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Structural Studies of Analgesics and Their Interactions.
III. The Crystal and Molecular Structure of Amidopyrine†

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Amidopyrine (1-phenyl-2,3-dimethyl-4-dimethylaminopyrazolone), $C_{13}H_{17}N_3O$, a dimethylamino derivative of antipyrine and an important analgesic and antipyretic agent, crystallizes in the triclinic space group $P\bar{1}$ with four molecules in a unit cell of dimensions $a=7{\cdot}458$ (5), $b=10{\cdot}744$ (5), $c=17{\cdot}486$ (15) Å, $\alpha=98{\cdot}6$ (2), $\beta=85{\cdot}6$ (3), $\gamma=108{\cdot}6$ (2)°. The structure was solved by direct methods and refined to an R value of 0·055 for 3706 photographically observed reflexions. The dimensions of the two crystallographically independent molecules are very nearly the same. The pyrazolone moiety in the molecule has dimensions comparable to those in antipyrine. Unlike antipyrine, the molecular dimensions of amidopyrine in the free state (the present structure) are close to those found in some of its hydrogen-bonded complexes. Thus it appears that the presence of the dimethylamino group makes the molecule more resistant to changes in its dimensions resulting from molecular association. An attempt has also been made to correlate the polar nature of the pyrazolone moiety and the hybridization state of the hetero nitrogen atoms in antipyrine, amidopyrine and their complexes.

Introduction

Several pyrazole derivatives are used as analgesic and anti-inflammatory agents. In our earlier communications we have reported the X-ray analysis of antipyrine, the first pyrazole derivative to be introduced as a drug (Singh & Vijayan, 1973), and a molecular complex between antipyrine and salicylic acid (Singh & Vijayan, 1974). The crystal structure analysis of amidopyrine (1-phenyl-2,3-dimethyl-4-dimethylaminopyrazolone), a dimethylamino derivative of antipyrine, is presented here. Amidopyrine is more potent than antipyrine in its pharmacological action and is also less toxic. A preliminary note on the analysis has been published (Singh & Vijayan, 1975).

Experimental

Large, transparent, plate-like crystals of amidopyrine were grown by slow evaporation at room temperature of its solution in 95% alcohol. The space group and unit-cell dimensions were determined from oscillation, Weissenberg and precession photographs taken along crystallographic axes. The reciprocal cell constants a^*,b^*,c^*, cos α^* and cos γ^* were refined by a least-squares method (*International Tables for X-ray Crystallography*, 1959) using 22 0*kl* and 16 *hk*0 high-angle reflexions. The crystal density was measured by flotation in an aqueous solution of potassium iodide.

Crystal data

Amidopyrine, $C_{13}H_{17}N_3O$; space group $P1$ or $P\bar{1}$; $a=7{\cdot}458\pm0{\cdot}005$, $b=10{\cdot}744\pm0{\cdot}005$, $c=17{\cdot}486\pm0{\cdot}015$ Å; $\alpha=98{\cdot}6\pm0{\cdot}2$, $\beta=85{\cdot}6\pm0{\cdot}3$, $\gamma=108{\cdot}6\pm0{\cdot}2°$. $M=231{\cdot}20$, $U=1312{\cdot}665$ Å^3; $D_m=1{\cdot}176\pm0{\cdot}005$, $Z=4$, $D_c=1{\cdot}171$ g cm^{-3}; $\lambda=1{\cdot}5418$ Å, μ(Cu $K\alpha$)$=6{\cdot}89$ cm^{-1}.

The intensity data were recorded on multiple-film equi-inclination Weissenberg photographs with nickel-filtered copper radiation for reciprocal levels *Hkl*, $H=0$ through 6 and *hkL*, $L=0$ through 10 from nearly cylindrical crystals of mean radii 0·035 and 0·050 cm, cut and ground along **a** and **c** respectively. The intensities were estimated visually with calibrated film strips. Out of a total of 5575 independent reflexions in the copper sphere, 4308 were recorded, of which 3706 were in the measurable range. The data were corrected for Lorentz and polarization effects and spot-shape distortions. The two sets of data were also corrected for absorption ($\mu r_a=0{\cdot}241, \mu r_c=0{\cdot}345$) using the analytical formula given by Palm (1964). The common reflexions in the two data sets were used for inter-level scaling. The absolute scale and the overall temperature factor were initially obtained from Wilson's statistics. The statistical distribution of $|E|$ values indicated the space group to be centrosymmetric and hence $P\bar{1}$, which was confirmed by subsequent structure analysis in this space group.

Structure determination

With space group $P\bar{1}$ and four molecules in the unit cell, there are two crystallographically independent molecules consisting of 34 non-hydrogen atoms in the asymmetric unit. The structure was solved with the

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program *MULTAN* originally written by Germain, Main & Woolfson (1971) and modified by S. Ramakumar and M. R. N. Murthy for the IBM 360/44 computer system at the Institute; 290 reflexions with $|E| \geq 1{\cdot}56$ were used for sign determination. Information obtained from packing considerations and Patterson distributions was also used, along with the conventional figures of merit (ABSFOM and *R*), to choose the correct set of signs from the *MULTAN* output. The correct solution (ABSFOM = 1·21, *R* = 18·6) turned out to be the second best non-trivial solution on the basis of the figures of merit.

The structure was first refined isotropically to an *R* value of 0·164 with the modified version of a block-diagonal *SFLS* program written by R. Shiono. Further refinement of the structure with individual anisotropic temperature factors of the form $\exp[-(b_{11}h^2+b_{22}k^2+b_{33}l^2+2b_{12}hk+2b_{13}hl+2b_{23}kl)]$ reduced *R* to 0·098. All the hydrogen atoms were located on a difference synthesis computed at this stage. The positional and isotropic thermal parameters of the hydrogen atoms were also included in the subsequent refinement cycles. The refinement was terminated when all the shifts became much smaller than the corresponding standard deviations. The final *R* value for 3706 observed reflexions was 0·055. The weighting function used in the final cycles had the form $1/(a+bF_o+cF_o^2)$, where $a = 0{\cdot}371$, $b = 0{\cdot}152$ and $c = 0{\cdot}0015$. The atomic scattering factors were those of Cromer & Waber (1965) for carbon, nitrogen and oxygen and of Stewart, Davidson & Simpson (1965) for hydrogen. The final positional and thermal parameters of the non-hydrogen atoms and those of the hydrogen atoms are listed in Tables 1 and 2 respectively.*

Discussion

Description of the structure

The crystal structure of amidopyrine as viewed along the *a* axis is shown in Fig. 1. Perspective views of the two crystallographically independent molecules, referred to hereafter as molecule *A* and molecule *B*, as seen along the normal to the planes of the respective pyrazolone rings, are shown in Fig. 2. Equations of the mean planes of various planar groups were calculated

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* A list of structure factors has been deposited with the British Library Lending Division as Supplementary Publication No. SUP 31735 (15 pp., 1 microfiche). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 13 White Friars, Chester CH1 1NZ, England.

Table 1. *Final positional and thermal parameters for the non-hydrogen atoms*

(*a*) Final positional coordinates (× 10^4) of non-hydrogen atoms. The estimated standard deviations are given in parentheses.

	x	*y*	*z*
N(1)	1506 (5)	4325 (3)	1436 (2)
N(2)	− 144 (4)	4566 (3)	1222 (2)
C(3)	484 (6)	5842 (4)	1023 (2)
C(4)	2408 (6)	6341 (4)	1040 (3)
C(5)	3130 (6)	5353 (4)	1284 (4)
C(6)	− 1742 (6)	4246 (5)	1793 (3)
C(7)	− 900 (6)	6485 (5)	824 (3)
O(8)	4768 (4)	5340 (3)	1337 (2)
N(9)	3527 (5)	7590 (3)	817 (2)
C(10)	4794 (8)	8421 (5)	1432 (4)
C(11)	4553 (10)	7459 (7)	93 (5)
C(12)	1469 (6)	2984 (5)	1448 (3)
C(13)	2815 (7)	2768 (5)	1888 (3)
C(14)	2820 (9)	1469 (6)	1889 (4)
C(15)	1504 (10)	414 (6)	1482 (5)
C(16)	1602 (10)	638 (6)	1067 (4)
C(17)	132 (7)	1920 (5)	1040 (3)
N(21)	4565 (5)	4296 (3)	3908 (2)
N(22)	1316 (5)	4500 (3)	3614 (2)
C(23)	2049 (6)	5858 (4)	3561 (3)
C(24)	689 (6)	6450 (4)	3720 (3)
C(25)	− 1068 (6)	5458 (4)	3923 (3)
C(26)	2422 (7)	3827 (5)	3969 (4)
C(27)	4094 (7)	6458 (5)	3346 (4)
O(28)	− 2684 (4)	5533 (3)	4059 (2)
N(29)	911 (6)	7805 (4)	3672 (3)
C(30)	371 (10)	8513 (6)	4387 (4)
C(31)	− 31 (11)	7965 (6)	3008 (4)
C(32)	− 1889 (6)	3004 (4)	3839 (3)
C(33)	− 3452 (7)	2758 (5)	4353 (4)
C(34)	− 4795 (8)	1511 (6)	4298 (4)
C(35)	− 4580 (10)	503 (6)	3733 (5)
C(36)	− 3026 (10)	740 (6)	3234 (5)
C(37)	− 1675 (8)	1993 (5)	3278 (3)

(*b*) Anisotropic thermal parameters (× 10^4) of non-hydrogen atoms. The estimated standard deviations are given in parentheses.

	b_{11}	b_{22}	b_{33}	b_{12}	b_{13}	b_{23}
N(1)	107 (6)	82 (4)	41 (2)	43 (4)	3 (3)	15 (2)
N(2)	100 (6)	85 (4)	37 (2)	35 (2)	9 (3)	20 (2)
C(3)	121 (8)	84 (4)	28 (2)	42 (5)	6 (3)	8 (2)
C(4)	113 (7)	75 (4)	37 (2)	28 (5)	5 (3)	11 (2)
C(5)	107 (7)	86 (4)	37 (5)	41 (2)	13 (3)	12 (2)
C(6)	117 (8)	119 (6)	44 (3)	41 (6)	8 (4)	25 (3)
C(7)	133 (8)	102 (5)	43 (2)	49 (5)	1 (4)	18 (3)
O(8)	112 (6)	112 (4)	65 (2)	46 (4)	34 (3)	28 (2)
N(9)	138 (7)	74 (4)	47 (2)	24 (4)	8 (3)	17 (2)
C(10)	214 (12)	81 (5)	65 (3)	13 (6)	− 13 (5)	5 (3)
C(11)	285 (16)	141 (7)	49 (3)	21 (9)	28 (6)	27 (4)
C(12)	158 (9)	87 (5)	37 (2)	56 (5)	21 (4)	20 (3)
C(13)	179 (10)	110 (6)	42 (3)	68 (6)	14 (4)	22 (3)
C(14)	265 (14)	133 (7)	58 (3)	104 (9)	21 (6)	39 (4)
C(15)	358 (18)	91 (6)	62 (4)	80 (8)	21 (6)	25 (4)
C(16)	294 (16)	89 (6)	59 (4)	37 (8)	18 (6)	15 (3)
C(17)	195 (11)	89 (5)	40 (2)	25 (6)	7 (4)	20 (3)
N(21)	115 (7)	76 (4)	38 (4)	17 (4)	6 (3)	14 (2)
N(22)	131 (7)	76 (4)	41 (2)	24 (4)	1 (3)	15 (2)
C(23)	130 (8)	81 (5)	33 (2)	18 (5)	− 1 (3)	11 (2)
C(24)	139 (8)	74 (4)	33 (2)	29 (5)	6 (3)	12 (2)
C(25)	123 (8)	80 (4)	36 (2)	21 (5)	− 5 (4)	9 (2)
C(26)	175 (10)	100 (5)	45 (3)	51 (6)	− 8 (4)	17 (3)
C(27)	132 (9)	99 (5)	54 (3)	19 (6)	11 (4)	20 (3)
O(28)	138 (6)	104 (4)	57 (2)	37 (4)	11 (3)	22 (2)
N(29)	176 (8)	72 (4)	47 (2)	34 (5)	12 (3)	13 (2)
C(30)	321 (17)	93 (6)	54 (3)	55 (8)	21 (6)	4 (3)
C(31)	373 (20)	128 (7)	50 (3)	95 (10)	10 (6)	36 (4)
C(32)	152 (9)	17 (4)	36 (2)	13 (5)	− 6 (4)	14 (2)
C(33)	176 (11)	96 (6)	47 (3)	20 (6)	10 (4)	14 (3)
C(34)	209 (13)	116 (7)	60 (4)	7 (7)	25 (5)	22 (4)
C(35)	255 (15)	89 (6)	81 (4)	− 18 (8)	− 7 (7)	20 (4)
C(36)	275 (16)	82 (6)	67 (4)	12 (8)	− 22 (6)	4 (4)
C(37)	197 (11)	96 (5)	39 (3)	27 (6)	− 3 (4)	12 (3)

Table 2. *Final positional coordinates* ($\times 10^3$) *and isotropic temperature factors of hydrogen atoms*

The estimated standard deviations are given in parentheses.

	x	y	z	B
H(13)	375 (9)	350 (6)	220 (4)	5 (2)
H(14)	373 (9)	132 (6)	217 (4)	6 (2)
H(15)	157 (12)	−40 (8)	142 (5)	9 (2)
H(16)	−88 (11)	−10 (7)	74 (4)	8 (2)
H(17)	−82 (7)	207 (5)	76 (3)	4 (1)
H(61)	−286 (9)	458 (6)	168 (4)	6 (2)
H(62)	−108 (10)	474 (7)	235 (4)	7 (2)
H(63)	−224 (9)	320 (6)	187 (4)	6 (2)
H(71)	−180 (9)	665 (6)	124 (3)	5 (1)
H(72)	−9 (10)	744 (7)	61 (4)	7 (2)
H(73)	−180 (10)	591 (7)	34 (4)	7 (2)
H(101)	438 (9)	932 (6)	130 (4)	6 (1)
H(102)	389 (10)	843 (7)	195 (4)	7 (2)
H(103)	589 (9)	807 (6)	153 (4)	5 (1)
H(111)	511 (10)	837 (7)	−12 (4)	8 (2)
H(112)	565 (13)	699 (9)	13 (6)	11 (3)
H(113)	384 (12)	684 (8)	−38 (5)	9 (2)
H(33)	−366 (9)	344 (6)	473 (4)	5 (1)
H(34)	−599 (9)	147 (6)	469 (4)	6 (1)
H(35)	567 (10)	−37 (7)	377 (4)	7 (2)
H(36)	−259 (12)	6 (8)	299 (5)	9 (2)
H(37)	−55 (8)	215 (5)	294 (3)	4 (1)
H(261)	261 (13)	424 (9)	454 (5)	9 (2)
H(262)	188 (9)	292 (6)	392 (4)	6 (2)
H(263)	373 (8)	403 (5)	373 (3)	4 (1)
H(271)	422 (8)	727 (6)	318 (3)	5 (1)
H(272)	500 (12)	640 (8)	381 (5)	9 (2)
H(273)	447 (12)	602 (8)	287 (5)	9 (2)
H(301)	66 (10)	949 (7)	419 (4)	7 (2)
H(302)	126 (16)	868 (10)	486 (6)	12 (3)
H(303)	−81 (9)	814 (6)	451 (4)	6 (2)
H(311)	30 (10)	897 (7)	300 (4)	7 (2)
H(312)	−147 (13)	764 (9)	308 (5)	9 (2)
H(313)	67 (12)	754 (8)	258 (4)	8 (2)

with Blow's (1960) method. In the structure, the phenyl ring and the pyrazolone ring are oriented with respect to each other at 37·7 and 40·1° in molecules *A* and *B* respectively. The orientation is determined essentially by steric factors as in the case of antipyrine (Singh & Vijayan, 1973). On account of the proximity of the carbonyl oxygen atom O(8) and the methyl carbon atom C(7), the sterically most favourable orientation of the dimethylamino group is one in which the two methyl groups lie on opposite sides of the pyrazolone ring. In this orientation, the two methyl groups could point towards either O(8) or C(7). The observed conformation in the structure corresponds to the former possibility. This conformation is sterically more favourable on account of the larger van der Waals radius of the methyl group compared to that of the oxygen atom. The dihedral angles which define the conformation of the dimethylamino group [namely, O(8)–C(4)–N(9)–C(10) and O(8)–C(4)–N(9)–C(11)] are −58·2 and 68·0° in molecule *A* and −57·4 and 70·6° in molecule *B*.

The hetero nitrogen atoms are pyramidal in both molecules. The nitrogen atom N(1) deviates from the plane of the three surrounding atoms by −0·199 ± 0·005 and N(2) by 0·404 ± 0·006 Å in molecule *A*. The corresponding values for the nitrogen atoms N(21) and N(22) in molecule *B* are −0·199 ± 0·005 and 0·362 ± 0·006 Å respectively. The phenyl ring attached to N(1) and the methyl group attached to N(2) lie on opposite sides of the mean plane of the five-membered pyrazolone ring. The dihedral angles C(12)–N(1)–N(2)–C(6) and C(32)–N(21)–N(22)–C(26) which define their mutual orientation are 68·2 (in molecule *A*) and 61·9° (in molecule *B*).

Average dimensions of the molecules in comparison with the molecular dimensions of antipyrine

The dimensions of the two crystallographically independent molecules in the structure are very nearly the same. Therefore their average values will be used in the further discussion. The average bond lengths and bond angles of the molecule are given in Fig. 3.

As mentioned earlier, the two methyl groups of the dimethylamino group lie on opposite sides of the plane of the five-membered ring. The line joining the two methyl carbon atoms is approximately normal to the plane of this ring. Thus, the lone pair of the amino nitrogen atom is nearly perpendicular to the *p* orbitals of the ring atoms and the resonance interaction of the amino nitrogen atom with the ring is expected to be negligible. Therefore, the electronic effect of the sub-

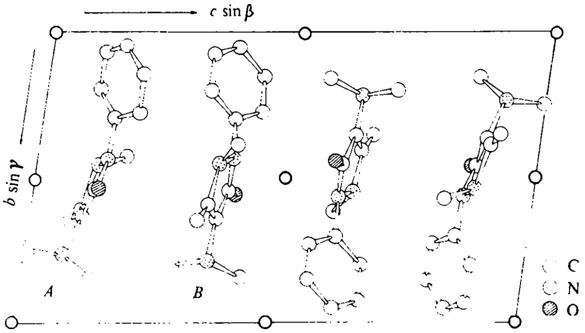

Fig. 1. The crystal structure of amidopyrine as viewed along the *a* axis.

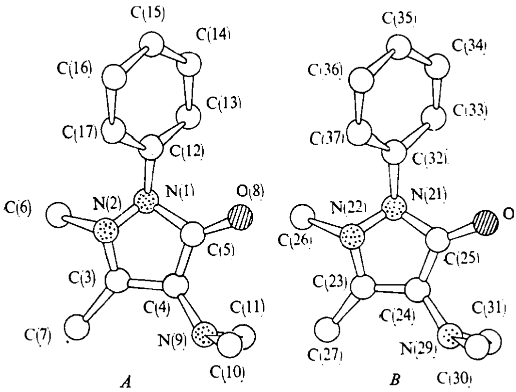

Fig. 2. Perspective views of the molecules *A* and *B* in the structure, as seen normal to the planes of the respective pyrazolone rings.

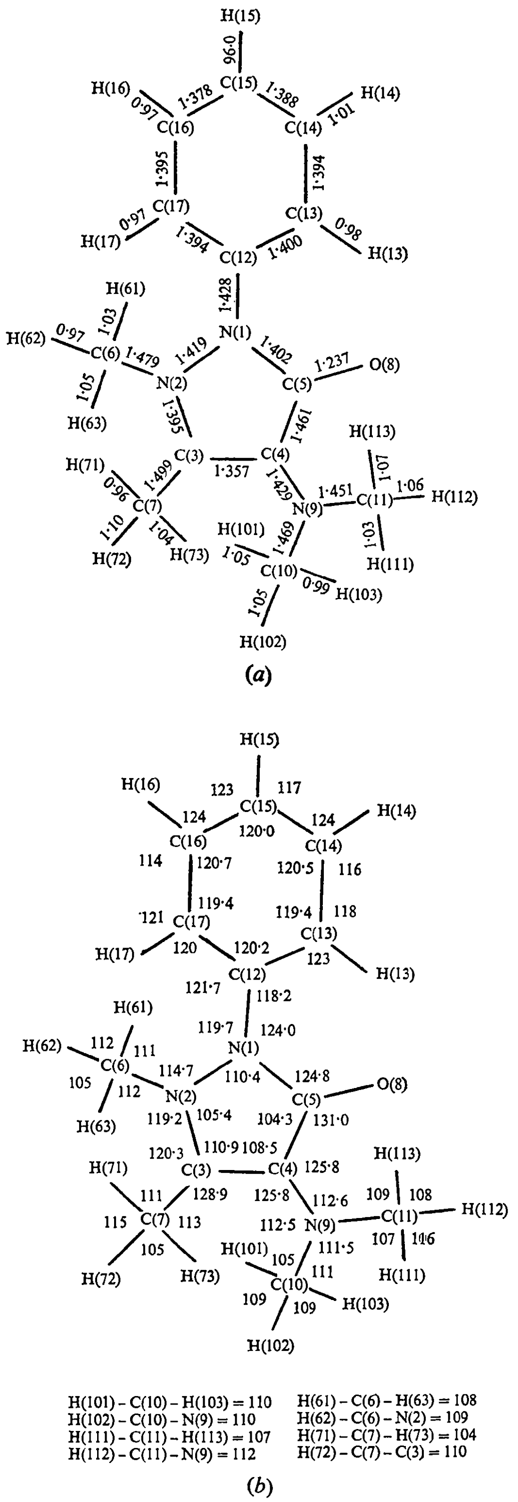

Fig. 3. (*a*) Average bond lengths (Å), (*b*) average bond angles (°). Mean standard deviations for the bond lengths are: σ(C–O) = 0·006, σ(N–N) = 0·006, σ(N–C) = 0·007, σ(C–C) = 0·008, σ(C–H) = 0·08 Å. The e.s.d.'s of bond angles involving non-hydrogen atoms vary between 0·3 and 0·6°, whereas the mean e.s.d.'s of C–C–H (or N–C–H) and H–C–H angles are 4·0 and 5·5° respectively.

stitution of the dimethylamino group at the 4-position is likely to be limited to the inductive effect through σ orbitals. These considerations indicate that the resonance forms I, II and III, used in the case of antipyrine (Singh & Vijayan, 1973), and shown in Fig. 4, are perhaps adequate to describe, in an approximate semi-quantitative manner, the structure of the pyrazolone moiety in amidopyrine. In fact, the observed bond lengths in this moiety can be satisfactorily explained (Table 3), employing the bond length–bond order curves used earlier (Singh & Vijayan, 1973), if the contributions from forms I, II and III are fixed at 68, 16 and 16% respectively. These contributions are comparable to those used in the case of antipyrine (66, 22 and 12% respectively), indicating the essential structural similarity of the pyrazolone moiety in the two compounds. A detailed comparison of individual bond lengths, valency angles and dihedral angles also clearly brings out this structural similarity. Minor differences do exist in the dimensions of the pyrazolone group between the two compounds. These differences give rise to the small variations in the relative contributions of the resonance forms I, II and III.

Table 3. *Observed and calculated bond lengths* (Å) *of the pyrazolone moiety in amidopyrine*

	Observed	Calculated
N(1)–N(2)	1·419	1·440
N(2)–C(3)	1·395	1·395
C(3)–C(4)	1·357	1·352
C(4)–C(5)	1·461	1·467
C(5)–N(1)	1·402	1·395
C(5)–O(8)	1·237	1·246

Molecular dimensions of amidopyrine in its crystalline complexes

The structures of two crystalline complexes involving amidopyrine, one with barbital (Kiryu, 1971) and the other with cyclobarbital (Kiryu, Hirayama & Iguchi, 1974), have been reported so far. In both these complexes, the association is achieved through a hydrogen bond with the carbonyl oxygen atom of the amidopyrine molecule. The molecular geometry of amidopyrine is very similar in the two compounds and hence the weighted average dimensions of the molecule will be used in the following discussion. The bond lengths and angles in the molecule, averaged using Topping's (1961) formula, are given in Fig. 5.

Examination of Figs. 3 and 5 shows that the dimensions of the molecule in the complexes are surprisingly close to those found in free amidopyrine. For example, the mean value of the differences between the bond lengths in the pyrazolone moiety in the two cases is 0·009 Å, the maximum difference being 0·025 Å. The small differences that exist can again be expressed qualitatively in terms of the resonance forms considered earlier. The average bond lengths of the pyrazolone group in the complexes can best be explained if the contributions of forms I, II and III are assumed to be 68, 20 and 12% respectively. These values are indeed very close to those calculated for free amidopyrine (68, 16 and 16%). The hybridization states of the two hetero nitrogen atoms are also somewhat similar in these two cases. In the complexes, N(1) and N(2) deviate from the planes of the three surrounding atoms by −0·234 ± 0·004 and 0·348 ± 0·019 Å respectively. The corresponding values in amidopyrine are −0·199 ± 0·004 and 0·383 ± 0·021 Å respectively. The close similarity between the dimensions of the pyrazolone moiety in free amidopyrine and in its complexes became rather intriguing when compared with the considerable differences between the molecular dimensions of antipyrine in the free state and those in its hydrogen-bonded complex with salicylic acid (Singh & Vijayan, 1974). Thus it appears that the attachment of the dimethylamino group at the 4-position makes the molecule more resistant to changes in its dimensions resulting from interactions at the carbonyl group.

The polar nature of the pyrazolone group and the hybridization state of the nitrogen atoms in antipyrine, amidopyrine and their complexes

The crystal structures of antipyrine, amidopyrine and a few of their hydrogen-bonded and metallic complexes were examined in this and the preceding papers in this series. The dimensions of the pyrazolone moiety in these crystals were also discussed in terms of the relative contributions from three resonance structures. The differences in the relative contributions are obviously related to the differences in the polar nature of the molecule. The changes in the hybridization state of the two hetero nitrogen atoms in the pyrazolone moiety resulting from the interactions at the carbonyl group were also discussed in some detail. In antipyrine, as well as in amidopyrine, a phenyl ring and a methyl group are attached to the two nitrogen atoms and, therefore, changes in the pyramidal nature of the latter lead to considerable changes in the geometry of the molecule. An attempt is made here to correlate the polar nature of the pyrazolone moiety and the hybridization state of the nitrogen atoms in the crystal structures examined so far. The attempt is again based on the relative contributions of three resonance forms. Admittedly, rigorous deductions cannot be made on the basis of contributions from different resonance forms calculated with empirical bond length–bond order curves. However, such calculations, when used carefully, can be very helpful in explaining broad structural features and in identifying the general trends of changes in molecular dimensions resulting from intermolecular interactions.

The displacements of the two hetero nitrogen atoms in the pyrazolone ring from the planes of the surrounding atoms and the sums of the angles around them (the nitrogen atoms), in antipyrine, amidopyrine and

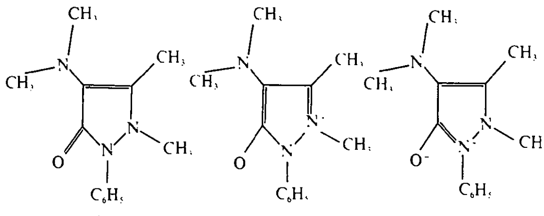

Fig. 4. Canonical structures of amidopyrine.

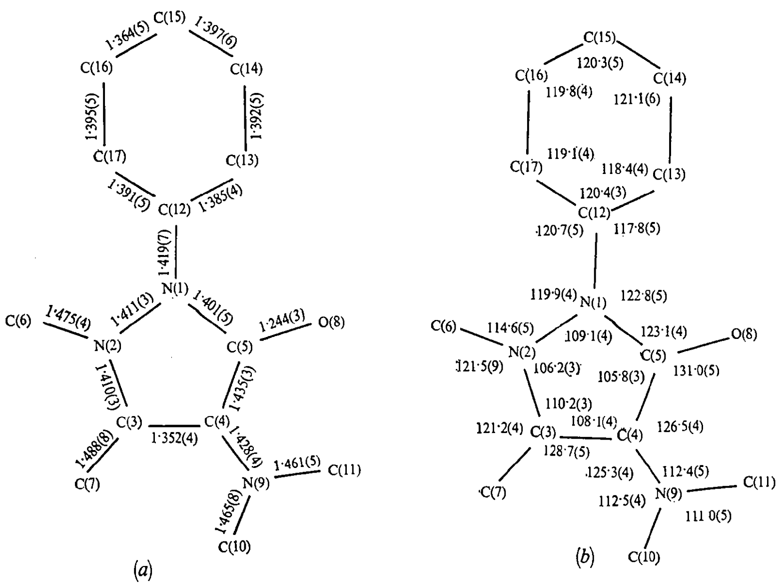

Fig. 5. (*a*) Weighted average bond lengths (Å) and (*b*) angles (°) of amidopyrine in its hydrogen-bonded complexes. The standard deviations are given in parentheses.

Table 4. *The displacements* (Å) *of the hetero nitrogen atoms from the planes of their nearest neighbours, the sum of the angles around them and the percentage contributions of the three canonical forms in amidopyrine and its complexes, and antipyrine and its complexes*

	Nearest neighbours	Amidopyrine	Amidopyrine in complexes	Antipyrine	Salipyrine	Calcium hexa-antipyrine perchlorate
Displacement of N(1)	N(2)–C(5)–C(12)	−0·199 (5)	−0·234 (5)	−0·247 (5)	−0·154 (8)	−0·098 (11)
Displacement of N(2)	N(1)–C(3)–C(6)	0·383 (21)	0·348 (19)	0·347 (5)	0·295 (8)	0·188 (12)
Sum of angles around N(1)		354·2	352·2	350·8	356·6	358·8
Sum of angles around N(2)		339·2	343·8	342·3	347·0	354·7
Form I (%)		68	68	66	45	41
Form II (%)		16	20	20	34	37
Form III (%)		16	12	12	21	22

their complexes are given in Table 4. The contributions of the three resonance forms in each structure, determined from bond length–bond order curves, are also listed in Table 4. In form I, all the bonds around N(1) and N(2) are single whereas forms II and III have a double bond each, adjacent to N(2) and N(1) respectively. The presence of these double bonds is likely to make N(1) and N(2) more planar. Thus, the deviations of N(1) and N(2) from the planes of their nearest neighbours may be expected to be inversely related to the relative contributions of (III) and (II) respectively. An examination of Table 4 shows that a general, though not rigorous, inverse relationship exists between the deviation of N(1) and the percentage contribution of (III) and between the deviation of N(2) and the percentage contribution of (II). It may be mentioned that the degree of planarity introduced by an adjacent bond having a given double-bond character differs between N(1) and N(2). For example, in amidopyrine each of these nitrogen atoms has a bond adjacent to it with a bond order of 1·16. But N(1) deviated from the plane of the neighbouring atoms by −0·199 ± 0·004 Å whereas the corresponding value for N(2) is 0·383 ± 0·021 Å. This disparity arises presumably because of the substituents at N(1) and N(2), and hence the steric constraints, being different. Also, the effect of the polar forms II and III on the hybridization state of the nitrogen atoms appears to be more pronounced in the metal complexes compared with that in the hydrogen-bonded complexes and in the free molecules. However, to sum up, there appears to be a reasonably good qualitative inverse correlation between the contribution of polar forms II and III and the pyramidal nature of hetero nitrogen atoms N(2) and N(1).

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References

Blow, D. M. (1960). *Acta Cryst.* **13**, 168.

Cromer, D. T. & Waber, J. T. (1965). *Acta Cryst.* **18**, 104–109.

Germain, G., Main, P. & Woolfson, M. M. (1971). *Acta Cryst.* A**27**, 368–376.

International Tables for X-ray Crystallography (1959). Vol. II, pp. 326–332. Birmingham: Kynoch Press.

Kiryu, S. (1971). *J. Pharm. Sci.* **60**, 699–703.

Kiryu, S., Hirayama, F. & Iguchi, S. (1974). *Chem. Pharm. Bull.* **22**, 1588–1592.

Palm, J. H. (1964). *Acta Cryst.* **17**, 1326–1327.

Singh, T. P. & Vijayan, M. (1973). *Acta Cryst.* B**29**, 714–720.

Singh, T. P. & Vijayan, M. (1974). *Acta Cryst.* B**30**, 557–562.

Singh, T. P. & Vijayan, M. (1975). *Curr. Sci.* **40**, 153–154.

Stewart, R. F., Davidson, E. R. & Simpson, W. T. (1965). *J. Chem. Phys.* **42**, 3175–3187.

Topping, J. (1961). *Errors of Observations and Their Treatment*. London: Chapman and Hall.