Structure of 3-(2-aminothiazol-4-yl)coumarin

V. N. Nesterov,[a] Yu. T. Struchkov,[b] S. N. Kovalenko,[c] Yu. A. Sharanin,[a] and I. A. Zhuravel'[c]*

[a]T. G. Shevchenko Lugansk State Pedagogical Institute,
2 ul. Oboronnaya, Lugansk, 348011 Ukraine.
Fax: +7 (064 2) 53 3127
[b]A. N. Nesmeyanov Institute of Organoelement Compounds, Russian Academy of Sciences,
28 ul. Vavilova, 117813 Moscow, Russian Federation.
Fax: +7 (095) 135 5085
[c]Ukrainian Pharmaceutical Academy, 53 ul. Pushkinskaya, Kharkov, 310002 Ukraine.
Tel.: +7 (057 2) 67 5082

The structure of 3-(2-aminothiazol-4-yl)coumarin has been established by X-ray structural analysis. The data obtained were compared with the results of molecular mechanics calculations.

Key words: coumarin, X-ray structural study, molecular mechanics.

A series of works devoted to the synthesis, spectral properties, and biological activity of thiazolylcoumarins has been reported recently.[1–5] Among the compounds of this class, highly efficient laser dyes[3,4] and promising biologically active compounds[1,5] have been found. Information on the spatial structures of these compounds is required to construct new theoretical models describing the structural dependence of their spectral properties and biological activity. For this purpose, 3-(2-aminothiazol-4-yl)coumarin (**1**) was studied by X-ray structural analysis, and the data obtained were compared with the results of molecular mechanics calculations (the MMX program).[6]

The overall view of the molecule is shown in Fig. 1; the bond lengths and bond angles are given in Tables 1 and 2. The molecule is approximately planar: the dihedral angle between the coumarin bicycle (planar within ±0.027 Å) and the thiazole substituent (planar within ±0.009 Å) is 9.2°. The slight twisting of the molecule around the C(3)—C(9) bond is apparently caused by shortened intramolecular nonbonded contacts: O(2)...C(11) 2.846(3) Å; C(2)...C(11) 3.011(3) Å; and N(1)...C(4) 2.839(3) Å (the sums of O and C, C and C, and N and C van der Waals radii are 3.22, 3.40, and 3.25 Å, respectively).[7] Steric hindrances are also partially relieved owing to an increase in the external bond angles O(2)C(2)C(3) (126.8(3)°) and C(3)C(9)C(11) (126.7(2)°).

The coplanar arrangement of the substituents in the coumarin molecule is favorable for π,π conjugation between the heterocycles and leads to the formation of a short intramolecular nonbonded O(2)...H(11) contact, which can be considered to be an intramolecular hydrogen bond of the C—H...O type with the parameters

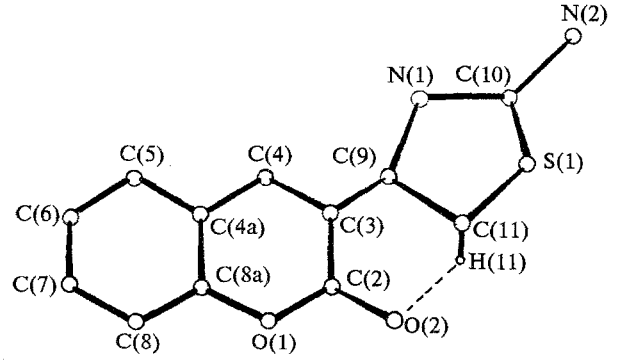

Fig. 1. The overall view of molecule **1**. Dashed line indicates the intramolecular C—H...O hydrogen bond.

Table 1. Experimental and calculated bond lengths in molecule **1**

Bond	*d*/Å		Bond	*d*/Å	
	X-ray structural analysis	MMX		X-ray structural analysis	MMX
O(1)—C(2)	1.373(3)	1.35	C(6)—C(7)	1.387(4)	1.40
O(1)—C(8a)	1.379(3)	1.36	C(7)—C(8)	1.377(4)	1.40
C(2)—O(2)	1.213(3)	1.22	C(8)—C(8A)	1.386(4)	1.40
C(2)—C(3)	1.464(3)	1.48	C(9)—N(1)	1.391(3)	1.43
C(3)—C(4)	1.353(3)	1.37	C(9)—C(11)	1.356(3)	1.36
C(3)—C(9)	1.469(3)	1.48	N(1)—C(10)	1.307(3)	1.31
C(4)—C(4a)	1.434(3)	1.46	C(10)—S(1)	1.748(3)	1.77
C(4A)—C(5)	1.407(3)	1.41	C(10)—N(2)	1.344(4)	1.39
C(4A)—C(8a)	1.385(3)	1.41	C(11)—S(1)	1.724(3)	1.77
C(5)—C(6)	1.380(4)	1.40			

Translated from *Izvestiya Akademii Nauk. Seriya Khimicheskaya,* No. 3, pp. 492—494, March, 1995.

1066-5285/95/4403-0475 $12.50

Table 2. Bond angles ω (deg) in molecule **1**

Angle	ω	
	X-ray structural analysis	MMX
C(2)O(1)C(8a)	123.2(2)	123.46
O(1)C(2)O(2)	115.5(2)	118.42
O(1)C(2)C(3)	117.6(2)	119.50
O(2)C(2)C(3)	126.8(2)	122.07
C(2)C(3)C(4)	118.6(2)	117.83
C(2)C(3)C(9)	119.4(2)	123.46
C(4)C(3)C(9)	121.9(2)	118.71
C(3)C(4)C(4a)	122.5(2)	120.64
C(4)C(4a)C(5)	124.4(2)	121.68
C(4)C(4a)C(8a)	117.9(2)	118.64
C(5)C(4a)C(8a)	117.7(2)	119.68
C(4a)C(5)C(6)	120.1(2)	120.09
C(5)C(6)C(7)	120.4(3)	120.15
C(6)C(7)C(8)	120.7(3)	120.08
C(7)C(8)C(8a)	118.4(3)	120.18
C(8)C(8a)O(1)	117.2(2)	120.47
C(4a)C(8a)O(1)	120.1(2)	119.71
C(4a)C(8a)C(8)	122.7(2)	119.82
C(3)C(9)N(1)	117.8(2)	120.99
C(3)C(9)C(11)	126.7(2)	127.24
N(1)C(9)C(11)	115.4(2)	111.71
C(9)N(1)C(10)	110.5(2)	114.73
N(1)C(10)S(1)	114.6(2)	112.55
N(1)C(10)N(2)	124.9(2)	122.19
N(2)C(10)S(1)	120.5(2)	125.27
C(10)S(1)C(11)	88.9(1)	88.82
S(1)C(11)C(9)	110.5(2)	112.14

Table 3. Atomic coordinates ($\times 10^4$, $\times 10^3$ for H atoms) in the structure of **1**

Atom	*x*	*y*	*z*
S(1)	2163(1)	2390(1)	5347(1)
O(1)	−4899(4)	3050(1)	8308(1)
O(2)	−1689(4)	2118(1)	7879(1)
N(1)	−583(4)	3869(1)	5711(1)
N(2)	1715(6)	3995(2)	4454(2)
C(2)	−3021(5)	2825(2)	7728(1)
C(3)	−2823(5)	3451(2)	7002(1)
C(4)	−4424(5)	4228(2)	6951(2)
C(4a)	−6283(5)	4465(2)	7585(1)
C(5)	−7938(5)	5276(2)	7568(2)
C(6)	−9705(5)	5435(2)	8201(2)
C(7)	−9887(6)	4795(2)	8855(2)
C(8)	−8271(6)	4001(2)	8893(2)
C(8a)	−6491(5)	3851(2)	8256(1)
C(9)	−950(4)	3210(2)	6342(1)
C(10)	968(5)	3528(2)	5141(1)
C(11)	389(5)	2386(2)	6256(1)
H(4)	−433(5)	462(2)	649(1)
H(5)	−777(5)	571(2)	712(2)
H(6)	−1086(6)	598(2)	818(2)
H(7)	−1112(5)	490(2)	927(2)
H(8)	−825(6)	354(2)	932(2)
H(11)	42(5)	184(2)	662(2)
H(21)*	241(6)	371(2)	405(2)
H(22)*	127(6)	457(2)	439(2)

* Hydrogen atoms of the $N(2)H_2$ group.

(O(2)...C(11) 2.846(3); C(11)—H(11) 0.96(3); H(11)...O(2) 2.34(2) Å; C(11)—H(11)...O(2) angle 112(3)°), which agree with the data from Ref. 8.

The trigonal nitrogen atom of the $N(2)H_2$ group (the sum of the bond angles is 359°) lies in the plane of the heterocycle. This is favorable for n,π conjugation of the lone electron pair of the nitrogen atom with the cycle, which is borne out by the C(10)—N(2) bond length (1.344(4) Å), which corresponds to a conjugated C_{sp^2}—N_{sp^2} bond.[9] The remaining bond lengths and bond angles in the coumarin system and in the thiazole heterocycle have normal values[9] and agree with those found in unsubstituted coumarin[10] and thiazole.[11]

The NH_2 hydrogen atoms are involved in intermolecular hydrogen bonding: N(2)—H(21)...O(2′) (0.5+*x*, 0.5−*y*, −0.5+*z*) (N(2)...O(2′) 3.097(3); N(2)—H(21) 0.84(3); H(21)...O(2′) 2.27(3) Å; N(2)—H(21)...O(2′) 168(3)°), N(2)—H(22)...N(1′) (−*x*, 1−*y*, 1−*z*) (N(2)...N(1′) 3.108(3), N(2)—H(22) 0.86(3), H(22)...N(1′) 2.25(3) Å, N(2)—H(22)...N(1′) 173(3)°), through which the molecules are linked into layers.

The results of MMX calculations of molecule **1** with full geometry optimization predict two conformers differing in energy by ΔE = 0.30 kcal/mol; the *s-trans* rotamer is more stable, which is in agreement with the experimental data. The C(4)C(3)C(9)C(11) torsion angle (159.2°), which corresponds to bending of the thiazole ring out from the plane of the coumarin cycle, exceeds the experimental value. Because the parametrization used in the calculations assumes medium with a permittivity of 1.5, this result is reasonable and corresponds to the well-known flattening of π conjugated assemblies of cycles in the crystalline state. The results of the calculation of the geometry of the most stable conformer are given in Tables 1 and 2.

Experimental

Crystals of **1** are monoclinic, at 20°C *a* = 4.839(2), *b* = 14.287(6), *c* = 15.800(6) Å, β = 94.00(2)°, *V* = 1090(1) Å^3, d_{calc} = 1.489 g/cm^3, *Z* = 4, the space group is $P2_1/n$. The unit-cell parameters and intensities of 2243 independent reflections were measured on a four-cycle automated Siemens P3/PC diffractometer (Mo *Kα* radiation, a graphite monochromator, θ/2θ scan technique, θ_{max} = 28°). The structure was solved by the direct method and refined anisotropically by the full-matrix least-squares method for nonhydrogen atoms using 2233 reflections with $I > 2\sigma(I)$. Hydrogen atoms were located from the difference syntheses and included in the refinement with isotropic thermal parameters. The final *R* value is 0.037 (R_w = 0.037). All calculations were performed using the SHELXTL PLUS program package (PC version). Atomic coordinates are given in Table 3 (atomic thermal parameters may be obtained from the authors).

References

1. V. P. Chernykh, I. S. Gritsenko, V. I. Gridasov, and S. N. Kovalenko, *Farmatsevticheskii Zhurnal* [*Pharmaceutical Journal*], 1991, **4**, 48 (in Russian).
2. I. A. Zhuravel', S. N. Kovalenko, V. P. Chernykh, A. O. Porokhnyak, E. K. Ryadnykh, and V. M. Markova, *Farmatsevticheskii Zhurnal* [*Pharmaceutical Journal*], 1991, **4**, 72 (in Russian).
3. M. M. Asimov, V. P. Gavrilenko, V. M. Nikitchenko, S. N. Kovalenko, A. I. Novikov, and A. N. Rubinov, *Izv. Akad. Nauk Belorussii, Ser. Fiz.-Mat. Nauk* [*Bull. Belorussian Acad. Sci., Div. Phys.-Mathem. Sci*], 1992, **1**, 44 (in Russian).
4. M. M. Asimov, V. M. Katarkevich, S. N. Kovalenko, V. M. Nikitchenko, and A. N. Rubinov, *Optika i Spektroskopiya* [*Optics and Spectroscopy*], 1987, **63**, 3, 606 (in Russian).
5. I. A. Zhuravel', S. N. Kovalenko, V. P. Chernykh, and I. V. Barannik, *Sbornik trudov Ryazanskogo Meditsinskogo Instituta* [*Collection of Papers of the Ryazan' Medical Institute*], Ryazan', 1991, 75 (in Russian).
6. U. Burkert and N. L. Allinger, *Molecular Mechanics*, Washington, DC, ASC, 1982.
7. A. Bondi, *J. Phys. Chem.*, 1966, **70**, 3006.
8. Z. Berkovitch-Yellin and L. Leiserowitz, *Acta Crystallogr.*, 1984, **B40**, 159.
9. F. H. Allen, O. Kennard, D. G. Watson, L. Brammer, A. G. Orpen, and R. Taylor, *J. Chem. Soc., Perkin Trans. II*, 1987, *S1*.
10. E. Gavuzzo, F. Mazza, and E. Giglio, *Acta Crystallogr.*, 1974, **B30**, 1351.
11. L. Nygaard, E. Asmussen, J. H. Hog, R. C. Maheshwari, C. N. Nielsen, I. B. Petersen, J. Rastrup-Andersen, and G. O. Sorensen, *J. Mol. Struct.*, 1971, 225.

Received May 12, 1994;
in revised form October 3, 1994