Acknowledgements. This work has been supported by the Swedish Natural Science Research Council. I am indebted to Dr. C. R. Creveling for most valuable discussions of this manuscript and to Drs. S. Agurell and J. E. Lindgren for assistance in recording the mass spectra. Invaluable technical assistance of Miss E. Hansson is gratefully acknowledged.

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Received March 11, 1972

## The Structure of 2,5-Diphenyl-3methyl-6a-thiathiophthene ASBJØRN HORDVIK, ODDVAR SJØLSET and LEIF J. SÆTHRE

Chemical Institute, University of Bergen, N-5000 Bergen, Norway

NDO/2 calculations on mono-methyl Jand mono-phenyl substituted 6a-thiathiophthenes show that a 3-methyl group causes a shortening of the S(1) - S(6a) bond relative to that in 6a-thiathiophthene, while a twisted 2-phenyl group causes a lengthening of this bond.<sup>1,2</sup> The lengthening effect of the 2-phenyl group on S(1) - S(6a)varies with the twist angle, being negligible at twist angle 0° and most pronounced at 90°.1

investigation 2.5 structure diphenyl-3-methyl-6a-thiathiophthene (I) has been carried out in order to test the CNDO/2 predictions; the preliminary results are given.

The sulphur-sulphur bonds in I are S(1) - S(6a) = 2.255(1) Å and S(6a) - S(6)=2.398(1) Å, and the 2- and 5-phenyl groups are twisted 56.7 and 23.7° about the respective connecting bonds. Thus, the effect of phenyl group 2 on the S-S bonding is opposed by the effect of phenyl group 5, and it seems likely that it is the 3methyl group which has caused the shortening of S(1) - S(6a) in agreement with the results from the CNDO/2 calculations.

Other bond lengths in the 6a-thiathiophthene system of I are: S(1) - C(2) =A, S(6a) - C(3a) = 1.749(2)1.714(2)S(6) - C(5) = 1.698(2) Å, C(2) - C(1.377(2) Å, C(3) - C(3a) = 1.429(3)C(2) - C(3) =C(3a) - C(4) = 1.406(2) Å, and C(4) - C(5)=1.374(3) Å.

A sample of 2,5-diphenyl-3-methyl-6athiathiophthene was generously supplied by M. Stavaux.<sup>3</sup> The crystals are dark red and belong to the monoclinic space group  $P2_1/c$ . The cell dimensions are a = 15.463(2)Å, b=8.015(1) Å, c=13.076(2) Å, and  $\beta=106.38(1)^{\circ}$ . There are four molecules per unit cell; density, calculated 1.393 g/cm<sup>3</sup>, found 1.388 g/cm<sup>3</sup>.

The structure analysis is based on X-ray data collected on a paper-tape controlled Siemens AED diffractometer using  $CuK\alpha$ radiation. 2865 reflections were observed within  $\theta = 71^{\circ}$ .

The structure was solved by the heavy atom (S) method and refined by full matrix least squares. The final R factor is 0.033.

The authors are indebted to Dr. M. Stavaux, Faculté des Science de Caen, France, for providing a sample of 2,5-diphenyl-3-methyl-6athiathiophthene.

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Received March 8, 1972.