organic compounds

3-(4-Bromophenyl)-5-(4-dimethyl-aminophenyl)-1-phenyl-2-pyrazoline: X-ray and density functional theory (DFT) studies

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In the crystal structure of the title compound, $C_{23}H_{22}BrN_3$, a strong conjugation of the pyrazoline chromophore with the aromatic rings at positions 1 and 3 is observed, as well as a significant shift in the synclinal→synperiplanar direction. The absolute structure was unequivocally determined. In the absence of clasical hydrogen-bond donors, the structure is stabilized by weak $C-H\cdots\pi$ interactions. This paper also reports the electronic structure of the title compound using NBO (natural bond order) analysis. The contributions of lone pairs to the relevant bonds were revealed.

Comment

Pyrazolines have been reported to show a broad spectrum of biological activities, including antibacterial (Nauduri & Reddy, 1998; Azarifar & Shaabanzadeh, 2002), antifungal (Korgaokar *et al.*, 1996), antiprotozoal (Cetin *et al.*, 2003), anti-inflammatory, analgesic (Udupi, Kushnoor *et al.*, 1998; Udupi, Rao *et al.*, 1998) and antidepressant (Bilgin *et al.*, 1993) activities. Moreover, pyrazolines are useful synthons in organic synthesis. In this context, we have prepared several 1,3,5-triaryl-2-pyrazolines using the most straightforward method for the synthesis of 1,3,5-triphenyl-2-pyrazolines involving the one-pot condensation of chalcones with phenylhydrazine in glacial acetic acid. We report here the absolute structure determination of one of them, the title compound, (I), with a 4-bromophenyl group at position 3 of the pyrazoline ring (Fig. 1).

The values of relevant bond lengths (Table 1) in the C11/N1/N2/C3/C31 structural fragment indicate strong conjugation of the pyrazoline chromophore with the aromatic rings at the N1 and C3 positions. These observations are in good agreement with those reported for 1,3-diphenyl-5-[4-(dimethylamino)phenyl]-2-pyrazoline (Rurack *et al.*, 2000) with an

unsubstituted phenyl ring at atom C3. Comparing this compound and (I), the Ar/C3/N2/N1 fragments are nearly planar in both cases, but in the case of compound (I), the
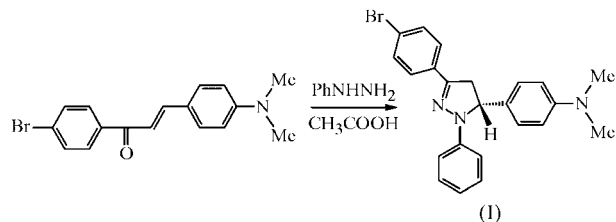
phenyl ring at N1 is directed by *ca* 8° more to coplanarity with the Ar/C3/N2/N1 fragment. Additionally, although in both cases a synclinal orientation of the Ar/C5 group to the pyrazoline ring is observed, the values of the relevant dihedral angles [36.6° for N1—C5—C51—C56 in (I) *versus* 76.5° for the analogous dihedral angle in 1,3-diphenyl-5-[4-(dimethylamino)phenyl]-2-pyrazoline (Rurack *et al.*, 2000)] indicate a significant shift in the synclinal→synperiplanar direction for (I), in contrast with a synclinal→anticlinal direction for 1,3-diphenyl-5-[4-(dimethylamino)phenyl]-2-pyrazoline. A similar orientation of the Ar/C5 group was demonstrated by the value of the relevant dihedral angle (−34.6°) observed for the *S* isomer of 1-(4-cyanophenyl)-3-phenyl-5-[4-(diethylamino)phenyl]-2-pyrazoline (Fahrni *et al.*, 2003), while the values of the relevant dihedral angles for the other 5-[4-(diethylamino)phenyl]-2-pyrazolines of this series vary from −47 to −63°.

The angles between rings 1–4, defined in Fig. 1, are summarized in Table 2. In the absence of classical hydrogen-bond donors, the structure is stabilized by weak $C-H\cdots\pi$ interactions, two of them in an edge-to-face manner (Table 3 and Fig. 2).

Natural bond orbital (NBO) analysis (Foster & Weinhold, 1980) of the electronic structure of (I) shows that the bond orders (Wiberg indices) are very close to the expected values.
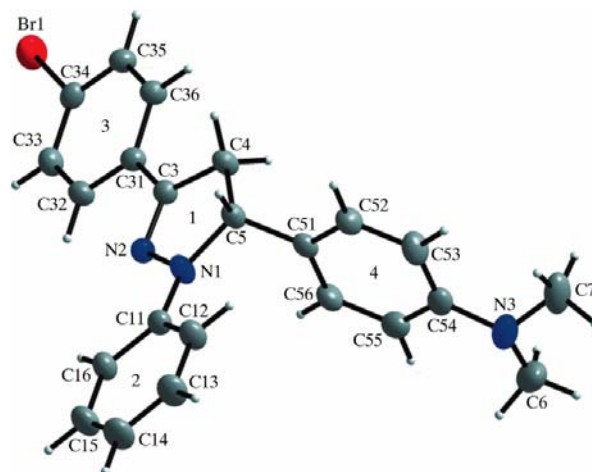

Figure 1
A perspective drawing of the *R* isomer of (I), showing the atomic numbering scheme. Displacement ellipsoids are drawn at the 50% probability level and H atoms are shown as small spheres of arbitrary radii. Central numbers define the rings.

The exceptions are the Br1—C34 (1.042), N2═C3 (1.679), N1—N2 (1.135), N1—C11 (1.072) and N3—C54 (1.123) bonds, where their bond orders are between a single and double bond and indicate electronic delocalization. A detailed analysis of the NBO results reveals that the electrons of the lone pair on atom Br1 contribute slightly to the Br1—C34 bond only, the electrons of the N2 lone pair are mainly delocalized on a double N2═C3 bond, and the electrons of the N1 lone pair contribute to the electronic density of the N1—C11 bond, lending it a partially double-bond character. The N1—N2 bond also has such double-bond character as a consequence of the partial contributions of the two lone pairs on atoms N1 and N2 to this bond. The lone pair on atom N3 makes a dominant contribution to the N3—C54 bond. This electronic redistribution leads to a shortening of the N1—C11, N1—N2, N2═C3 and N3—C54 bonds.
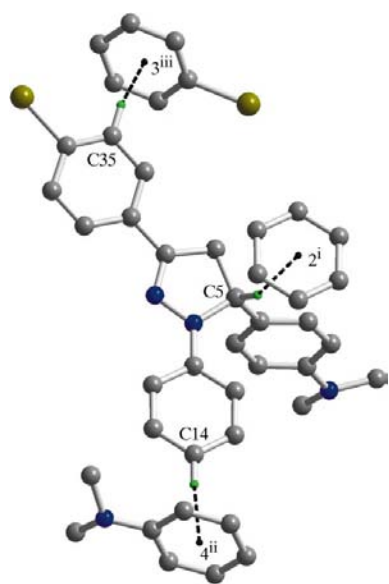

Figure 2
C—H$\cdots\pi$ interactions in the structure of (I). For clarity, H atoms not included in these interactions have been omitted and only the acceptor aromatic rings, with numbers in their centres (see Fig. 1), are shown. For symmetry codes, see Table 3.

Experimental

For the preparation of compound (I) (see scheme), 1-(4-bromophenyl)-3-[4-(dimethylamino)phenyl]prop-2-en-1-one (Koóš *et al.*, 1984) and phenylhydrazine in glacial acetic acid were heated to reflux according to the previously described procedure of Koóš *et al.* (1990). Compound (I) (m.p. 459–460 K) crystallized from the solution during its cooling. ^{1}H NMR (DMSO-d_6): δ 6.62–7.68 (*m*, 13H, aromatic), 5.36 (*dd*, 1H, *J* = 6.2 and 12.2 Hz, 5-H), 3.81 (*dd*, 1H, *J* = 12.2 and 17.4 Hz, 4-H$_{cis}$), 3.02 (*dd*, 1H, *J* = 6.2 and 17.4 Hz, 4-H$_{trans}$), 2.81 (*s*, 6H, Me$_2$N); ^{13}C NMR (DMSO-d_6): δ 149.8, 144.1, 131.8, 131.6, 129.6, 128.9, 127.5, 126.4, 121.6, 118.7, 113.2, 112.8 (aromatic), 146.1 (C-3), 63.1 (C-5), 42.8 (C-4), 39.7 (Me$_2$N). Yellow single crystals of adequate quality for diffraction analysis were obtained by slow crystallization from ethanol.

Crystal data

C$_{23}$H$_{22}$BrN$_3$	V = 7816.04 (17) Å^3
M_r = 420.35	Z = 16
Orthorhombic, *Fdd*2	Mo *K*α radiation
a = 32.3762 (4) Å	μ = 2.12 mm^{-1}
b = 43.4056 (2) Å	T = 183 (2) K
c = 5.5618 (1) Å	0.78 × 0.21 × 0.08 mm

Data collection

Siemens SMART CCD area-detector diffractometer	34545 measured reflections
Absorption correction: multi-scan (*SADABS*; Sheldrick, 2003)	6946 independent reflections
T_{min} = 0.289, T_{max} = 0.849	5926 reflections with $I > 2\sigma(I)$
	R_{int} = 0.034

Refinement

$R[F^2 > 2\sigma(F^2)]$ = 0.044	H-atom parameters constrained
$wR(F^2)$ = 0.113	$\Delta\rho_{max}$ = 0.41 e Å^{-3}
S = 1.00	$\Delta\rho_{min}$ = −0.56 e Å^{-3}
6946 reflections	Absolute structure: Flack (1983),
268 parameters	with 3062 Friedel pairs
1 restraint	Flack parameter: −0.003 (7)

Table 1
Selected geometric parameters (Å, °).

Br1—C34	1.908 (2)	N1—C5	1.485 (3)
N1—N2	1.378 (3)	N2—C3	1.297 (3)
N1—C11	1.393 (3)	N3—C54	1.399 (3)
N2—N1—C5—C51	−129.50 (19)	N2—C3—C31—C32	−6.2 (3)
N2—N1—C11—C16	13.0 (4)	N1—C5—C51—C56	36.6 (3)

Table 2
Dihedral angles between pairs of rings (°) in (I).

The rings are as defined in Fig. 1.

Planes defining the dihedral angle	Angle
1,2	8.79
1,3	5.75 (12)
1,4	74.28 (12)
2,3	13.83 (12)
2,4	82.73 (12)
3,4	68.90 (11)

Table 3
C—H$\cdots\pi$ interactions (Å, °).

CgX is the centroid of ring X and ring numbers are as defined in Fig. 1.

D—H$\cdots CgX$	H$\cdots CgX$	D—H$\cdots CgX$
C5—H5$\cdots Cg2^i$	2.80	157
C14—H14$\cdots Cg4^{ii}$	2.85	150
C35—H35$\cdots Cg3^{iii}$	2.73	133

Symmetry codes: (i) $x, y, z - 1$; (ii) $x + \frac{1}{4}, -y - \frac{1}{4}, z - \frac{1}{2}$; (iii) $x - \frac{1}{2}, -y, z - \frac{1}{2}$.

H atoms were constrained to the ideal geometry using an appropriate riding model (C—H = 0.95–0.99 Å) and were refined isotropically. For the methyl groups, the C—H distances (0.98 Å) and N—C—H angles (109.5°) were kept fixed, while the torsion angles were allowed to refine with the starting position based on the threefold averaged circular Fourier synthesis.

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NBO (natural bond orbital) calculations were carried out by means of the *NBO* program (Glendening *et al.*, 1993) included in the *GAUSSIAN98* package (Frisch *et al.*, 1998), after full optimization of the geometric parameters of the isolated molecule at the B3LYP/6-31G+ level of theory.

Data collection: *SMART* (Bruker, 2003); cell refinement: *SAINT* (Bruker, 2003); data reduction: *SAINT* and *SADABS* (Sheldrick, 2003); program(s) used to solve structure: *SHELXTL* (Bruker, 2003); program(s) used to refine structure: *SHELXTL*; molecular graphics: *DIAMOND* (Brandenburg, 2006); software used to prepare material for publication: *SHELXTL*.

Supplementary data for this paper are available from the IUCr electronic archives (Reference: DN3043). Services for accessing these data are described at the back of the journal.

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