

# Crystal Structure Determination of *N*-Phenyl-(5-anilino-2,4-pentadienyldene) ammonium Bromide Hemihydrate. A Test on the Applicability of a Relation between Structure Factor, Triple Products and a Single Patterson Vector

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The crystal structure of one modification of *N*-phenyl-(5-anilino-2,4-pentadienyldene)ammonium bromide hemihydrate has been determined by the heavy-atom method. In order to test a procedure based on a relation between structure factor, triple products and a single Patterson vector, the positions of the bromine atoms were determined with the aid of this procedure. The crystals are monoclinic, space group  $C2/c$ ,  $Z=8$ , with  $a=14.01$ ,  $b=13.92$ ,  $c=16.59$  Å,  $\beta=96.27^\circ$ . Intensities were measured on an automatic 4-circle diffractometer. A block-diagonal least-squares refinement led to a final  $R$  of 0.064. The molecule is nearly planar and is in an all-*trans* configuration. There are no alternating C-C bond distances in the pentadienyldene chain which thus has aromatic character. The water molecule lies on a twofold axis and participates in four weak hydrogen bonds of the type  $O-H \cdots Br^-$  and  $O \cdots H-C$  in a pseudo-tetrahedral arrangement. The bromine ion is connected by hydrogen bonds to one water molecule and to two nitrogen atoms; this arrangement is nearly planar and is asymmetric.

## Introduction

Several modifications of the compound *N*-phenyl-(5-anilino-2,4-pentadienyldene)ammonium bromide

hemihydrate,  $(Ph-N=C-C=C-C=C-N-Ph)Br^- \cdot \frac{1}{2}H_2O$

(hereinafter called: PAPAB), are known (König, 1904). Our first aim was to determine the crystal structure of a monoclinic modification of PAPAB, in order to establish the geometry of the molecule and the bonding character in the pentadienyldene chain. Secondly we wanted to test the applicability of a procedure to determine the heavy-atom positions, employing a relation between structure factor, triple products and a single (heavy-atom) Patterson vector (Krabbendam & Kroon, 1971).

## Experimental

A sample of PAPAB was kindly supplied by Professor J. F. Arens, who also suggested the X-ray analysis. The block-shaped crystals obtained by slow evaporation of a glacial acetic acid solution (König, 1904) show a blue metallic shine and are ruby-red in transmitted light. They apparently belong to the  $\alpha$  modification described by Shimidzu (1927). Space group, cell constants and structure factors were deduced from measurements on a four-circle automatic Enraf-Nonius diffractometer with Cu  $K\alpha$  radiation ( $\lambda=1.5418$  Å).

### Crystal data

$[Ph-NH-(CH)_5-NH-Ph]Br \cdot \frac{1}{2}H_2O$ , M.W. 338.24.  
Monoclinic

$a=14.01$ ,  $b=13.92$ ,  $c=16.59$  Å,  $\beta=96.27^\circ$ ,  
 $V_{cell}=3218$  Å<sup>3</sup>,  $D_c=1.39$  g cm<sup>-3</sup>,  $Z=8$ .  $F(000)=1384$ .  
Systematic absences:  $hkl$  with  $h+k=2n+1$ ,  $h0l$  with  $l=2n+1$ .

The symmetry test of Ramachandran & Srinivasan (1959) revealed the presence of a centre of symmetry. Thus the space group is  $C2/c$ .

The  $\omega$  scan mode was used for recording the intensities. A hemisphere of the reciprocal lattice was scanned, up to  $\theta=70^\circ$ , and, after averaging, 2810 independent intensities were available for the structure determination. No correction for absorption ( $\mu=36.4$  cm<sup>-1</sup>) was applied; the dimensions of the crystal used were  $0.15 \times 0.07 \times 0.05$  mm.

## Structure determination

In a preceding paper (Krabbendam & Kroon, 1971) we established a relation between a structure factor, triple products and a single Patterson vector  $U$  by comparing the Fourier coefficients of the structure with the Fourier coefficients of the Hoppe section at a single vector  $U$  in the double Patterson.

It reads:

$$F_h = \frac{\sum_{h'} F_h F_{h'} F_{\bar{h}+\bar{h}'} \cos 2\pi h' \cdot U}{\sum_{h'} f_h^M f_{\bar{h}+\bar{h}'}^M \cos 2\pi h \cdot U/2}, \quad (1)$$

in which  $U$  is a single vector between atoms  $M$  with form factor  $f_h^M$ . Employing absolute values of the triple products, each provided with a weighting factor  $P_{+-}P_-$ , this relation has been modified to:

$$F_h = \frac{\sum_{h'} |F_h F_{h'} F_{\bar{h}+\bar{h}'}| \tanh N(|U_h U_{h'} U_{\bar{h}+\bar{h}'}|) \cos 2\pi h' \cdot U}{\sum_{h'} f_h^M f_{\bar{h}+\bar{h}'}^M \cos 2\pi h \cdot U/2}. \quad (2)$$

We expected to find the single vectors  $\mathbf{U}$  by searching for those values of  $\mathbf{U}$  which minimize the measure of fit  $R_A$ , defined as:

$$R_A = \frac{\sum_{\mathbf{h}} |F_{\mathbf{h}}^O| - |F_{\mathbf{h}}^C|}{\sum_{\mathbf{h}} |F_{\mathbf{h}}^O|}, \quad (3)$$

in which  $F_{\mathbf{h}}^C$  stands for the right-hand side of (2). However, in a test run on a two-dimensional example (plane group  $pgg$ ), it became apparent that the function  $R_A(\mathbf{U})$  showed minima at the positions of double peaks as well. We then made use of the fact that all hypersections of the double Patterson belong to plane group  $p2$ , with the exception of the hypersections at the single peaks, which retain the symmetry of the structure. This led to a measure of fit  $R_B$ , which required the Fourier coefficients of a hypersection to obey the symmetry relations of the plane group  $pgg$ . The function  $R_B(\mathbf{U})$  also showed a few false minima in addition to the correct ones, but not on the positions of the double vectors, as was the case in  $R_A(\mathbf{U})$ . We devised a third measure of fit  $R_C$ , a combination of  $R_A$  and  $R_B$ , which indeed showed its lowest minima at the positions of the single vectors.

We have employed equation (2), together with  $R_A$ ,  $R_B$  and  $R_C$ , to determine the structure of a derivative of chloranilic acid of unknown chemical composition, space group  $C2/c$  (Kroon & Krabbendam, 1973). For this space group  $R_B$  and  $R_C$  were defined as:

$$R_B = \frac{\sum_{\mathbf{h}} \sum_{\mathbf{k}} \sum_{\mathbf{l}} [|F_{\mathbf{hkl}}^C| - (-1)^l |F_{\mathbf{hkl}}^C|]}{\sum_{\mathbf{h}} \sum_{\mathbf{k}} \sum_{\mathbf{l}} |F_{\mathbf{hkl}}^C|} \quad (4)$$

$$R_C = \frac{\sum_{\mathbf{h}} \sum_{\mathbf{k}} \sum_{\mathbf{l}} [|F_{\mathbf{hkl}}^O| - (|F_{\mathbf{hkl}}^C| + (-1)^l |F_{\mathbf{hkl}}^C| \cdot \frac{1}{2})]}{\sum_{\mathbf{h}} \sum_{\mathbf{k}} \sum_{\mathbf{l}} |F_{\mathbf{hkl}}^O|} \quad (5)$$

Searching for a chlorine-chlorine single vector, we scanned  $\mathbf{U}$  at regular intervals through Patterson space, found a minimum in  $R_C(\mathbf{U})$ , calculated the signs of  $F_{\mathbf{h}}$  from the triple products by equation (2), and derived from the resulting  $F_{\text{obs}}$  map the structure (which appeared to be potassium chloranilate monohydrate).

As the scanning procedure was rather time-consuming, we wanted to test a simpler procedure on the structure determination of PAPAB: The coordinates of the 18 highest Patterson peaks were introduced into equation (2), using the bromine scattering factors;  $R_A$ ,  $R_B$  and  $R_C$  were calculated in each case. Owing to the limited size of the computer storage only 684 equations, each with 1007 terms, were employed. The result is shown in Table 1. In this table each search vector  $(u, v, w)$  goes with a vector  $(\frac{1}{2} - u, \frac{1}{2} - v, -w)$ . The reason for this is that the centres of symmetry in  $C2/c$  belong to one of two different equivalence classes, so that for each single vector  $(u, v, w)$ , which connects two atoms related by a centre of symmetry in one equivalence class, there is a second vector  $(\frac{1}{2} - u, \frac{1}{2} - v, -w)$ , which connects two atoms related by a centre of symmetry in the other equivalence class. The symmetry relations

between structure factors, and consequently the expressions for  $R_B$  and  $R_C$ , depend on the equivalence class; once these expressions are chosen only one of a pair of possible single vectors will give a minimum in  $R_B$  and  $R_C$ , but we have to check both vectors of each pair. If we take this into consideration and also disregard the rather special Harker vector at (0-0000, 0-3889, 0-5000) then we find, from Table 1, for the lowest value of  $R_B$  ( $100R_B = 43$ ) and of  $R_C$  ( $100R_C = 35$ ) the bromine-bromine single vector at  $\mathbf{U} = (0-1667, 0-3889, 0-2639)$ . To investigate the influence of overlap from neighbouring hypersections in the Hoppe section, we applied a sharpening function  $\exp 5s^2$  to the  $F$ 's and  $f^{\text{Br}}$ 's in equation (2). As a result there was a considerable decrease in the  $R_A$  values for all search vectors, whereas  $R_B$  showed a significant decrease only at the position of the single vector.

Table 1. *The measures of fit  $R_A$ ,  $R_B$  and  $R_C$  as a function of the Patterson vectors  $(u, v, w)$*

For each  $R$  the first column is calculated with unsharpened, the second with sharpened reflexions.  $u, v$  and  $w$  are  $\times 10^4$ .

$u$	$v$	$w$	$100R_A$	$100R_B$	$100R_C$				
5000	1111	5000	23	13	121	56	53		
0000	3889	5000	23	13	0	0	24	13	
3277	5000	2388	24	14	114	112	54	50	
1723	0000	7612	24	14	108	107	52	48	
3333	1111	7361	33	26	127	130	55	53	
1667	3889	2639	33	26	43	33	35	26	single vector
3236	3500	9055	57	57	88	86	64	65	
1764	1500	0945	57	57	130	126	71	72	
4527	3263	8263	62	62	110	112	71	73	
0473	1737	1737	62	62	128	127	74	75	
3650	3150	8477	65	67	115	111	74	77	
1350	1850	1523	65	67	129	128	75	79	
2819	4250	8055	68	66	91	90	74	74	
2181	0750	1945	68	66	129	121	78	78	
2388	3444	9361	64	63	103	105	72	73	
2612	1556	0639	64	63	135	126	76	76	
3416	2638	9722	71	74	138	127	80	83	
1584	2362	0278	71	74	126	125	78	83	
0153	5000	8277	64	66	116	113	79	81	
4847	0000	1723	64	66	116	113	79	81	
1805	5000	5944	65	64	108	109	79	78	
3195	0000	4056	65	64	103	105	78	78	
4888	2819	7583	62	64	133	126	71	74	
0112	2181	2417	62	64	134	137	71	75	
1722	2555	6250	63	62	130	133	75	74	
3278	2445	3750	63	62	132	130	74	74	
3819	4888	0833	67	76	110	120	76	84	
1181	0112	9167	67	76	125	126	77	84	
0777	4305	3861	65	68	112	120	74	79	
4223	0695	6139	65	68	114	118	74	78	
2014	2916	0583	75	78	119	116	81	84	
2986	2084	9417	75	78	127	130	82	86	
3805	5000	4666	76	73	113	113	85	85	
1195	0000	5334	76	73	96	95	84	83	
2847	2708	5556	68	72	126	131	77	82	
2153	2292	4444	68	72	122	125	77	81	

It appears that  $R_B(\mathbf{U})$  is an excellent criterion to identify the heavy-atom single vector. However, care must be taken to avoid special vectors such as, in the present case, the Harker vector at (0-0000, 0-3889, 0-5000). It is not difficult to show that, in general, Harker vectors

that originate from glide-plane operations correspond to hypersections with the exact space-group symmetry (that is: with  $R_B=0$ ). These special vectors are known for each space group and can be excluded from the analysis.

A heavy-atom map, with all observed structure factors, and signs calculated from the bromine positions at  $\frac{1}{2}U$ , revealed the structure at once. Another Fourier map, with signs obtained directly from the triple products by application of equation (2), was inferior to the first. The  $F_{obs}$  Fourier map in the structure determination of potassium chloranilate monohydrate, with signs calculated from the triple products, had revealed the structure very clearly. The inferiority of the Fourier map in the present case is due to the small number of reflexions. This follows from the fact that the signs obtained by (2), for this small number of structure factors, agree remarkably well with the signs obtained from the heavy-atom positions.

Another problem in the calculation of  $F_h^C$ , and thus of  $R_C$ , is the fact that sometimes  $\cos 2\pi\mathbf{h} \cdot U/2$  in the denominator of (1) and (2) is close to zero. In this case equation (1), and equation (2) correspondingly, should be replaced by the equivalent relation:

$$F_h = \frac{-\sum_{h'} F_h F_{h'} F_{h+h'} \sin 2\pi\mathbf{h}' \cdot U}{\sum_{h'} f_h^M f_{h+h'}^M \sin 2\pi\mathbf{h} \cdot U/2} \quad (6)$$

We have not done this yet; we merely left out  $F_h^C$  in the calculation of  $R_B$  and  $R_C$  if this happened.

However, our main concern is with the relatively few reflexions we could handle in our computer program. Since the relations (1) and (6) are algebraic, they are valid only if all structure factors are included. We do not plan to make the program handle more reflexions. Instead, we will proceed by employing a recently derived statistical relation, based on the joint probability distribution  $P(E_k, E_{-k}, \cos 2\pi\mathbf{k} \cdot U)$ , which in-

Table 2. Fractional coordinates and thermal parameters

Estimated standard deviations in parentheses. The anisotropic temperature factor is in the form  $\exp [10^{-5} \sum_i \sum_j h_i h_j \beta_{ij}]$ .

	x	y	z	$\beta_{11}$	$\beta_{22}$	$\beta_{33}$	$2\beta_{12}$	$2\beta_{23}$	$2\beta_{31}$
Br	0.08158 (4)	0.19648 (4)	0.13182 (4)	467	506	394	149	161	141
O	0.0000	0.3683 (4)	0.2500	567	535	510	0	0	67
N(1)	0.6007 (3)	0.1708 (3)	-0.0394 (3)	377	491	333	62	156	119
N(2)	0.2469 (3)	0.0448 (3)	0.2259 (3)	382	410	373	88	84	148
C(1)	0.5702 (4)	0.1212 (4)	0.0207 (3)	463	440	312	-22	40	95
C(2)	0.4811 (4)	0.1320 (4)	0.0446 (3)	400	510	379	92	99	179
C(3)	0.4486 (4)	0.0800 (4)	0.1084 (3)	392	524	394	118	23	183
C(4)	0.3585 (4)	0.0895 (4)	0.1341 (3)	484	442	401	100	102	236
C(5)	0.3318 (4)	0.0358 (4)	0.1973 (3)	396	431	387	-26	86	131
C(6)	0.6923 (3)	0.1677 (3)	-0.0684 (3)	417	381	308	-8	-57	154
C(7)	0.7667 (4)	0.1126 (4)	-0.0314 (3)	448	608	337	234	59	129
C(8)	0.8541 (4)	0.1129 (5)	-0.0636 (4)	472	714	457	188	149	198
C(9)	0.8670 (4)	0.1659 (4)	-0.1322 (4)	523	653	473	-92	-95	366
C(10)	0.7917 (4)	0.2210 (4)	-0.1684 (3)	571	578	400	-82	84	264
C(11)	0.7039 (4)	0.2210 (4)	-0.1364 (3)	473	454	369	-66	119	103
C(12)	0.2137 (3)	-0.0032 (3)	0.2925 (3)	416	355	314	-2	-55	121
C(13)	0.1238 (3)	0.0228 (4)	0.3124 (3)	379	457	375	-25	91	168
C(14)	0.0867 (4)	-0.0227 (4)	0.3756 (4)	422	549	449	-68	33	251
C(15)	0.1375 (4)	-0.0942 (4)	0.4192 (3)	629	497	373	-150	74	321
C(16)	0.2264 (4)	-0.1199 (4)	0.3984 (3)	650	482	382	130	186	213
C(17)	0.2657 (4)	-0.0749 (4)	0.3349 (3)	486	444	383	101	42	155

Table 2 (cont.)

	x	y	z	$B(\text{\AA}^2)$	Bonded to
H(1)	0.005	0.330	0.210	5	O
H(2)	0.560	0.215	-0.075	4	N(1)
H(3)	0.205	0.095	0.207	4	N(2)
H(4)	0.617	0.075	0.057	4	C(1)
H(5)	0.433	0.174	0.020	4	C(2)
H(6)	0.490	0.025	0.127	4	C(3)
H(7)	0.305	0.133	0.105	4	C(4)
H(8)	0.375	-0.010	0.228	4	C(5)
H(9)	0.765	0.093	0.027	4	C(7)
H(10)	0.910	0.073	-0.025	4	C(8)
H(11)	0.930	0.170	-0.170	4	C(9)
H(12)	0.793	0.270	-0.235	4	C(10)
H(13)	0.655	0.272	-0.165	4	C(11)
H(14)	0.085	0.058	0.275	4	C(13)
H(15)	0.020	0.000	0.393	4	C(14)
H(16)	0.107	-0.133	0.465	4	C(15)
H(17)	0.265	-0.165	0.437	4	C(16)
H(18)	0.328	-0.105	0.313	4	C(17)

volves a conditional average over only the larger  $E$  values (Heinerman, Krabbendam & Kroon, 1974).

### Structure refinement

The atomic coordinates, deduced from the heavy-atom Fourier synthesis, were refined by block-diagonal least-squares calculations. The hydrogen-atom positions were found from a difference synthesis. They were given a  $B$  of  $4 \text{\AA}^2$ , except for the water-molecule hydrogen atoms, which were assigned a  $B$  of  $5 \text{\AA}^2$ . These values were kept fixed during further block-diagonal least-squares refinement, in which all positional parameters and the anisotropic thermal parameters of the non-hydrogen atoms were varied. The scattering factors for the heavy atoms were obtained from Cromer & Mann (1968); for hydrogen the analytical form of



Table 3 (cont.)

Table with multiple columns of numerical data, organized in groups. Each group contains several rows of numbers, some with small letters (a, b, c) and subscripts (1, 2, 3) indicating specific entries or conditions. The data appears to be a continuation of a larger table.

Moore (1963) was used. The anomalous part of the scattering factor of  $\text{Br}^-$  was taken from Rietveld (1966). The refinement was considered to be completed when all shifts were far below the estimated standard deviations; the resulting  $R$  was 0.064. The final positional and thermal parameters are presented in Table 2. Observed and calculated structure factors are given in Table 3.

### Discussion of the structure

The molecular dimensions are given in Fig. 1. The molecule, which is in the all-*trans* configuration, is

nearly planar, with a maximum distance to the least-squares plane of 0.14 Å; the torsion angles are relatively small (Fig. 1). It appears that there are, within the limit of error, no alternating C-C bond distances in the pentadienylidene chain. This cannot be ascribed to disorder; in that case we would expect non-planar bond configurations around the nitrogen atoms. Consequently we have here a linear bonding system of an aromatic character with an equal contribution of two mesomeric forms which are equivalent by symmetry. The same situation was found in dipyrrolidyl-trime-thincyanin perchlorate ethanol (Zedler & Kulpe, 1970).

Table 4. Environment of the water molecule

Distance	Symmetry transformation	Angle
$\cdots\text{Br}(1)$	$x, y, z$	$\text{Br}(1)-\text{O}-\text{Br}(1')$ 89.3°
$\cdots\text{Br}(1')$	$-x, y, \frac{1}{2}-z$	$\text{C}(5)-\text{O}-\text{C}(5')$ 93.7
$\cdots\text{C}(5)$	$-\frac{1}{2}+x, \frac{1}{2}+y, z$	$\text{Br}(1)-\text{O}-\text{C}(5)$ 128.1
$\cdots\text{C}(5')$	$\frac{1}{2}-x, \frac{1}{2}+y, \frac{1}{2}-z$	$\text{Br}(1)-\text{O}-\text{C}(5')$ 111.8

Table 5. Geometry of the hydrogen bonds

D	H	A	Symmetry transformation of A	D-H	H $\cdots$ A	D $\cdots$ A	D-H $\cdots$ A
O	H(1)	Br	$x, y, z$	0.86 Å	2.56 Å	3.364 Å	155.6°
N(1)	H(2)	Br	$\frac{1}{2}-x, \frac{1}{2}-y, -z$	0.99	2.43	3.387	159.5
N(2)	H(3)	Br	$x, y, z$	0.94	2.46	3.387	166.1
C(5)	H(8)	O	$\frac{1}{2}+x, -\frac{1}{2}+y, z$	0.98	2.44	3.367	156.8

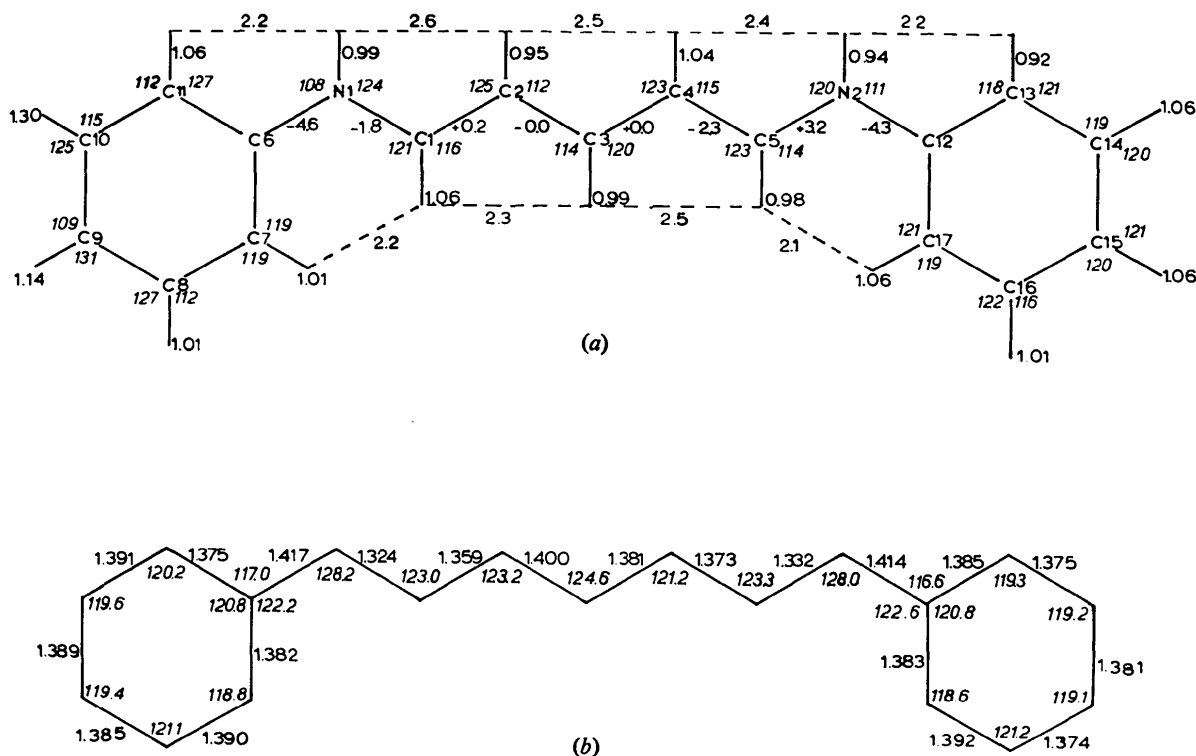


Fig. 1. Interatomic distances and bond angles. (a) Torsion angles in the chain calculated from the heavy-atom positions are given by numbers provided with a sign. The estimated standard deviations of the other values that give bond lengths, bond angles and non-bonded distances in which hydrogen atoms are involved are 0.08 Å, 4° and 0.1 Å respectively. (b) Bond lengths and bond angles involving the heavy atoms. The e.s.d.'s are 0.008 Å and 0.5° respectively.

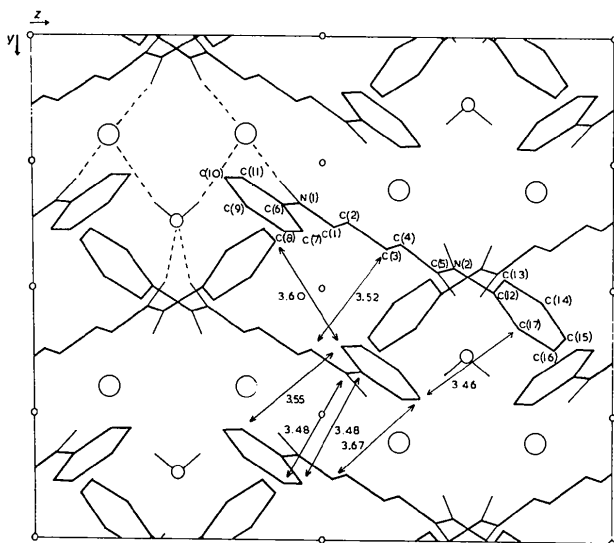


Fig. 2. The structure of *N*-phenyl-(5-anilino-2,4-pentadienylidene)ammonium bromide hemihydrate projected along the *a* axis. Some of the hydrogen bonds are depicted; the shortest intermolecular contacts are indicated.

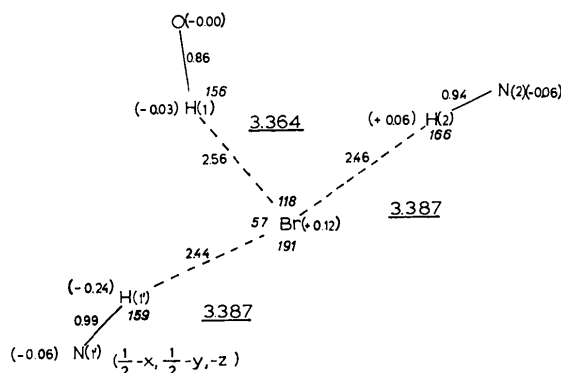


Fig. 3. The environment of the bromine ion. The underlined values are related to the distances between the bromine ion and the O and N atoms. The values in parentheses give the distances of the atoms to the mean plane through Br, N(1'), N(2) and O.

It can also be expected in the structure of 3,3'-diethylthiacarbocyanine bromide (Wheatley, 1959); here, however, the accuracy of the X-ray results did not permit conclusions about the bond orders in the methyne chain to be drawn.

The fact that the angle C(7)C(6)N(1) is significantly larger than the angle C(11)C(6)N(1) can be explained by the repulsion between H(4) and H(9). The same holds for the angle C(17)C(12)N(2) with respect to C(13)C(12)N(2), which will be influenced by the small contact between H(8) and H(18). A similar effect is found in the centric molecule diphenyl-1,3,5,7-octatetraene (Drenth & Wiebenga, 1955). The values of the pertinent angles are 122.7 and 119.2° respectively.

The water molecule (O-H=0.86 Å; ∠H-O-H=102°), which is situated on the twofold axis, plays a role as proton donor for two bromine ions, and has two close contacts involving hydrogen atoms from symmetry-related carbon atoms which are bonded to the nitrogen atoms in the pentadienylidene chain (Fig. 2). Thus the water molecule participates in four bonds of the type X-H...Y in a pseudo-tetrahedral arrangement (Table 4).

Another hydrogen-bonding system consists of two N-H...Br<sup>-</sup> contacts (Table 5), which, with a third hydrogen bond to a water molecule, form a nearly planar asymmetric arrangement (Fig. 3).

The remaining intermolecular contacts, mainly involving one phenyl group, can be inferred from Fig. 2.

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