

## DETERMINATION OF THE STRUCTURE OF *p*-METHYLBENZAMIDINIUM FORMATE MONOHYDRATE

Bohumil KRATOCHVÍL<sup>a</sup>, Jan ONDRÁČEK<sup>a</sup>, Jindřich HAŠEK<sup>b</sup> and László CSORDÁS<sup>c</sup>

<sup>a</sup> Department of Mineralogy,

Prague Institute of Chemical Technology, 166 28 Prague 6, Czechoslovakia

<sup>b</sup> Institute of Macromolecular Chemistry,

Czechoslovak Academy of Sciences, 166 06 Prague 6, Czechoslovakia and

<sup>c</sup> Laboratory of Surface and Interface Physics,

Eötvös University, 1088 Budapest, Hungary

Received December 21st, 1987

Accepted February 8th, 1988

The molecular and crystal structure of *p*-methylbenzamidinium formate monohydrate,  $C_9H_{14}N_2O_3$ , was solved by direct methods. The positions of all the atoms were localized and the structure was refined anisotropically. The final value of the *R* factor equalled 0.043 for 1 150 observed reflections ( $I > 1.96\sigma(I)$ ). The substance crystallizes in the  $P2_1/c$  monoclinic space group with lattice parameters  $a = 1\ 038.9(4)$ ,  $b = 1\ 146.1(5)$ ,  $c = 912.4(3)$  pm,  $\beta = 94.77(3)^\circ$ ,  $Z = 4$ . The molecule contains an amidinium-carboxylate bond, formed by two intramolecular hydrogen bridges of the N—H...O type. Intermolecular hydrogen bonds are formed by the side hydrogen atoms of the amidine and the hydrogen atoms of the water molecule and are of the N—H...O and O—H...O types; they form a three-dimensional network in the crystal structure. In this, the structure of *p*-methylbenzamidinium formate monohydrate differs from the related structures of benzamidinium pyruvate and benzamidinium bromoacetate, characterized by infinite intermolecular chains formed through hydrogen bonding.

The specific interaction of an enzyme containing an arginine active site with a carboxylate substrate can depend on the formation of two parallel hydrogen bonds of the N—H...O—C type, as has been demonstrated, for example, for lactate dehydrogenase<sup>1</sup>. Through this interaction, the substrate is suitably fixed to the active site in the enzyme. In addition to this bond of the substrate to the enzyme, amidine-carboxylate interactions play an important role in fixing the tertiary structure of proteins or in the formation of nucleoproteins<sup>2</sup>. Amidinium carboxylates are suitable model molecules for simulation of this interaction. A great deal of attention has been paid to the structure of these compounds. So far, only the structures of bis(acetamidinium) carbonate monohydrate<sup>3</sup>, formamide oxime oxalate<sup>4</sup>, benzamidinium pyruvate<sup>5</sup> and benzamidinium bromoacetate<sup>6</sup> are known. The studied compound, *p*-methylbenzamidinium formate monohydrate, is a further member in the series of benzamidinium carboxylates. The structure of these compounds (see refs<sup>5,6</sup>) is character-

ized by two parallel intramolecular hydrogen bonds forming interactions between the nitrogen atoms of the amidinium group and the carboxyl oxygen atoms. The amidinium side-chain hydrogen atoms form two intermolecular hydrogen bonds, once again between nitrogen and oxygen atoms (in neighbouring molecules), so that the final crystal structure is characterized by infinite chains bonded together through van der Waals interactions.

The studied structure of *p*-methylbenzamidinium formate monohydrate is unusual in the presence of water molecules and their effect on the system of hydrogen bonds and the geometry of the amidinium-carboxyl interactions.

### EXPERIMENTAL

Synthesis of the crystals of the studied compound was based on *p*-methylbenzamidiniumchloride, prepared by the procedure of Glock<sup>7</sup>. *p*-Methylbenzamidinium chloride (1 g) was dissolved in 100 ml of water and applied to a column containing 30 g of Amberlite IRA - 400 (100–200 mesh) converted to the formate cycle. Elution with water and evaporation of the eluate yielded 1.02 g (97% of the theoretical yield) of *p*-methylbenzamidinium formate, m.p. 240–241°C. For C<sub>9</sub>H<sub>12</sub>N<sub>2</sub>O<sub>2</sub> (180.2) calculated 59.99% C, 6.71% H, 15.54% N and found 59.79% C, 6.71% H, 15.22% N. The product was recrystallized from aqueous acetone (acetone: water = 9 : 1). It was later found from solution of the crystal structure that the recrystallization did not yield the anhydrous salt (*p*-methylbenzamidinium formate), but rather the monohydrate. Chemical analysis was carried out on the anhydrous salt.

The studied crystals of *p*-methylbenzamidinium formate monohydrate, C<sub>9</sub>H<sub>14</sub>N<sub>2</sub>O<sub>3</sub> (198.2), were not very stable in the air and dehydrated after several weeks, reflected in whitening of the originally transparent crystals. The density of the transparent crystals of *p*-methylbenzamidinium formate monohydrate was found by the flotation method in a mixture of tetrachloromethane-hexane at 23°C.

The preliminary dimensions of the unit cell and the space group symmetry were determined from Weissenberg patterns (extinction  $h0l : l = 2n + 1$ ,  $0k0 : k = 2n + 1$ ). A single crystal with dimensions of 0.30 × 0.25 × 0.10 mm was employed for refinement of the lattice parameters (15 centred high angle reflections) and measurement of the intensities on the Syntex P2<sub>1</sub> four-circle diffractometer. Graphite-monochromated MoK<sub>α</sub> radiation ( $\lambda = 71.069$  pm) was employed and the measurement was carried out at a temperature of 23°C. No significant fluctuations in three intensities of the standard reflections were found during the measurement. A total of 1 423 reflections were measured in the range  $2\theta \geq 60^\circ$ , of which 1 150 were considered observed ( $I > 1.96 \sigma(I)$ ). Correction for absorption was neglected.

The phase problem was solved by direct methods. The SHELXS 86 program<sup>8</sup> yielded a set of coordinates for all the nonhydrogen atoms that was later complemented by the maximum in the differential synthesis, interpreted as the so-far neglected oxygen atom in the water molecule. The coordinates of all the hydrogen atoms were found from the differential maps. The complete structure was successfully refined using the SHELX 76 program<sup>9</sup>. In the final refinement cycle, the maximal value was  $(\Delta/\sigma) = 0.037$ . The highest residual maximum on the final  $\Delta F$  map had value of  $0.17 \text{ e}/(100 \text{ pm})^3$  and the lowest,  $-0.26 \text{ e}/(100 \text{ pm})^3$ . The final values of the reliability factors are  $R = 0.043$ ,  $wR = 0.043$ , where  $w = [\sigma^2(F_o) + 0.0009F_o^2]^{-1}$ . The geometry of the refined structure was calculated using the PARST program<sup>10</sup> and the structure was drawn by Dr Malý (Institute of Physics, Czechoslovak Academy of Sciences, Prague) using his own program. The computations were carried out on an EC 1033 computer.

## RESULTS AND DISCUSSION

The basic crystallographic data for *p*-methylbenzamidine formate monohydrate are listed in Table I. The fractional coordinates of all the atoms and their temperature vibrational parameters are given in Table II. Table III lists the interatomic distances and angles.

As expected, the structure of the *p*-methylbenzamidine formate monohydrate molecule is very similar to that of benzamidine pyruvate<sup>5</sup> and benzamidine bromoacetate<sup>6</sup>. The amidinium-carboxylate interaction occurs through two intramolecular hydrogen bonds at the H1N1 and H1N2 atoms (Fig. 1). However, a considerable difference was found between the molecular arrangement in the studied substance and in the above related salts. Originally, it was expected that the structure of the studied compound would also consist of infinite molecular chains connected by intermolecular hydrogen bonds through the side H2N1 and H2N2 atoms of the amidinium group (see refs<sup>5,6</sup>). The presence of the molecule of crystal water in *p*-methylbenzamidine formate monohydrate is apparently the main reason for the formation of the three-dimensional network of hydrogen bonds in the crystal structure of this substance (Fig. 2), rather than infinite chains. In the hydrogen bond network, the N1 and N2 atoms apparently act as double proton donors, the O1 atom as a double proton acceptor, the O2 atom as a triple proton acceptor and the oxygen atom of the molecule of crystal water (OW) both as an acceptor and double donor of protons.

The optimal (least squares) plane can be fitted through the molecule of the studied compound through the benzene ring and the atoms of the amidine group (Table IV). The angle between these planes equals 26.1(1)° and the torsion angles C8—C3—C2—N1 and C4—C3—C2—N2 equal 25.9(3)° and 26.0(4)°, respectively. These values are very different from those found for benzamidine pyruvate<sup>5</sup> (planar angle: 35.2(3)°, torsion angles: 36.5(2)° and 35.1(2)°) and for benzamidine bromoacetate<sup>6</sup> (33.4(4)°, 33.5(1.0)° and 32.9(9)°).

TABLE I

Basic crystallographic data

$a = 1\,038.9\ (4)\ \text{pm}$	$\rho_c = 1.22\ \text{Mg m}^{-3}$
$b = 1\,146.1\ (5)\ \text{pm}$	$\rho_o = 1.24\ \text{Mg m}^{-3}$
$c = 914.4\ (3)\ \text{pm}$	space group: $P2_1/c$
$\beta = 94.77\ (3)^\circ$	$\mu(\text{MoK}\alpha) = 0.086\ \text{mm}^{-1}$
$V = 1\,082.6\ (7) \cdot 10^6\ \text{pm}^3$	$F(000) = 424$
$Z = 4$	

The group of atoms including the carboxyl: C1, O1, O2, H1N1 and H1N2 exhibits large deviations from the optimal plane ( $\chi^2 = 1\ 104\cdot5$ ), while planes defined by the same atoms were found for benzamidinium pyruvate ( $\chi^2 = 68\cdot4$ ) and benzamidinium bromoacetate ( $\chi^2 = 13\cdot8$ ). Thus, the angle between the C1, O1, O2, H1N1 and C2, N1, N2, H1N1, H1N2 (amidinium group) planes is not considered here, but

TABLE II

The coordinates of the nonhydrogen ( $\cdot 10^4$ ) and hydrogen ( $\cdot 10^3$ ) atoms and their equivalent and isotropic temperature parameters. In brackets are given the values of e.s.d.  $U_{eq} = (U_{11} + U_{22} + U_{33} + 2U_{13} \cos \beta)/3$

Atom	x	y	z	$U_{eq}, \text{pm}^2$
O1	6 469 (2)	-1 947 (1)	1 845 (2)	687 (6)
O2	6 025 (1)	-3 829 (1)	2 069 (2)	610 (5)
OW	2 885 (2)	-5 239 (1)	5 110 (2)	714 (6)
N1	4 329 (2)	-1 285 (1)	3 373 (2)	572 (6)
N2	3 985 (2)	-3 176 (1)	3 949 (2)	533 (6)
C1	6 540 (2)	-2 979 (2)	1 495 (2)	554 (8)
C2	3 694 (2)	-2 070 (2)	4 075 (2)	438 (6)
C3	2 663 (2)	-1 698 (2)	4 994 (2)	429 (6)
C4	1 653 (2)	-2 436 (2)	5 269 (2)	582 (8)
C5	689 (2)	-2 055 (2)	6 118 (3)	655 (9)
C6	700 (2)	-943 (2)	6 714 (2)	547 (8)
C7	1 718 (2)	-221 (2)	6 448 (2)	554 (8)
C8	2 687 (2)	-589 (2)	5 601 (2)	507 (7)
C9	9 652 (3)	-538 (3)	7 645 (4)	797 (12)
				$U_{iso} \cdot 10^{-1}, \text{pm}^2$
H1W	311 (2)	-584 (2)	441 (3)	102 (8)
H2W	313 (3)	-549 (2)	594 (3)	106 (9)
H1N1	503 (2)	-150 (2)	279 (3)	82 (7)
H2N1	413 (2)	-53 (2)	340 (2)	78 (7)
H1N2	461 (2)	-339 (2)	335 (2)	64 (6)
H2N2	363 (2)	-372 (2)	444 (2)	63 (6)
HCl	709 (2)	-315 (2)	63 (2)	74 (7)
HC4	162 (2)	-317 (2)	484 (2)	68 (6)
HC5	-4 (3)	-260 (2)	629 (3)	86 (8)
HC7	174 (2)	54 (2)	689 (2)	67 (6)
HC8	339 (2)	-8 (2)	545 (2)	56 (6)
H1C9	-78 (4)	-123 (4)	802 (4)	145 (15)
H2C9	-90 (4)	-5 (3)	721 (4)	124 (14)
H3C9	2 (3)	-9 (3)	855 (4)	130 (12)

only that between the C1, O1, O2 plane and the plane of the amidinium group (see Table IV). This angle has a value of  $16.2(2)^\circ$  and is much larger than that found for

TABLE III

Interatomic distances (in pm) and angles (in  $^\circ$ ). In brackets are given the values of e.s.d. Symmetry code: *i*)  $1 - x, y - 1/2, 1/2 - z$ ; *ii*)  $1 - x, -y - 1, 1 - z$ ; *iii*)  $1 - x, y + 1/2, 1/2 - z$

C9—H1C9	98 (4)	H1C9—C9—H2C9	112 (3)
C9—H2C9	87 (4)	H1C9—C9—H3C9	106 (3)
C9—H3C9	102 (3)	H2C9—C9—H3C9	103 (3)
C9—C6	150.9 (4)	C9—C6—C7	120.9 (2)
C6—C7	138.0 (3)	C9—C6—C5	121.4 (2)
C7—HC7	96 (2)	C6—C7—C8	121.3 (2)
C7—C8	138.5 (3)	C7—C8—C3	120.8 (2)
C8—HC8	95 (2)	C8—C3—C4	118.4 (2)
C8—C3	138.6 (3)	C3—C4—C5	120.1 (2)
C3—C4	138.7 (3)	C4—C5—C6	121.8 (2)
C4—HC4	93 (2)	C5—C6—C7	117.6 (2)
C4—C5	138.7 (3)	C8—C3—C2	120.1 (2)
C5—HC5	100 (3)	C4—C3—C2	121.5 (2)
C5—C6	138.5 (3)	C3—C2—N1	119.8 (2)
C3—C2	147.7 (3)	H1N1—N1—H2N1	116 (2)
C2—N1	131.4 (3)	C3—C2—N2	120.8 (2)
N1—H1N1	97 (2)	H1N2—N2—H2N2	119 (2)
N1—H2N1	89 (2)	N1—C2—N2	119.4 (2)
C2—N2	131.0 (3)	O1—C1—O2	127.3 (2)
N2—H1N2	91 (2)		
N2—H2N2	87 (2)		
C1—O1	122.9 (3)		
C1—O2	124.8 (3)		
C1—HC1	103 (2)		

## Intramolecular hydrogen bonds

N1...O1	282.4 (3)	N1—H1N1...O1	174 (2)
N2...O2	293.2 (3)	N2—H1N2...O2	179 (2)
N2...OW	286.7 (2)	N2—H2N2...OW	164 (2)

## Intermolecular hydrogen bonds

OW...O1 <sup><i>i</i></sup> } O1...OW <sup><i>iii</i></sup> }	276.8 (2)	OW—H1W...O1 <sup><i>i</i></sup> } O1—H1W <sup><i>iii</i></sup> ...OW <sup><i>iii</i></sup> }	179 (2)
O2...N1 <sup><i>i</i></sup> } N1...O2 <sup><i>iii</i></sup> }	286.3 (2)	O2—H2N1 <sup><i>i</i></sup> ...N1 <sup><i>i</i></sup> } N1—H2N1...O2 <sup><i>iii</i></sup> }	163 (2)
OW...O2 <sup><i>ii</i></sup>	292.6 (3)	OW—H2W...O2 <sup><i>ii</i></sup>	172 (3)

the corresponding plane in benzamidinium pyruvate molecule ( $5\cdot6(3)^\circ$ ) and in benzamidinium bromoacetate ( $3\cdot7(6)^\circ$ ).

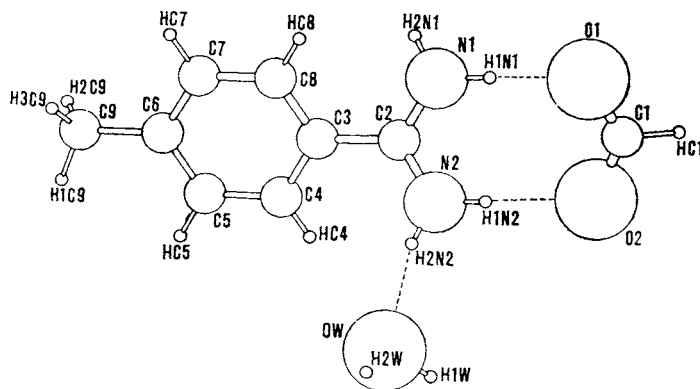


FIG. 1

The molecule of *p*-methylbenzamidinium formate monohydrate with numbered atoms

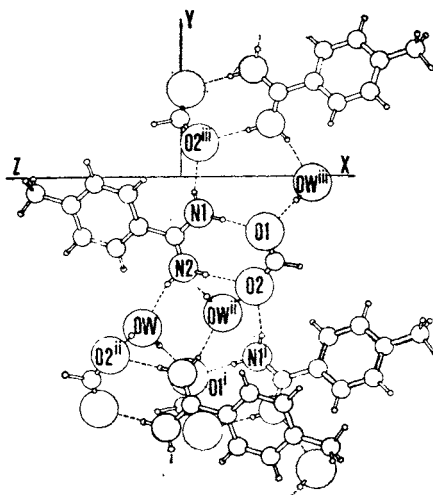


FIG. 2

The intramolecular and intermolecular hydrogen bonds (designated by dashed lines) in the crystal structure of *p*-methylbenzamidinium formate monohydrate. View perpendicular to the *Y*-axis

TABLE IV

The optimal least squares planes fitted through the atoms in the molecule. Each plane is defined as  $AX + BY + CZ + D = 0$ . The e.s.d. values are given in brackets. The planes are fitted only through the atoms designated by an asterisk

Benzene ring plane <sup>a</sup>		Amidine group plane <sup>b</sup>		Carboxyl group plane <sup>c</sup>	
atom	deviation from the plane, pm	atom	deviation from the plane, pm	atom	deviation from the plane, pm
C3*	0.5 (2)	C2*	0.01 (21)	C1*	0
C4*	-0.3 (2)	N1*	0.02 (21)	O1*	0
C5*	-0.3 (3)	N2*	0.03 (21)	O2*	0
C6*	0.5 (2)	H1N1*	-3 (2)	H1N1	-61 (2)
C7*	-0.3 (2)	H1N2*	3 (2)	H1N2	-50 (2)
C8*	-0.2 (2)				

<sup>a</sup>  $-0.4551(8)X + 0.3432(9)Y - 0.8217(5)Z + 5.491(2) = 0$ ;  $\chi^2 = 18.44$ ; <sup>b</sup>  $-0.608(3)X - 0.078(2)Y - 0.790(2)Z + 4.888(8) = 0$ ;  $\chi^2 = 3.08$ ; <sup>c</sup>  $0.760(3)X - 0.108(2)Y + 0.641(3)Z - 6.31(1) = 0$ .

The authors wish to thank Dr S. Smrčková from the Department of Organic Chemistry of the Prague Institute of Chemical Technology for preparing the crystals of the studied compound.

## REFERENCES

- Adams M. J., Buehner M., Chandrasekhar K., Ford G. C., Hackert M. L., Liljas A., Rossman M. G., Smiley I. E., Allison W. S., Everse J., Kaplan N. O., Taylor S. S.: *Proc. Natl. Acad. Sci. U.S.A.* **70**, 1968 (1973).
- Smrčková S.: *Chem. Listy* **82**, 337 (1988).
- Norrestam R.: *Acta Crystallogr.*, **C 40**, 297 (1984).
- Kjoeller Larsen I.: *Acta Crystallogr.*, **C 41**, 749 (1985).
- Kratochvíl B., Ondráček J., Krechl J., Hašek J.: *Acta Crystallogr.*, **C 43**, 2184 (1987).
- Kratochvíl B., Ondráček J., Malý K., Csordás L.: *Collect. Czech. Chem. Commun.* **53**, 294 (1988).
- Glock G.: *Ber. Dtsch. Chem. Ges.* **21**, 2653 (1888).
- Sheldrick G. M.: *SHELXS 86. A Fortran-77 Program for the Solution of Crystal Structures from Diffraction Data*. University of Cambridge, England 1986.
- Sheldrick G. M.: *SHELX 76. A Program for Crystal Structure Determination*. University of Cambridge, England 1976.
- Nardelli M.: *PARST. A System of Computer Routines for Calculating Molecular Parameters from Results of Crystal Structure Analysis*. University of Parma, Italy 1984.

Translated by M. Štulíková.