports Online
ISSN 1600-5368

[(1-Methylcytosine)$_2$H]I, an asymmetric base pair

Jens Müller[a]* and Eva Freisinger[b]

[a]University of Dortmund, Inorganic Chemistry, Otto-Hahn-Straße 6, 44227 Dortmund, Germany, and [b]University of Zürich, Institute of Inorganic Chemistry, Winterthurerstrasse 190, 8057 Zürich, Switzerland

Correspondence e-mail: mueller@muellerlab.org

Key indicators

Single-crystal X-ray study
T = 163 K
Mean σ(C–C) = 0.005 Å
R factor = 0.020
wR factor = 0.043
Data-to-parameter ratio = 13.8

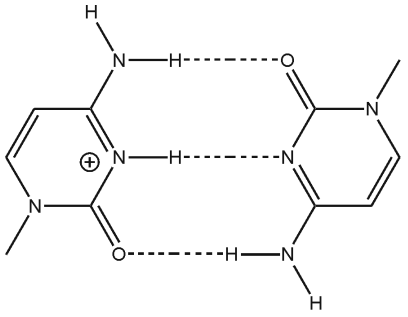
For details of how these key indicators were automatically derived from the article, see http://journals.iucr.org/e.

The X-ray crystal structure of the title compound, 1-methylcytosinium iodide 1-methylcytosine, [(1-MeC)$_2$H]I (1-MeC is 1-methylcytosine) or $C_5H_8N_3O^+\cdot I^-\cdot C_5H_7N_3O$, has been determined at 163 K. In this compound, one protonated (1-MeCH$^+$) and one neutral methylcytosine (1-MeC) moiety form an asymmetric base pair comprising three hydrogen bonds. A previous structure determination [Krüger, Bruhn & Steinborn (2004). *Org. Biomol. Chem.* **2**, 2513–2516] showed the same cell parameters but a centrosymmetric base pair in space group $P2_1/c$. At low temperature, however, we discovered the title compound to be a racemic twin showing pseudo-centrosymmetry.

Received 4 January 2005
Accepted 10 January 2005
Online 22 January 2005

Comment

Hydrogen bonds are a common structural feature in nucleic acids (Lavery & Zakrzewska, 1999). Although typically two different nucleobases undergo base pairing (*e.g.* guanine:cytosine, adenine:thymine), several hydrogen-bonding patterns are known with base pairing between identical nucleobases. The i-motif, consisting of two parallel-stranded intertwined double helices made up entirely of cytosine, is a well known example (Patel *et al.*, 1999). A recent publication describes the crystal structure of a centrosymmetric hemiprotonated methylcytosine:methylcytosine base pair, [(1-MeC)$_2$H]I (Krüger *et al.*, 2004). Concomitant DFT calculations suggest the formation of an asymmetric base pair, however. We report here the crystal structure of this compound in a different crystal configuration, determined at 163 K, displaying the theoretically predicted asymmetric base pairing pattern (Fig. 1). The crystal was obtained in the course of our studies of model systems for metal-mediated base pairs (Müller *et al.*, 2005).



(I)

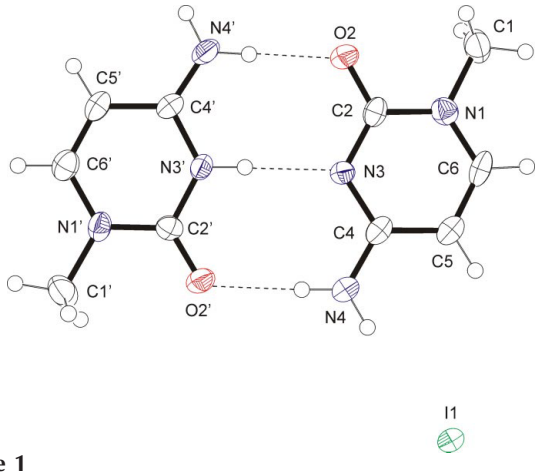


Figure 1
View of the cation of the title compound with the atom numbering scheme. Displacement ellipsoids are drawn at the 50% probability level.

The hydrogen-bonded nucleobases of the title compound are almost coplanar [1.6 (2)°]. Two base pairs are bridged *via* the iodide counter-ion (Fig. 2), which forms hydrogen bonds to the exocyclic amine groups of both bases [3.633 (2) and 3.717 (3) Å]. Two crystallographically independent 1-MeC moieties of neighbouring base pairs stack at a distance of approximately 3.4 Å, leading to the formation of a chain structure with two individual chains I and II (Fig. 3).

The H atom at the N3 position of 1-MeCH$^+$ was located in difference Fourier maps. The protonation site is further corroborated by an increase in the C2—N3—C4 angle [125.1 (3)° in 1-MeCH$^+$ and 119.6 (2)° in 1-MeC]. In addition, the two N4(H)···O hydrogen bonds display different bond lengths, resulting in a 2.762 (4) Å distance for the stronger bond involving N4(H) of 1-MeCH$^+$ and 2.901 (3) Å for the weaker bond (see Table 2 for hydrogen-bond geometries). Accordingly, both the C4—N4 and the C2—O2 bonds are significantly shorter in 1-MeCH$^+$ than in 1-MeC [1.291 (5) *versus* 1.333 (4) Å and 1.219 (3) *versus* 1.245 (3) Å]. The N3···N3′ distance is 2.808 (4) Å. All these experimental values correlate well with those of the DFT study (Krüger *et al.*, 2004).

A comparison of the two different crystal forms of [(1-MeC)$_2$H]I with related structures of hemiprotonated cytosine dimers containing a variety of other counter-ions or solvent molecules reveals that in almost all cases asymmetric base pairs are observed (Salam & Aoki, 2000; Schimanski *et al.*, 1998; Kistenmacher *et al.*, 1980; Fujinami *et al.*, 1979; Kistenmacher *et al.*, 1979). Only one of the crystallographically independent 1-MeCH$^+$:1-MeC pairs in the structure of cytosine hemitrichloroacetate has been proposed as truly symmetric (Gdaniec *et al.*, 1988), whereas in the other centrosymmetric structures known to date this symmetry appears to be a consequence of a disordered H atom in the central hydrogen bond (Krüger *et al.*, 2004; Gdaniec *et al.*, 1988). The difference between the crystal structure presented in this work and its symmetric counterpart (Krüger *et al.*, 2004) is presumably based on a temperature-dependent change from disorder to order, supporting this assumption.

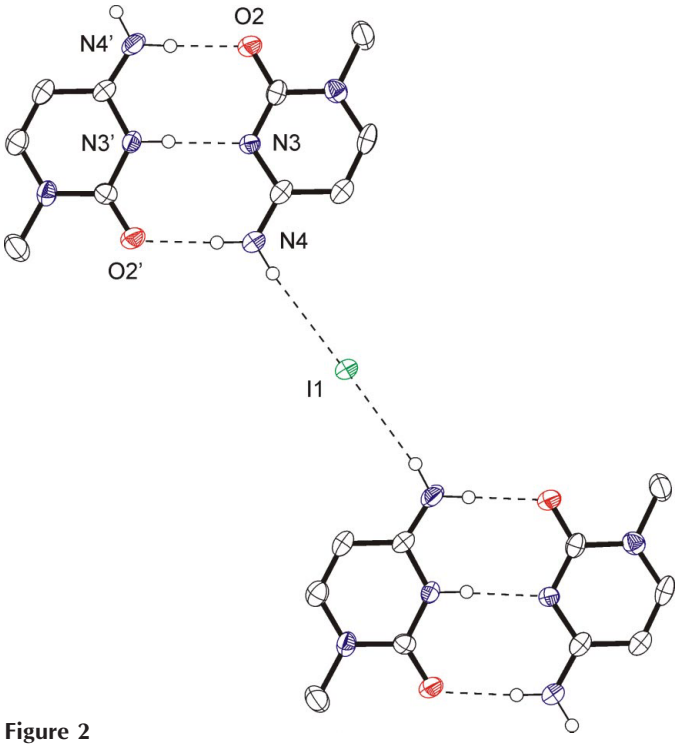


Figure 2
Two base pairs bridged *via* an iodide counter-ion. Displacement ellipsoids are drawn at the 50% probability level. The unlabelled asymmetric pair is related by the symmetry operator ($x+1$, y, $z+1$). Dashed lines indicate hydrogen bonds.

Experimental

The title compound was synthesized according to published protocols (Kistenmacher *et al.*, 1979).

Crystal data

$C_5H_8N_3O^+\cdot I^-\cdot C_5H_7N_3O$
M_r = 378.18
Monoclinic, $P2_1$
a = 7.195 (1) Å
b = 8.629 (2) Å
c = 11.522 (2) Å
β = 97.59 (3)°
V = 709.1 (2) Å^3
Z = 2
D_x = 1.771 Mg m^{-3}
Mo $K\alpha$ radiation
Cell parameters from 4452 reflections
θ = 2.9–25.4°
μ = 2.27 mm^{-1}
T = 163 (2) K
Block, colourless
0.50 × 0.40 × 0.38 mm

Data collection

Nonius KappaCCD diffractometer
ω scans
Absorption correction: multi-scan (*SCALEPACK*; Otwinowski & Minor, 1997)
T_{min} = 0.358, T_{max} = 0.427
4462 measured reflections
2519 independent reflections
2291 reflections with $I > 2\sigma(I)$
R_{int} = 0.022
θ_{max} = 25.4°
$h = -8 \rightarrow 8$
$k = -10 \rightarrow 10$
$l = -13 \rightarrow 13$

Refinement

Refinement on F^2
$R[F^2 > 4\sigma(F^2)]$ = 0.020
$wR(F^2)$ = 0.043
S = 0.98
2519 reflections
183 parameters
H atoms treated by a mixture of independent and constrained refinement
$w = 1/[\sigma^2(F_o^2) + (0.0118P)^2]$ where $P = (F_o^2 + 2F_c^2)/3$
$(\Delta/\sigma)_{max}$ = 0.001
$\Delta\rho_{max}$ = 0.31 e Å^{-3}
$\Delta\rho_{min}$ = −0.27 e Å^{-3}
Extinction correction: *SHELXL97*
Extinction coefficient: 0.0174 (9)
Absolute structure: Flack (1983), 1166 Friedel pairs
Flack parameter: 0.52 (2)

Table 1
Selected geometric parameters (Å, °).

C2—O2	1.245 (3)	C2′—O2′	1.219 (3)
C2—N3	1.359 (4)	C2′—N3′	1.368 (4)
N3—C4	1.342 (3)	N3′—C4′	1.355 (3)
C4—N4	1.333 (4)	C4′—N4′	1.291 (5)
O2—C2—N3	122.3 (3)	O2′—C2′—N3′	121.8 (3)
O2—C2—N1	118.6 (3)	O2′—C2′—N1′	121.7 (4)
N3—C2—N1	119.2 (3)	N3′—C2′—N1′	116.5 (3)
C4—N3—C2	119.6 (2)	C4′—N3′—C2′	125.1 (3)
N4—C4—N3	117.9 (3)	N4′—C4′—N3′	119.7 (3)
N4—C4—C5	119.9 (2)	N4′—C4′—C5′	123.2 (3)
N3—C4—C5	122.2 (3)	N3′—C4′—C5′	117.0 (3)

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

D—H···*A*	*D*—H	H···*A*	*D*···*A*	*D*—H···*A*
N3′—H3′···N3	0.82 (4)	1.99 (4)	2.808 (4)	171 (4)
N4′—H4′1···O2	0.86	1.92	2.762 (4)	166
N4—H4*A*···O2’	0.86	2.07	2.901 (3)	161
N4—H4*B*···I1	0.86	2.87	3.717 (2)	169
N4′—H4’2···I1^{i}	0.86	2.78	3.633 (2)	171
C5—H5···O2′^{ii}	0.93	2.47	3.088 (4)	124
C5′—H5′···O2^{iii}	0.93	2.48	3.085 (4)	123

Symmetry codes: (i) $x-1, y, z-1$; (ii) $-x+1, y+\frac{1}{2}, -z+1$; (iii) $-x, y-\frac{1}{2}, -z$.

H atoms, except H3′, were included in calculated positions with distances ranging from 0.86 to 0.96 Å and included in the refinement in the riding-model approximation with refined isotropic displacement parameters. Atom H3′ was found in the difference Fourier map and refined without restraints.

Data collection: *KappaCCD Software* (Nonius, 1998); cell refinement: *DENZO* and *SCALEPACK* (Otwinowski & Minor, 1997); data reduction: *DENZO* and *SCALEPACK*; program(s) used to solve structure: *SHELXS86* (Sheldrick, 1990*a*); program(s) used to refine structure: *SHELXL97* (Sheldrick, 1997); molecular graphics: *SHELXTL-Plus* (Sheldrick, 1990*b*); software used to prepare material for publication: *SHELXL97*.

This work was supported by the Deutsche Forschungsgemeinschaft (Emmy Noether-Programme), the Department of Chemistry at the University of Dortmund and the Fonds der Chemischen Industrie. The authors thank Professor Dr Bernhard Lippert for his continuous support.

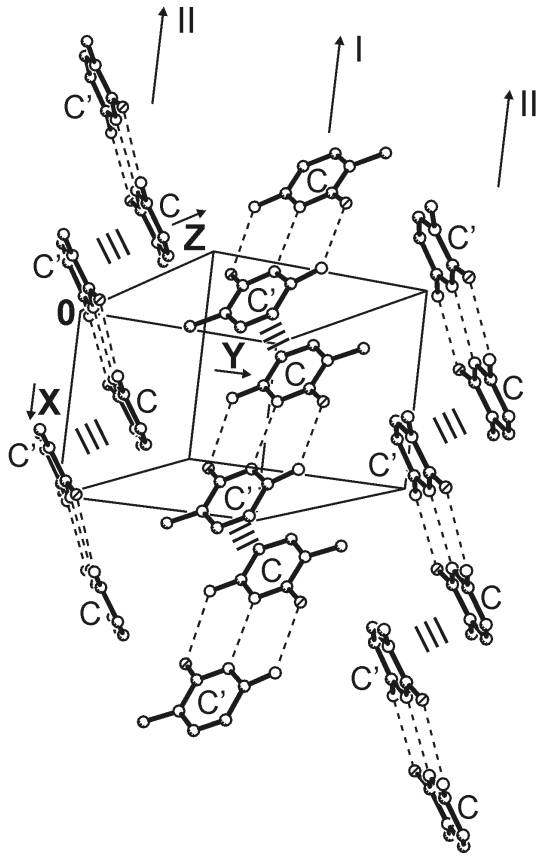


Figure 3
Chain structure formed by base stacking of crystallographically independent 1-MeC moieties. Dashed lines indicate hydrogen bonds.

References

Flack, H. D. (1983). *Acta Cryst.* A**39**, 876–881.
Fujinami, F., Ogawa, K., Arakawa, Y., Shirotake, S., Fuji, S. & Tomita, K.-I. (1979). *Acta Cryst.* B**35**, 968–970.
Gdaniec, M., Brycki, B. & Szafran, M. (1988). *J. Chem. Soc. Perkin Trans.* 2, pp. 1775–1779.
Kistenmacher, T. J., Rossi, M., Caradonna, J. P. & Marzilli, L. G. (1979). *Adv. Mol. Relax. Interact. Proc.* **15**, 119–133.
Kistenmacher, T. J., Rossi, M., Chiang, C. C., Caradonna, J. P. & Marzilli, L. (1980). *Adv. Mol. Relax. Interact. Proc.* **17**, 113–134.
Krüger, T., Bruhn, C. & Steinborn, D. (2004). *Org. Biomol. Chem.* **2**, 2513–2516.
Lavery, R. & Zakrzewska, K. (1999). *Oxford Handbook of Nucleic Acid Structure*, edited by S. Neidle, pp. 39–76. New York: Oxford University Press Inc.
Müller, J., Polonius, F.-A. & Roitzsch, M. (2005). *Inorg. Chim. Acta.* In the press (doi: 10.1016/j.ica.2004.11.038).
Nonius (1998). *KappaCCD Software*. Nonius BV, Delft, The Netherlands.
Otwinowski, Z. & Minor, W. (1997). *Methods in Enzymology*, Vol. 276, *Macromolecular Crystallography*, Part A, edited by C. W. Carter Jr & R. M. Sweet, pp. 307–326. New York: Academic Press.
Patel, D. J., Bouaziz, S., Kettani, A. & Wang, Y. (1999). *Oxford Handbook of Nucleic Acid Structure*, edited by S. Neidle, pp. 389–453. New York: Oxford University Press Inc.
Salam, M. A. & Aoki, K. (2000). *Inorg. Chim. Acta*, **311**, 15–24.
Schimanski, A., Freisinger, E., Erxleben, A. & Lippert, B. (1998). *Inorg. Chim. Acta*, **283**, 223–232.
Sheldrick, G. M. (1990*a*). *Acta Cryst.* A**46**, 467–473.
Sheldrick, G. M. (1990*b*). *SHELXTL-Plus* (VMS). Siemens Analytical X-ray Instruments Inc., Madison, Wisconsin, USA.
Sheldrick, G. M. (1997). *SHELXL97*. University of Göttingen, Germany.