

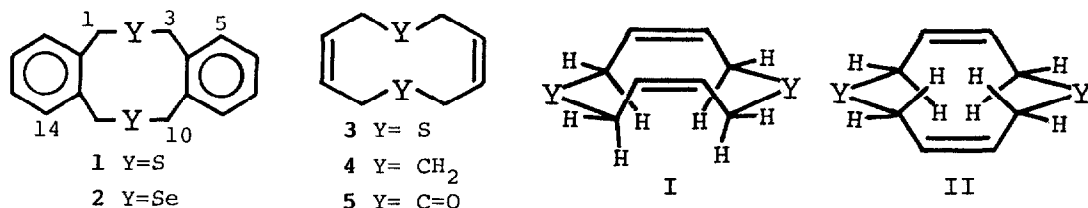
## STRUCTURES OF 2,11-DITHIA[3.3]ORTHO CYCLOPHANE AND ITS DISELENA ANALOGUE

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**Abstract:** Structures of 2,11-Dithia[3.3]orthocyclophane(1) and its diselenium analogue(2) are confirmed to be anti by X-ray analysis and ring current method.

Recently, Y. H. Lai and co-worker reported the conformational studies of 2,11-dithia[3.3]-orthocyclophane(1),<sup>1)</sup> using dynamic NMR analysis. They concluded that the most stable conformer of 1 should be syn. This conclusion attracted our attention because we have deduced completely different result as long as the most stable conformer is concerned.

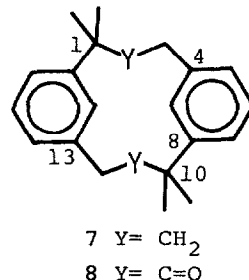
In this paper, we report our result which verifies that the most stable conformation of 1 is not the syn but the anti in both the crystalline state and the solution phase. We also report that the same conclusion is true for diselenium analogue(2).<sup>2)</sup>



The conformation of *cis,cis*-1,6-cyclodecadiene, the fundamental skeleton for 1, has been particular interest for the past two decades,<sup>3)</sup> and it was discussed in terms of boat(I) and chair(II) conformers. The boat and the chair correspond to the syn and anti structures for 1, respectively. X-ray crystallographic analysis of the mercuric chloride complex of 4,9-dithia-*cis,cis*-1,6-cyclodecadiene(3) disclosed that 3 adopted the chair conformation in the crystalline state.<sup>4)</sup>

It is also known that the chair conformer predominates over the boat both in *cis,cis*-1,6-cyclodecadiene(4)<sup>5)</sup> and its 4,9-diketo derivative(5).<sup>6)</sup> The rationale for these results stems from the difference of intramolecular steric repulsion between the two diametrically arranged double bonds.<sup>3)</sup> While the boat form has the repulsion, the chair form seems to be strain free. It is rather natural to assume that the situation should be accentuated when two benzene rings are condensed onto these two double bonds. However, the previous authors concluded quite the reverse.

Bathochromic shift and broadening of absorption bands in the UV spectrum can sometimes be a prove for "stacked" arrangement of two benzene rings.<sup>7)</sup> The previous authors applied this observation as the experimental evidence for the predominance of the syn structure<sup>1)</sup> by comparing the spectrum of 1 with that of 2,11-dithia[3.3]metacyclophane (6), whose preferred conformation has been established to be syn. However, the comparison of the UV spectra is not straightforward and



sometimes gives misleading conclusions. It is exemplified by the fact that, although two spectra of 1,1,10,10-tetramethyl[3.3]metacyclophane(7) and its 2,11-diketo derivative(8) are not different extensively with each other, the preferred conformation of the two are quite different; they are syn<sup>8)</sup> and anti,<sup>9)</sup> respectively.

One more evidence employed by the previous authors is the result of the MM2 calculation, which predicted that the stacked arrangement of the two benzenes in the syn conformer is preferred than the distant arrangement in the anti form. Unreasonable van der Waals attractive interaction between the facing two benzene rings should be the reason of these results. Quite recently, it is pointed out by Liljefors<sup>10)</sup> and Allinger<sup>11)</sup> independently that MM2 has false inclination for a stacked arrangement of two benzenes because of the lack of electrostatic repulsion term between them. To improve this inclination, Allinger has developed MM3 program, which can handle the benzene-benzene interaction correctly with added electrostatic interaction term.

In order to obtain information for the most stable conformation of 1, molecular mechanics calculations were performed. All the plausible initial geometries were generated by our MMRS program.<sup>12)</sup> They were then subjected to MM2 calculations which include extra electrostatic interaction term between the two benzenes correctly. Contrary to the previous calculations,<sup>1)</sup> any one of the three possible syn conformer has significantly larger steric energy than the anti structure(A1). The energy difference between A1 and the lowest syn conformer(S1) is 3.8 kcal/mol.<sup>13)</sup> This value is large enough to exclude any one of the syn structures. It is also found that A1 is the global minimum conformer, since it lies almost 2.8 kcal/mol below the next best anti structure(A2). These three structures(S1,A1,A2) are shown in Figure 1.

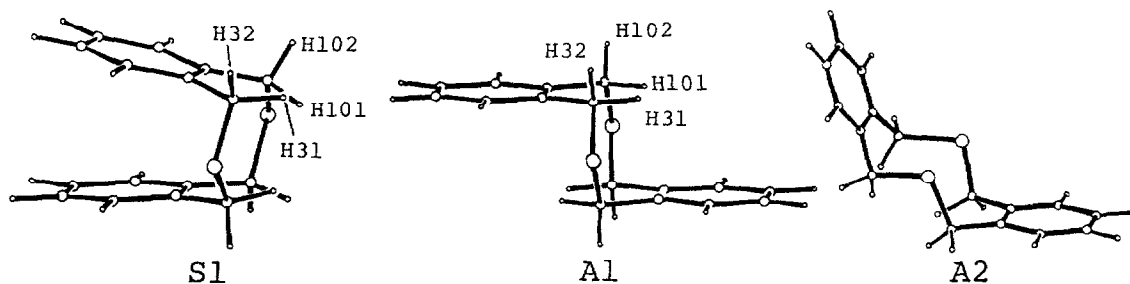


Fig.1. Stable conformers of 1 by MM2 calculation.

Further support for predominance of the anti structure was obtained by X-ray crystallographic analysis.<sup>14)</sup> Molecular geometries of 1 and 2 are shown in Figure 2. As can be clearly seen in the figure, both 1 and 2 have the almost identical anti structure in the crystalline state. Although the molecular mechanics calculations predicted a highly symmetrical  $C_{2v}$  structure(A1), the structure found in the crystal has small deviation from the  $C_{2v}$  symmetry. The benzene rings shift sideways as can be seen in Figure 2. The same deviation can also be observed in 2. This experiment, however, can not be a conclusive evidence for the most stable conformer in these molecules, since it is not always true that the structure obtained in the crystalline state is the true global energy minimum. It is especially so in flexible molecules such as macrocyclic compounds. In fact, [2.2]orthocyclophane is such a case. It is anti in crystal,<sup>15)</sup> whereas syn predominates over anti in solution.<sup>16)</sup>

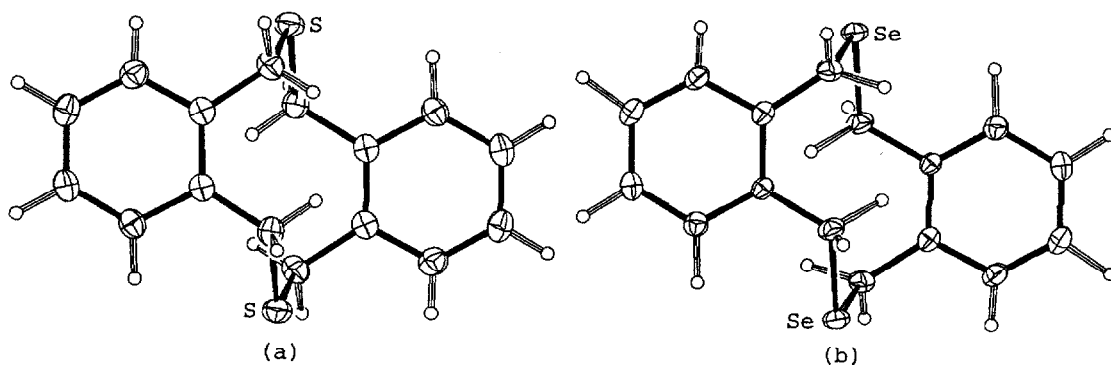


Fig.2. ORTEP drawing of 1(a) and 2(b).

In order to clarify the predominant conformation in solution,  $^1\text{H-NMR}$  spectral data for 1 and 2 were compared to those of respective reference compounds; 1,2-bis(methylthiomethyl)benzene(9) and 1,2-bis(methylselenomethyl)benzene(10). Table 1 summarizes these NMR data. Relative arrangement of the two benzenes can be obtained by the chemical shift differences of the benzene protons from those of reference compound. Small down field shifts (0.39, 0.07ppm for ortho and meta, respectively) of the aromatic protons of 1 cannot be compatible with the general features of the syn structure (small upfield shifts). These can be explained reasonably only by the anti orientation of the two benzenes.

Table 1.  $^1\text{H-NMR}$  chemical shifts of 1, 2, 9 and 10. ( $\delta$ , ppm)

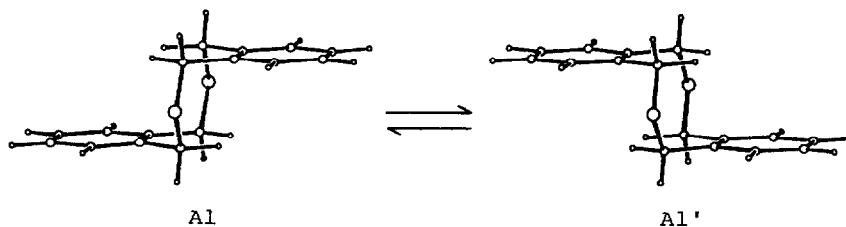
compound	CH <sub>2</sub>	aromatic	
		ortho-	meta-
1	3.44	7.61	7.27
9	3.85	7.22	7.21
2	3.66	7.50	7.22
10	3.91	7.16	7.16

Conclusive evidence for the anti conformation of 1 can be obtained from the upfield shift values of  $-\text{CH}_2-$  protons. In the anti structure, one of the two hydrogens of each methylene attached on the opposite benzene ring sticks out in the shielding region of the benzene ring, (Figure 1) On the other hand, the syn structure does not have such a hydrogen as can be seen in the side view of the conformer S1. The upfield shift values of these hydrogens were estimated by our newly developed ring current method<sup>17)</sup> and summarized in Table 2. Since 1 has dynamic processes which equalize all of the methylene hydrogens, these values should be averaged for comparison with the observed shift value. While the averaged upfield shift in the syn structure is very small (0.03ppm), that for the anti (0.38ppm) is very close to the observed one (0.41ppm).

Table 2. The calculated shift values. (- sign denotes upfield shift)

	anti(X-ray)	syn(S1)
H 31	-0.84	-0.00
H 32	-0.28	-0.09
H101	-0.37	+0.08
H102	-0.03	-0.13
av.	-0.38	-0.03

The close resemblance of these values can be the evidence for the predominance of the anti structure. The same discussion is true in 2. The dynamic processes discussed in the previous paper should then be replaced by  $\text{A1} \rightleftharpoons \text{A1}'$ .



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**1**: Monoclinic,  $P2_1/a$ ,  $a=16.604(5)\text{\AA}$ ,  $b=4.950(2)$ ,  $c=8.304(2)$ ,  $\beta=100.28(2)^\circ$ ,  $Z=2$ ,  $R=0.034$ .  
**2**: Monoclinic,  $P2_1/a$ ,  $a=17.038(4)\text{\AA}$ ,  $b=4.899(1)$ ,  $c=8.256(2)$ ,  $\beta=98.60(2)^\circ$ ,  $Z=2$ ,  $R=0.062$ .
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