Le cycle benzénique est plan et régulier, la distance moyenne de liaison est de 1,39 Å et les angles de liaison ont une valeur moyenne de 120°. Ce noyau est per-perpendiculaire au cycle C(1)–C(2)–C(3)–C(4)–C(5), l'angle formé entre les deux plans moyens est de 89°. Cette orientation résulte d'un empêchement stérique dû à la présence du méthyle et du pont oxotriméthylène.

Enfin la Fig. 3 montre les distances intermoléculaires les plus courtes. La cohésion cristalline est donc assurée uniquement par des liaisons de type van der Waals.

Configuration relative de la molécule

La configuration relative de la forme racémique de point de fusion $F = 228\,°C$ du composé étudié est représentée sur la Fig. 2.

Cette configuration est précisément celle qui a été proposée par Moïse & Tirouflet (1970) à partir des résultats de spectroscopie de résonance magnétique nucléaire (Tableau 8).

Le noyau phényle se trouve situé du côté du radical méthyle et son orientation sensiblement perpendiculaire au plan cyclopentadiénique C(1)–C(2)–C(3)–C(4)–C(5) (89°) est favorable au blindage des protons du groupe CH₃ et explique donc la valeur du déplacement chimique du radical méthyle (Tableau 8).

Dans la nomenclature (R.S.) de Cahn, Ingold & Prelog (1966) adaptée en série métallocénique par

Schlögl (1966) et systématisée par Gautheron & Broussier (1971) la configuration relative de la cétone racémique correspond aux deux possibilités énantiomères $R_p S_c$ ou $S_p R_c$.

Cette étude apporte donc un élément sûr, indispensable pour établir la stéréochimie dynamique de la réaction: celle-ci se fait avec rétention de la configuration. Elle permet par ailleurs de vérifier l'ensemble des configurations des composés I, II, III, IV etc. et apporte d'autres données strictement conformationnelles qui viennent étayer les hypothèses formulées dans l'interprétation des spectres de résonance magnétique nucléaire.

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The Crystal Structure of a Homolog of Acetylcholine: 3-Acetoxypropyltrimethyl-ammonium Bromide

By B. M. CRAVEN AND G. HITE

Crystallography Department, University of Pittsburgh, Pittsburgh, Pa 15260, U.S.A.

The crystal structure of 3-acetoxypropyltrimethylammonium bromide, $[CH_3COOCH_2CH_2CH_2N(CH_3)_3]^+Br^-$, is orthorhombic with space group $P2_12_12_1$ and $a = 10·62$, $b = 15·06$, $c = 7·050$ Å. There are four formula units per cell. The molecular ion is nearly in the extended conformation except for the acetoxy group. There is a synclinal conformation about the C(2)–C(3) bond so that the C(1) and O(ether) atoms are separated by only 2·78 Å.

Introduction

The preferred conformation of the choline moiety $(CH_3)_3N^+$–CH_2–CH_2–O– is known to be synclinal with respect to the C–C bond. The consistently short intramolecular $N\cdots O$ and $NCH_3\cdots O$ distances (3·2 and 3·0 Å) which have been observed in crystal structures containing glycerylphosphorylcholine (Abrahamsson & Pascher, 1965; Sundaralingam & Jensen, 1965, acetylcholine (Herdklotz & Sass, 1970; Canepa, Pauling & Sørum, 1966), most cholinergic ligands (Shefter,

1971) and choline itself (Hjortås & Sørum, 1971) are evidence of an attractive interaction.

It has been suggested that this is primarily Coulombic in nature, involving the positively charged quaternary ammonium group and the electron distribution about the oxygen atom (Sundaralingam, 1968). There have been extensive molecular orbital calculations on the energy and electronic structure of acetylcholine over a range of different conformations (Kier, 1967; Liquori, Damiani & deCoen, 1968). More recent studies (Beveridge & Radna, 1971; Ajo, Bossa, Damiani,

Fidenzi, Gigli, Lanzi & Lapiccerella, 1972; Pullman, Courriere & Coubeils, 1971) satisfactorily account for the acetylcholine conformations which have been observed both in the crystalline state and in aqueous solution (Partington, Feeny & Burgen, 1972; Culvenor & Ham, 1970). These calculations show that the positive charge is delocalized in a uniform way over the choline CH_2 and CH_3 groups. The nitrogen atom is slightly deficient in charge (0·1 e) and both the ester oxygen atoms carry a significant excess (0·3 e).

We report the crystal structure determination of 3-acetoxypropyltrimethylammonium bromide, $(CH_3COOCH_2CH_2CH_2N(CH_3)_3)^+Br^-$, a homolog of acetylcholine in which there is an additional methylene group between the quaternary ammonium and ester group. Hereafter, we refer to the ion as acetylhomocholine. Our aim was to seek a possible relationship between the observed conformation and the increased intramolecular separation of the polar groups.
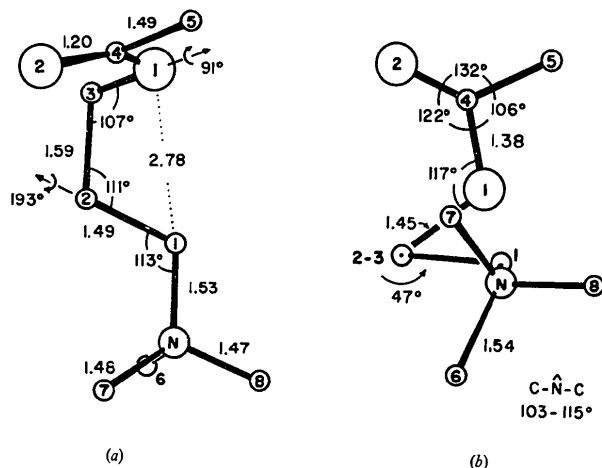

Fig. 1. Structure of the acetylhomocholine ion. Distances are given in Å units. (a) The view projected on the plane of atoms C(1), C(2) and C(3). (b) The view down the bond C(2) → C(3).

Experimental

Acetylhomocholine bromide was synthesized by acetylation of 3-dimethylaminopropanol (Eastman Kodak Co., New York) followed by quaternization using methyl bromide. The second step was carried out in ethereal solution, so that the required salt was obtained as a precipitate. The salt was recrystallized from dry acetone, with care to exclude atmospheric moisture. Crystals of acetylhomocholine bromide were obtained as strongly hygroscopic, transparent, orthorhombic prisms elongated on c. The X-ray data thus had to be collected with the crystal mounted in a sealed Lindemann glass capillary. The lattice parameters are $a = 10·62(2)$, $b = 15·06(3)$, $c = 7·050(8)$ Å. The space group is $P2_12_12_1$ and there are four formula units $(C_8H_{18}NO_2Br)$ per cell. Although a number of crystals were mounted, X-ray photographs revealed that they were invariably of poor quality, exhibiting slight splitting of the diffracted beams. Examination of the crystals under polarized light gave no indication of the reason for these diffraction effects. The X-ray intensity data were measured from a crystal of dimensions approximately $0·2 \times 0·3 \times 0·6$ mm using a four-circle computer-controlled diffractometer and graphite monochromated Mo $K\alpha$ radiation. Each reflection was scanned in the $\theta/2\theta$ mode over an angular range (2° in 2θ) sufficient to record the intensity of both components of the split beam. The data were of poorer than usual quality and were restricted to 486 observed and 278 unobservably weak reflections which were all within $\sin\theta/\lambda \le 0·57$ Å^{-1}. A reflection was considered to be unobservably weak if the integrated intensity, I, was less than $2\sigma(I)$. Such reflections were assigned values of $I = \sigma(I)/2$. The available data proved to be adequate for the crystal structure determination. The phase problem was solved by the heavy atom method.

Refinement of the structure parameters was by a block-diagonal least-squares procedure. Hydrogen atoms were located in a difference electron density map and were arbitrarily assigned temperature factors of

Table 1. Atomic parameters

(a) Non-hydrogen atoms

Positional parameters are given as fractional coordinates. Thermal parameters are given in according to the expression $T = \exp(-\sum_i \sum_j \beta_{ij}h_ih_j)$. The e.s.d.'s given in parentheses refer to the least significant figures in the parameter values. The parameters are $\times 10^4$ for the Br atom, and $\times 10^3$ for the remaining non-hydrogen atoms.

	x	y	z	β_{11}	β_{22}	β_{33}	β_{12}	β_{13}	β_{23}
Br	1383 (3)	1592 (2)	2347 (4)	120 (3)	41 (1)	284 (8)	10 (2)	−1 (6)	−8 (3)
O(1)	569 (2)	2 (1)	291 (3)	13 (2)	8 (1)	21 (6)	−1 (1)	6 (4)	−4 (2)
O(2)	745 (3)	−51 (2)	431 (4)	19 (4)	12 (2)	48 (10)	2 (3)	3 (6)	−10 (4)
N	352 (2)	121 (1)	739 (4)	11 (2)	3 (1)	33 (7)	−1 (1)	−10 (6)	4 (3)
C(1)	418 (3)	85 (2)	560 (5)	8 (3)	3 (1)	32 (10)	−2 (1)	7 (5)	−6 (3)
C(2)	552 (3)	113 (2)	545 (6)	12 (4)	6 (2)	36 (13)	−1 (2)	5 (7)	−3 (4)
C(3)	605 (3)	93 (2)	339 (6)	12 (4)	8 (2)	48 (14)	−6 (2)	−4 (6)	−10 (4)
C(4)	653 (3)	−64 (2)	336 (6)	7 (3)	9 (2)	51 (15)	−4 (2)	8 (6)	−2 (5)
C(5)	600 (3)	−148 (2)	255 (6)	14 (4)	6 (2)	34 (9)	1 (2)	3 (7)	4 (5)
C(6)	334 (3)	222 (2)	744 (5)	16 (4)	5 (1)	24 (8)	−1 (2)	10 (7)	−0 (4)
C(7)	427 (4)	103 (2)	911 (5)	25 (5)	5 (2)	20 (9)	6 (3)	−13 (6)	1 (3)
C(8)	230 (2)	76 (1)	755 (5)	9 (2)	2 (1)	24 (8)	−1 (1)	0 (5)	1 (3)

Table 1 (*cont.*)

(*b*) Hydrogen atoms

	x	*y*	*z*
H(11)	0·380	0·030	0·50
H(12)	0·395	0·145	0·42
H(21)	0·620	0·090	0·64
H(22)	0·560	0·180	0·50
H(31)	0·700	0·090	0·33
H(32)	0·555	0·145	0·23
H(51)	0·650	−0·200	0·22
H(52)	0·525	−0·150	0·30
H(53)	0·585	−0·145	0·11
H(61)	0·240	0·240	0·65
H(62)	0·400	0·275	0·75
H(63)	0·255	0·245	0·85
H(71)	0·438	0·035	0·93
H(72)	0·500	0·125	0·85
H(73)	0·360	0·140	1·00
H(81)	0·235	0·015	0·76
H(82)	0·160	0·090	0·87
H(83)	0·180	0·100	0·63

4·5 Å^2. Subsequently, hydrogen atom parameters were not refined. The reflections were weighted in the least-squares refinement as the inverses of the variances $\sigma^2(F)=18\cdot1-1\cdot1(F)+0\cdot024|F|^2$. Atomic scattering factors were taken from *International Tables for X-ray Crystallography* (1962), including $\Delta f'=-0\cdot3$ and $\Delta f''=2\cdot5$ for the bromide ion. The data were not sufficiently accurate to allow descrimination between the structure and its inverse, although an attempt was made to refine them both, by including the anomalous scattering effect of the bromide ion. Both refinements converged with a final *R* index of 0·14 for all reflections, or 0·10 excluding those which were unobservably weak. The *R* index was found to increase continuously as a function of sin θ/λ, presumably because of deterioration in the quality of the intensity data with increasing separation of the split diffracted beams. Thus for the 150 reflections in the sin θ/λ range 0·11 to 0·30 Å^{-1}, the *R* index was 0·08 and for the 140 reflections in the range 0·49 to 0·56 Å^{-1} the *R* index was 0·28. Final atomic parameters are listed in Table 1, and the observed and calculated structure amplitudes are in Table 2.

Discussion

The bond lengths and angles and the observed conformation of the acetylhomocholine ion are shown in Fig. 1. The bond lengths and angles are similar to those in related crystal structures. They will not be discussed further because the interatomic distances and angles have large e.s.d.'s (0·04 Å in a bond length and 2° in a bond angle.)

The interesting aspects of the molecular framework are the twists of the planar acetoxy group and the tetrahedral trimethylammonium group with respect to the central trimethylene chain. The molecular ion is folded so that the N··O distance (4·3 Å) is approximately

Table 2. *Observed and calculated structure amplitudes*

Values listed in successive columns are *h*, $|F_{\text{obs}}|$, $|F_{\text{calc}}|$.

Reflections marked (*) were unobservably weak.

0, 0		
2	24	24
4	120	124
6	5*	3
8	30	31
10	25	25
1, 0		
1	33	35
2	44	46
3	11	9
4	15	17
5	53	55
6	34	32
7	5*	5
8	18	17
9	17	15
10	13	17
2, 0		
0	28	25
1	10	9
2	10	8
3	91	91
4	42	41
5	4*	5
6	44	37
7	48	47
8	11	12
9	6*	7
10	7*	4
3, 0		
1	131	121
2	4*	1
3	51	45
4	10	12
5	73	75
6	5*	3
7	5*	6
8	6*	2
9	32	33
10	7*	8
4, 0		
0	138	134
1	90	85
2	11	15
3	41	43
4	75	74
5	40	47
6	15	16
7	28	27
8	26	22
9	11	2
10	7*	8
5, 0		
1	12	7
2	93	90
3	8	6
4	27	23
5	35	31
6	38	41
7	6*	5
8	26	26
9	14	11
10	7*	9
6, 0		
0	51	47
1	4*	6
2	9	12
3	15	14
4	64	62
5	6*	7
6	28	26
7	6*	9
8	25	21
9	6*	4
10	16	13
7, 0		
1	35	38
2	63	56
4	22	19
5	72	61
6	32	29
7	6*	6
8	17	17
9	29	26
8, 0		
0	5*	6
1	80	77
2	27	28
4	5*	3
5	42	36
6	6*	6
7	33	32
8	6*	7
9	7*	2
9, 0		
1	29	31
2	19	18
3	30	32
4	6*	4
5	29	24
6	16	12
7	6*	5
8	7*	6
9	17	13
10, 0		
0	33	38
1	32	30
2	17	19
3	36	37
4	31	31
5	7*	6
6	14	17
7	21	19
8	23	22
9	7*	6
11, 0		
1	6*	2
2	48	51
3	6*	5
4	24	22
5	7*	6
6	31	30
7	7*	2
8	15	14
9	7*	1
12, 0		
0	45	46
1	26	29
2	6*	7
3	16	17
4	24	28
5	15	16
6	7*	3
7	7*	8
8	17	9
9	8*	5
13, 0		
1	26	30
2	18	21
3	7*	10
4	7*	13
5	13	16
6	7*	9
7	7*	6
14, 0		
0	13	11
1	19	20
2	7*	4
3	8*	26
4	7*	4
5	7*	3
6	7*	2
7	18	19
0, 1		
1	46	54
2	22	21
3	80	87
4	14	13
5	15	16
6	10	13
7	61	62
8	5*	3
9	11	6
10	6*	1
1, 1		
0	3*	1
1	62	55
2	119	138
3	47	52
4	9	10
5	49	54
6	41	39
7	13	10
8	17	17
9	21	24
10	12	4
2, 1		
0	16	16
1	66	63
2	22	18
3	64	65
4	59	64
5	4*	6
6	25	22
7	17	19
8	25	25
9	6*	4
10	7*	8
3, 1		
0	4*	0
1	9	7
2	123	126
3	4*	2
4	44	45
5	16	17
6	60	59
7	5*	4
8	28	24
9	6*	5
10	7*	16
4, 1		
0	106	106
1	67	63
2	31	31
3	39	39
4	39	43
5	24	21
6	20	18
7	27	29
8	24	21
9	6*	5
10	7*	17
5, 1		
0	8	9
1	88	84
2	27	23
3	48	48
4	18	16
5	44	44
6	5*	6
7	16	15
8	6*	6
9	21	20
10	7*	3
6, 1		
0	31	25
1	37	38
2	23	23
4	13	12
5	7*	9
6	6*	5
7	49	44
8	12	10
9	6*	6
7, 1		
0	28	24
1	71	71
2	70	65
4	5*	4
5	54	40
6	29	26
7	6*	6
8	6*	6
9	18	16
8, 1		
0	85	85
1	5*	5
2	17	18
4	53	53
5	18	11
6	25	24
7	6*	5
8	19	17
9	7*	3
9, 1		
0	5*	10
1	29	28
2	40	42
3	18	18
4	17	17
5	8*	8
6	30	30
7	7*	16
8	19	15
9	7*	6
10, 1		
0	38	37
1	29	29
2	6*	9
3	31	33
4	34	31
5	15	14
6	22	21
7	17	20
8	7*	9
9	7*	4
11, 1		
0	6*	7
1	44	44
2	6*	5
3	30	33
4	6*	8
5	43	42
6	7*	4
7	7*	4
8	7*	2
9	16	16
12, 1		
0	14	16
1	16	15
2	6*	6
3	22	22
4	14	19
5	14	12
6	7*	5
7	22	17
8	7*	8
9	7*	2
13, 1		
0	6*	2
1	16	13
2	29	36
3	7*	4
4	7*	3
5	7*	14
6	20	20
7	7*	5
8	8*	8
14, 1		
0	33	34
1	7*	2
2	7*	5
3	7*	1
4	25	28
5	7*	6
6	18	14
7	8*	3
0, 2		
0	179	169
1	46	50
2	27	33
3	7	6
4	84	94
5	16	14
6	32	35
7	11	9
8	31	30
9	6*	4
10	12	18
1, 2		
0	37	38
1	60	54
2	43	54
3	22	30
4	14	16
5	30	31
6	34	36
7	5*	6
8	6*	9
9	19	23
10	7*	12
2, 2		
0	57	49
1	91	89
2	26	28
3	42	55
5	31	32
6	19	17
7	26	24
8	11	16
9	6*	5
10	7*	5
3, 2		
0	42	41
1	84	77
2	26	28
3	56	55
5	61	59
6	5*	3
7	6*	3
8	11	11
9	21	26
10	7*	5
4, 2		
0	49	49
1	37	36
2	30	27
3	43	44
4	49	49
5	21	26
6	25	23
7	32	32
8	32	27
9	6*	3
10	7*	8
5, 2		
0	5*	5
1	16	19
2	63	63
4	29	26
5	27	26
6	42	41
7	11	6
8	24	21
9	6*	5
10	7*	10
6, 2		
0	73	87
1	23	21
2	5*	11
4	61	57
5	7*	10
6	11	10
7	6*	3
8	14	15
9	7*	5
7, 2		
0	5*	11
1	23	24
2	48	47
4	20	21
5	56	45
6	22	21
7	6*	7
8	19	22
9	13	17
8, 2		
0	5*	6
1	42	42
2	17	17
4	6*	4
5	20	16
6	15	12
7	38	36
8	7*	2
9	7*	3
9, 2		
0	6*	9
1	36	38
2	15	15
3	23	21
4	12	8
5	28	22
6	13	13
7	7*	11
8	7*	8
9	7*	13
10, 2		
0	42	43
1	27	26
2	6*	4
3	35	34
4	37	35
5	8*	4
6	7*	10
7	13	14
8	7*	14
9	16	6
11, 2		
0	6*	0
1	6*	6
2	47	46
3	7*	12
4	16	17
5	7*	3
6	21	21
7	7*	7
8	14	13
9	7*	3
12, 2		
0	34	34
1	19	16
2	6*	8
3	18	20
4	16	17
5	8*	10
6	7*	8
7	18	11
8	7*	9
13, 2		
0	7*	5
1	25	24
2	25	22
3	7*	6
4	7*	7
5	14	18
6	7*	9
7	8*	6
8	8*	5
14, 2		
0	7*	14
1	19	22
2	7*	4
3	25	25
4	7*	3
5	7*	9
6	8*	6
7	8*	13
0, 3		
1	16	19
2	4*	2
5	5*	4
6	5*	6
7	49	55
8	6*	8
9	6*	2
10	7*	6
1, 3		
0	22	23
1	45	38
2	40	52
5	34	34
6	26	27
7	6*	13
8	17	17
9	7*	13
10	7*	8
2, 3		
0	78	75
1	48	46
2	30	31
5	12	12
6	6*	10
7	6*	10
8	6*	12
9	6*	4
10	7*	10
3, 3		
0	5*	5
1	5*	5
2	91	82
5	11	12
6	42	42
7	13	13
8	20	19
9	6*	6
10	14	12
4, 3		
0	23	28
1	23	23
2	23	23
4	33	31
5	19	19
6	21	20
7	29	25
8	18	20
9	14	7
10	7*	9
5, 3		
0	16	20
1	52	64
2	31	29
4	5*	5
5	37	32
6	6*	5
7	11	11
8	6*	4
9	16	19
9	7*	6
10	7*	3
6, 3		
0	10	15
1	30	36
2	24	22
4	14	14
5	16	15
6	13	13
7	23	23
8	6*	6
9	7*	3
7, 3		
0	14	17
1	26	30
2	63	59
4	15	18
5	47	35
6	24	20
7	6*	3
8	7*	8
9	7*	14
8, 3		
0	41	50
1	6*	10
2	21	21
4	35	31
5	16	11
6	22	20
7	7*	4
8	19	18
9	7*	6
9, 3		
0	6*	6
1	17	14
2	33	29
3	6*	8
4	6*	7
5	14	10
6	24	22
7	7*	10
8	7*	8
9	7*	9
10, 3		
0	22	26
1	30	31
2	16	13
3	25	24
4	26	26
5	16	13
6	18	16
7	14	13
8	7*	4
9	8*	3
11, 3		
0	7*	12
1	30	31
2	7*	11
3	25	26
4	13	12
5	30	29
6	7*	5
7	7*	3
8	7*	6
12, 3		
0	7*	7
1	7*	10
2	7*	3
3	16	15
4	15	13
5	7*	5
6	7*	7
7	8*	15
8	8*	7
13, 3		
0	7*	6
1	15	15
2	24	21
3	7*	7
4	7*	5
5	8*	9
6	15	14
7	13	3
0, 4		
0	89	84
1	26	25
2	15	13
5	18	16
6	11	16
7	6*	0
8	15	18
9	7*	7
10	7*	11
1, 4		
0	5*	2
1	44	37
2	42	36
5	24	29
6	16	17
7	6*	10
8	13	12
9	7*	11
10	7*	8
2, 4		
0	24	28
1	36	34
2	16	13
5	19	17
6	18	17
7	13	15
8	6*	8
9	7*	7
10	7*	4
3, 4		
0	24	27
1	37	40
2	5*	10
5	41	38
6	11	6
7	6*	5
8	6*	4
9	12	15
10	7*	4
4, 4		
0	28	36
1	22	26
2	22	19
4	27	27
5	17	14
6	15	11
7	19	21
8	7*	17
9	7*	8
10	7*	7
5, 4		
0	6*	7
1	10	12
2	42	38
4	12	11
5	7*	9
6	23	24
7	7*	11
8	13	12
9	12	5
10	7*	8
6, 4		
0	39	51
1	13	19
2	6*	7
4	43	40
5	8*	7
6	13	10
7	7*	5
8	7*	9
9	7*	2
7, 4		
0	6*	8
1	14	16
2	35	32
4	18	17
5	30	22
6	19	17
7	17	8
8	7*	10
9	7*	10
8, 4		
0	6*	4
1	20	25
2	22	21
4	6*	9
5	19	14
6	7*	8
7	24	23
8	7*	4
9	7*	4
9, 4		
0	14	18
1	18	22
2	18	11
3	18	13
4	6*	7
5	21	14
6	7*	10
7	7*	8
8	7*	3
9	8*	11
10, 4		
0	22	27
1	16	17
2	16	14
3	19	21
4	22	22
5	8*	10
6	7*	5
7	7*	8
8	8*	9
11, 4		
0	7*	6
1	7*	7
2	31	29
3	7*	9
4	14	13
5	8*	4
6	20	15
7	8*	5
0, 5		
1	35	35
2	12	15
5	15	14
6	6*	10
7	16	22
1, 5		
0	12	13
1	33	26
2	26	25
5	14	16
6	14	15
7	6*	6
2, 5		
0	14	13
1	14	16
2	17	13
5	6*	11
6	17	16
7	7*	7
3, 5		
0	6*	2
1	6*	10
2	46	41
5	6*	4
6	22	23
7	7*	10
4, 5		
0	28	33
1	24	23
2	20	18
4	15	14
5	18	15
6	7*	4
7	7*	10
5, 5		
0	13	17
1	25	28
2	6*	11
4	6*	11
5	26	19
6	7*	6
7	7*	4
6, 5		
0	6*	5
1	6*	9
2	13	9
4	7*	9
5	8*	5
6	7*	11
7	17	14
7, 5		
0	14	16
1	15	22
2	30	24
4	13	13
5	20	17
6	7*	12
7	7*	3
8, 5		
0	30	37
1	7*	13
2	7*	6
4	25	23
5	9*	7
6	7*	5
9, 5		
0	7*	2
1	7*	10
2	19	15
4	7*	5
5	9*	4
6	16	10
10, 5		
0	7*	11
1	7*	9
2	7*	7
3	16	13
4	15	12
0, 6		
0	45	40
1	17	16
2	6*	6
1, 6		
0	7*	6
1	21	16
2	7*	11
2, 6		
0	7*	9
1	13	11
2	15	12
3, 6		
0	22	22
1	19	20
2	6*	2
4, 6		
0	18	19
1	7*	15
2	16	13
5, 6		
0	7*	3
1	7*	7
2	23	18
6, 6		
0	16	15
1	12	11
2	7*	3
7, 6		
0	7*	4
1	7*	12

1·0 Å shorter than would be the case in the fully extended conformation. Although the N···O distance could be decreased by twists about both C–C bonds in the central trimethylene chain, in fact only the twist (133° from *trans* or *antiperiplanar*) about the C(2)–C(3) bond is in this sense. The smaller twist (13° from *antiperiplanar*) about the C(1)–C(2) bond leads to a slight increase in N···O distance. The latter twist is probably associated with the strong interactions between quaternary ammonium groups and bromide ions (Fig. 2) Because of the sense of the twist about the C(1)–C(2) bond and because the observed intramolecular N···O and shortest NCH₃···O distances are about 1·1 Å and 2·0 Å longer than corresponding distances in the *synclinal* choline moiety, we conclude that O···N(CH₃)₃ interactions have a much reduced role in causing the folded conformation of the homocholine moiety.

However, the twist about the bond C(2)–C(3), which is only 47° from *synplanar*, brings atoms C(1) and O(1) close together (2·78 Å). Their separation is closer than the shortest NCH₃···O distances which have been reported for the choline moiety [2·87 Å in muscarine iodide (Jellinek, 1957); 2·88 Å in succinylcholine diiodide (Jensen, 1970)]. Although these distances suggest the possibility of CH···O hydrogen bonding, this is

not the case. In these crystal structures, including acetylhomocholine bromide, the C–H bonds are not directed towards the oxygen atom.

The other feature of conformational interest is the twist of 91° about the O(1)–C(3) bond. The twist about the corresponding bond in acetylcholine is 79° in the crystal structure of the bromide (Canepa, Pauling & Sørum, 1966) and 167° in the chloride (Herdklotz & Sass, 1970). It appears that the conformation about this bond depends upon crystal packing forces.

By analogy with the calculated electronic structure for acetylcholine, positive charge in acetylhomocholine is expected to extend over the trimethylammonium and trimethylene groups. Both steric and electronic factors would tend to keep this part of the molecule in the extended conformation. This is observed to be very nearly the case. The *synclinal* conformation about the C(2)–C(3) bond is compatible with an attractive interaction between a negatively charged O(1) atom and the positively charged cationic region, particularly the C(1) atom.
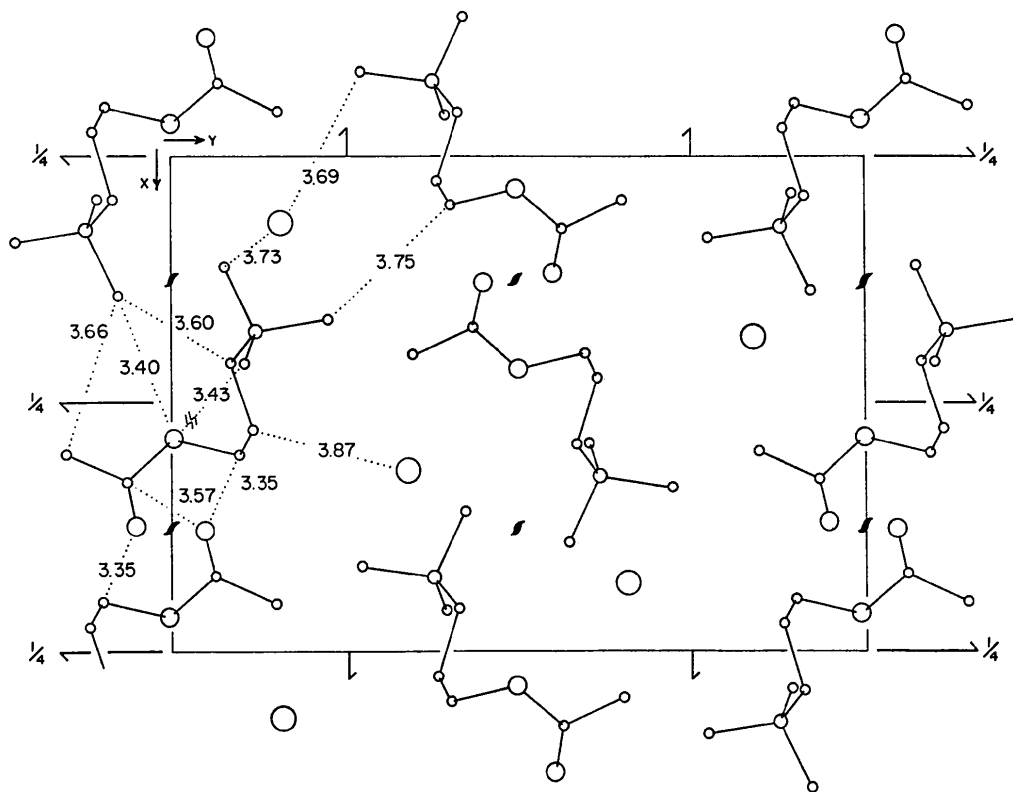
Fig. 2. The crystal structure of acetylhomocholine bromide. Circles of decreasing radius represent Br⁻, oxygen, nitrogen and carbon atoms. The shortest intermolecular distances are given in Å units.

1130 computer which were used were written by Drs R. Shiono and G. L. Gartland.

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The Metal Complexes of Peptides and Related Compounds. VII. The Crystal Structure of Bis-(6-aminohexanoato)copper(II) Dihydrate

BY BO SJÖBERG AND RAGNAR ÖSTERBERG

Department of Medical Biochemistry, University of Göteborg, Fack, S-400 33 Göteborg 33, Sweden

RUNE SÖDERQUIST

Research Institute of National Defence (FOA), Sweden

The crystal structure of bis-(6-aminohexanoato)copper(II) dihydrate has been determined from 993 independent, visually estimated reflexions, which were recorded using equi-inclination Weissenberg photographs and Cu $K\alpha$ radiation. The monoclinic, $P2_1/n$ unit cell has the dimensions $a = 8\cdot550$ (2), $b = 20\cdot068$ (3), $c = 5\cdot145$ (1) Å, and $\beta = 106\cdot85$ (2)°; it contains four asymmetric units. The structure was solved by using standard Fourier techniques, and refined by the method of least squares ($R = 0\cdot066$). Four aminohexanoate molecules are coordinated to a central copper atom, two of them via a carboxylate oxygen atom and the other two via a nitrogen atom [Cu–O = $1\cdot967$ (5) Å, Cu–N = $1\cdot994$ (6) Å]. These centrosymmetric ligand atoms form an almost square plane, and they are *trans* with respect to each other. The second oxygen atoms of the two carboxylate groups bound, one above and one below the 'square' plane, complete a distorted octahedron [Cu–O = $2\cdot768$ (6) Å]. Each ligand molecule binds two copper atoms, forming a two-dimensional network; the networks are connected by hydrogen bonds formed between the amino nitrogen atoms and carboxylate oxygen atoms, and via water molecules which are hydrogen bonded to nitrogen and carboxylate oxygen atoms.

Introduction

As part of a general study on copper–protein interaction, the copper ion complexes of 6-aminohexanoic acid are being investigated. This particular ligand is intended as a model for carboxylate and ε-amino side chains present in proteins. In a solution study, we have previously shown that the carboxylate group rather than the ε-amino group of aminohexanoic acid interacts with copper(II) ions (Österberg & Toftgård, 1972). In the corresponding copper(I) system, on the other

hand, our data indicate that copper(I) is bound to the ε-amino group (Österberg & Sjöberg, 1972). Here, we report the crystal structure of bis-(6-aminohexanoato)-copper(II) dihydrate, which clearly demonstrates that copper(II) ions interact with the ε-amino group in the solid state.

Experimental

The crystals used in this study were prepared by one of the methods developed by Sjöberg (doctoral dissertation, to be published): bis-(1,5-cyclooctadiene)-