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The Crystal Structures of Aflatoxin B₁. II. The Structure of an Orthorhombic and a Monoclinic Modification

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If aflatoxin B₁ is recrystallized from a chloroform-ethanol mixture, both an orthorhombic and a monoclinic modification are formed. The orthorhombic crystals have the unit-cell constants $a = 7.84$, $b = 6.36$ and $c = 28.35$ Å and the space group is $P2_12_12_1$, while the constants for the monoclinic crystals are $a = 7.93$, $b = 6.21$, $c = 14.04$ Å and $\alpha = 95.8^\circ$. Their space group is $P2_1$. The crystal structures of the two modifications have been solved with the aid of the structure of aflatoxin B₁·CHCl₃ already known. The orientations of the aflatoxin B₁ molecule were assumed to be the same in all three structures and the positions of the molecules were determined by calculating the value of the residual while they were moved systematically through the unit cell. Both structures consist (just as the structure of aflatoxin B₁·CHCl₃) of strings of coplanar molecules in the directions [110] and $\bar{1}\bar{1}0$. The molecules within a string have again two short CH₃···O contacts: 2.97 and 3.18 Å for the orthorhombic form and 3.00 and 3.10 Å for the monoclinic form. These short contacts point to an interaction between the molecules and may be called hydrogen bonds.

Introduction

If aflatoxin B₁ is recrystallized by diffusion of ethanol (in which it is only slightly soluble) into a saturated solution of the toxin in chloroform, crystals containing chloroform (modification I) are formed (van Soest & Peerdeman, 1970*a*). However, if a solution of the toxin in a mixture of chloroform and ethanol is slowly evaporated, two new modifications (II and III) are formed. Their crystal structures were determined in order to compare them with the crystal structures already found for aflatoxin B₂ (van Soest & Peerdeman, 1970*b*) and for aflatoxin B₁·CHCl₃.

Experimental

For both modifications, the unit-cell dimensions were determined from Weissenberg and rotation photographs; their space groups followed from the systematically absent reflexions. The intensities were measured automatically with a PAILRED diffractometer, using nickel-filtered copper radiation. The monochromator was not applied in view of the small scattering power of the crystals. The intensities were corrected for Lorentz and polarization factors.

Most of the crystals obtained from the chloroform-ethanol solution are thin pale-yellow platelets. They

are monoclinic with the space group P2₁. The unit cell angles are 95.8°; it contains two molecules. For the intercellular dimensions a=7.93, b=6.21, c=14.04 Å

Table 1(a). Observed and calculated structure factors (×10) and phase angles of the orthorhombic modification

Table with multiple columns for h, k, l, F_o, F_c, ARG, and F_o-F_c ARG. The table lists crystallographic data for various reflections, including observed and calculated structure factors and their phase angles.

with the aid of Fig. 5 of the preceding paper (van Soest & Peerdeman, 1970a). This figure shows a projection of the structure of aflatoxin B₁. CHCl₃ along the *a* axis. Within a period of 36.25 Å, there are two aflatoxin B₁ layers separated by a chloroform layer. The shortening of the *c* axis of the orthorhombic form to a value of 28.35 Å can be explained from the absence of the chloroform layers and a further shortening to a value of 14.04 Å in the case of the monoclinic form can be accounted for by 'removing' one of the two aflatoxin B₁ layers.

In view of this it seems likely that the orientations of the aflatoxin B₁ molecule will be the same in all three structures. This assumption was easily verified by making use of a simple technique. Coordinates of the molecules (calculated from those of the known structure I) were used to calculate the minimum residual functions $R(0YZ)$ and $R(XOZ)$. In other words, the *R* value defined as $\sum ||F_o| - |F_c|| / \sum |F_o|$ was repeatedly calculated for a number of reflexions when the molecule was systematically moved through the unit cell (e.g. van Soest & Peerdeman, 1970a). For the orthorhombic modification, 18 strong low-order *Ok*l reflexions and 20 strong low-order *h*0*l* reflexions were used. The minimum value of *R* was 0.10 for both functions. In this way, the approximate position of the molecule was determined and further refined by calculating $R(XYZ)$ for a small area with 47 strong low-order *hkl* reflexions. $R(XYZ)$ was 0.10 for the final position. The same procedure was followed for the monoclinic modification. For the space group $P2_1$, only the function $R(0YZ)$ needed to be calculated.

The structures were refined with the aid of an IBM 1800 computer, using a block-diagonal least-squares program. The *R* for the orthorhombic form decreased

without complications to a value of 0.053. The number of reflexions used was 1564. Thirty-five atomic positions, the anisotropic temperature factors of the 23 heavy atoms and one scaling factor were varied. During the refinement of the monoclinic form it appeared that the reflexions from 43*l* to 46*l* were systematically calculated too high. As they were measured separately from the others, a second scaling factor was introduced for these reflexions. The final *R* was 0.076 for the 1144 reflexions observed and 0.084 if the 64 zeros were included. The hydrogen atoms were given isotropic temperature factors equal to those of the carbon atoms to which they are bound; these factors were obtained from the refinement. The atomic scattering factors used in these refinements were taken from *International Tables for X-ray Crystallography* (1962). The final structure factors are detailed in Table 1 and the structural parameters in Tables 2 to 4. The arbitrary numbering of the atoms of the molecule is given in Fig. 1.

Table 3. Final parameters and e.s.d.'s ($\times 10^4$) and the isotropic temperature factors (Å) for the hydrogen atoms

Orthorhombic modification				
	<i>x/a</i>	<i>y/b</i>	<i>z/c</i>	<i>B</i>
H(1)	6093 (56)	5088 (73)	4987 (14)	2.9
H(2)	5182 (58)	6499 (73)	5368 (14)	2.9
H(3)	4639 (57)	2279 (77)	5281 (14)	2.7
H(4)	3835 (56)	3485 (71)	5700 (14)	2.7
H(5)	2110 (62)	6854 (79)	5715 (15)	4.1
H(6)	917 (63)	9179 (80)	5647 (15)	4.1
H(7)	1379 (63)	8441 (78)	6170 (15)	4.1
H(8)	3620 (57)	6354 (73)	6454 (14)	3.0
H(9)	9869 (60)	7368 (76)	6998 (14)	3.0
H(10)	8450 (59)	-5828 (74)	7203 (15)	3.4
H(11)	9113 (59)	403 (77)	7585 (15)	3.5
H(12)	7666 (61)	8057 (77)	8256 (15)	3.6

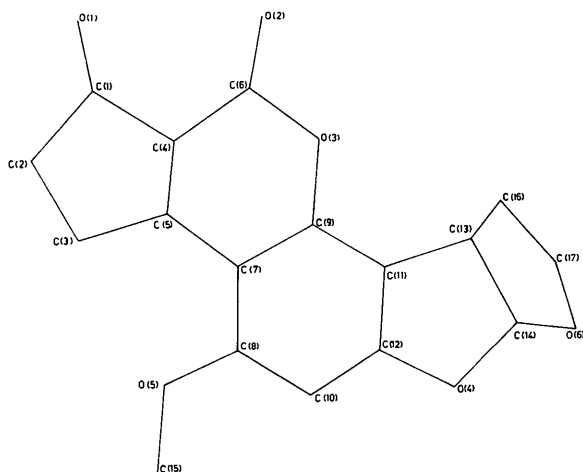
Table 2. Final positional parameters and e.s.d.'s ($\times 10^5$) for the non-hydrogen atoms

	Orthorhombic modification			Monoclinic modification		
	<i>x/a</i>	<i>y/b</i>	<i>z/c</i>	<i>x/a</i>	<i>y/b</i>	<i>z/c</i>
C(1)	75043 (58)	53704 (69)	55708 (13)	39165 (118)	63859 (117)	-60682 (45)
C(2)	58313 (58)	51418 (66)	53148 (13)	22927 (120)	62432 (119)	-55162 (50)
C(3)	49526 (55)	31993 (64)	55241 (12)	13910 (118)	41548 (119)	-59590 (48)
C(4)	76630 (53)	35499 (62)	58866 (13)	40810 (105)	44003 (110)	-67042 (44)
C(5)	62301 (49)	23397 (59)	58663 (12)	26747 (111)	31506 (107)	-66724 (41)
C(6)	90976 (58)	30920 (68)	61891 (14)	54811 (121)	37870 (125)	-73150 (51)
C(7)	60883 (50)	4999 (58)	61510 (12)	24975 (111)	11687 (102)	-72587 (43)
C(8)	46765 (51)	-8973 (64)	61602 (13)	10794 (110)	-2503 (116)	-72820 (47)
C(9)	74793 (47)	767 (60)	64570 (12)	38432 (110)	5746 (113)	-78751 (44)
C(10)	46459 (52)	-26617 (66)	64451 (13)	10715 (120)	-21867 (114)	-78671 (48)
C(11)	74637 (52)	-16816 (61)	67484 (12)	38441 (111)	-13016 (115)	-84782 (45)
C(12)	60720 (56)	-29825 (62)	67279 (13)	24454 (122)	-26361 (107)	-84383 (46)
C(13)	86793 (55)	-24198 (66)	71231 (13)	50393 (111)	-22523 (118)	-92471 (47)
C(14)	77945 (61)	-44821 (70)	72860 (14)	41316 (131)	-44311 (119)	-95696 (49)
C(15)	18581 (58)	-16057 (83)	58583 (18)	-16650 (120)	-8691 (142)	-66502 (67)
C(16)	86302 (62)	-11502 (68)	75705 (14)	49798 (123)	-11385 (117)	-1522 (41)
C(17)	78521 (61)	-22276 (83)	78990 (14)	42197 (135)	-23665 (131)	-8225 (54)
O(1)	85136 (47)	68025 (57)	55236 (12)	48846 (86)	79474 (81)	-59881 (35)
O(2)	4251 (42)	40052 (57)	62233 (12)	68384 (91)	46433 (99)	-73661 (44)
O(3)	88869 (35)	13244 (44)	64787 (9)	52632 (71)	18494 (76)	-79108 (31)
O(4)	62288 (40)	-46731 (44)	70200 (9)	25719 (89)	-44878 (75)	-90423 (34)
O(5)	33874 (37)	-3649 (37)	58685 (10)	-1792 (80)	4554 (83)	-66853 (37)
O(6)	73564 (44)	-42350 (52)	77662 (9)	36926 (96)	-43860 (87)	-5471 (34)

Table 3 (cont.)

Monoclinic modification

	<i>x/a</i>	<i>y/b</i>	<i>z/c</i>	<i>B</i>
H(1)	2880 (117)	6008 (112)	-4821 (53)	3.7
H(2)	1659 (123)	7543 (126)	-5491 (54)	3.7
H(3)	903 (126)	3154 (125)	-5400 (54)	3.7
H(4)	253 (121)	4444 (122)	-6289 (54)	3.7
H(5)	-1169 (137)	7317 (132)	-6305 (56)	4.4
H(6)	-2345 (133)	9946 (125)	-6169 (55)	4.4
H(7)	-2151 (134)	8698 (129)	-7217 (56)	4.4
H(8)	85 (123)	6819 (121)	-7901 (53)	3.7
H(9)	6358 (123)	7742 (123)	-9002 (50)	3.6
H(10)	4946 (123)	-6090 (124)	-9428 (55)	3.8
H(11)	5915 (121)	488 (128)	-115 (59)	3.8
H(12)	3784 (133)	7913 (127)	-1610 (57)	4.2

Fig. 1. Arbitrary numbering of the atoms of the aflatoxin B₁ molecule.

Discussion

The bond lengths and the bond angles (not corrected for thermal motion) of the aflatoxin B₁ molecules together with their standard deviations, are listed in Tables 5 and 6. Except for the outer dihydrofuran ring, the structure of the molecule is very similar to that of the aflatoxin B₂ molecule (*cf.* van Soest & Peerdeman, 1970*b*). Twenty of the 23 heavy atoms are approximately lying in one plane, just as the five atoms of the protruding dihydrofuran ring. The least-squares equations of these planes and the distances from the atoms to the planes are given in Table 7. Projections of the structures on the (100) plane are shown in Fig. 2(*a*) and (*b*). Comparison of the projection of the orthorhombic modification [Fig. 2(*a*)] with that of aflatoxin B₁·CHCl₃ shows that the first structure can be derived from the second by 'removing' the chloroform layers and by 'moving' the aflatoxin B₁ layers towards one another. The resulting packing of the cyclopentenone rings is rather close: the distances C(2)···O(1) and C(3)···O(1) are 3.24 and 3.32 Å respectively. If we also 'remove' one of the two aflatoxin B₁ layers, the monoclinic structure results [Fig. 2(*b*)] showing a different packing of the cyclopentenone rings. Except for the 3.35 Å of the C(3)···O(1) contact, none of its intermolecular distances is shorter than 3.40 Å.

The mode of packing of the aflatoxin B₁ layer has already been described (van Soest & Peerdeman, 1970*a*). It is now clear that this layer occurs in all three structures. It is characterized by strings of coplanar molecules in the directions [110] and $\bar{1}\bar{1}0$. The molecules within a string are coupled by an interac-

Table 4(*a*). Final thermal parameters and *e.s.d.*'s ($\times 10^5$) for the non-hydrogen atoms

Orthorhombic modification

The anisotropic temperature factor is defined as

$$\exp [-(\beta_{11}h^2 + \beta_{22}k^2 + \beta_{33}l^2 + 2\beta_{12}hk + 2\beta_{13}hl + 2\beta_{23}kl)].$$

	β_{11}	β_{22}	β_{33}	β_{12}	β_{13}	β_{23}
C(1)	1809 (80)	2171 (112)	104 (5)	-243 (94)	24 (18)	78 (21)
C(2)	1915 (82)	1816 (103)	98 (4)	-269 (91)	-44 (17)	73 (19)
C(3)	1655 (76)	1913 (106)	88 (4)	-170 (86)	-55 (17)	13 (19)
C(4)	1508 (72)	1864 (98)	90 (4)	-171 (78)	-3 (17)	12 (19)
C(5)	1210 (63)	1706 (93)	91 (4)	-47 (73)	32 (15)	-18 (18)
C(6)	1630 (78)	2103 (111)	129 (5)	-327 (90)	-11 (19)	84 (22)
C(7)	1355 (66)	1533 (89)	89 (4)	-190 (73)	31 (15)	31 (17)
C(8)	1342 (69)	2028 (126)	97 (4)	-302 (80)	-23 (16)	-21 (20)
C(9)	1080 (56)	1728 (93)	88 (4)	-30 (71)	17 (14)	-20 (18)
C(10)	1469 (72)	1971 (105)	105 (4)	-613 (83)	16 (16)	-0 (20)
C(11)	1335 (67)	1748 (96)	91 (4)	-46 (78)	-23 (16)	19 (18)
C(12)	1685 (77)	1684 (97)	93 (4)	-289 (84)	-6 (17)	69 (18)
C(13)	1501 (72)	2126 (110)	108 (4)	-136 (86)	1 (17)	122 (21)
C(14)	1932 (89)	2151 (116)	115 (5)	79 (100)	-29 (19)	68 (22)
C(15)	1438 (81)	3181 (150)	186 (7)	-763 (101)	-98 (22)	78 (30)
C(16)	1954 (92)	2262 (117)	116 (5)	-164 (98)	-111 (20)	82 (22)
C(17)	1889 (89)	3325 (150)	114 (5)	-33 (112)	-79 (19)	4 (26)
O(1)	2364 (74)	3468 (112)	205 (5)	-1382 (87)	-169 (18)	422 (21)
O(2)	1830 (64)	3600 (114)	227 (5)	-1493 (78)	-223 (17)	407 (23)
O(3)	1249 (47)	2114 (73)	128 (4)	-372 (55)	-56 (12)	118 (14)
O(4)	2132 (61)	1932 (75)	125 (4)	-466 (67)	-85 (14)	144 (15)
O(5)	1534 (53)	2494 (84)	160 (4)	-750 (63)	-149 (14)	154 (18)
O(6)	2343 (68)	3076 (96)	100 (3)	-617 (80)	11 (14)	114 (16)

tion between the methyl group and the carbonyl oxygen atoms O(1) and O(2), as is indicated by the short intermolecular distances of 2.97 and 3.18 Å of the or-

thorhombic modification and 3.00 and 3.10 Å of the monoclinic modification (see Fig. 2). Sutor (1963) has reported a number of crystal structures containing

Table 4(b). Final thermal parameters and *e.s.d.*'s ($\times 10^4$) for the non-hydrogen atoms

Monoclinic modification

The anisotropic temperature factor is defined as

$$\exp [-(\beta_{11}h^2 + \beta_{22}k^2 + \beta_{33}l^2 + 2\beta_{12}hk + 2\beta_{13}hl + 2\beta_{23}kl)] .$$

	β_{11}	β_{22}	β_{33}	β_{12}	β_{13}	β_{23}
C(1)	182 (18)	292 (21)	39 (3)	-13 (17)	-15 (6)	-6 (6)
C(2)	163 (18)	299 (22)	51 (3)	-36 (17)	13 (7)	-15 (7)
C(3)	159 (18)	291 (21)	47 (3)	-39 (16)	26 (7)	-19 (7)
C(4)	124 (16)	262 (19)	38 (3)	-30 (14)	-3 (6)	-10 (6)
C(5)	164 (17)	275 (19)	29 (3)	-14 (13)	-6 (6)	3 (6)
C(6)	174 (19)	329 (23)	49 (4)	-39 (18)	-0 (7)	-18 (8)
C(7)	143 (16)	225 (17)	35 (3)	-21 (14)	-5 (6)	-1 (6)
C(8)	137 (17)	279 (20)	44 (3)	-48 (15)	-8 (6)	10 (7)
C(9)	123 (16)	287 (19)	39 (3)	-27 (15)	-6 (6)	16 (6)
C(10)	178 (19)	247 (19)	48 (3)	-44 (15)	-1 (7)	-9 (7)
C(11)	132 (16)	286 (19)	40 (3)	-23 (15)	-5 (6)	-6 (7)
C(12)	200 (19)	232 (18)	43 (3)	-26 (16)	-3 (7)	-9 (6)
C(13)	147 (18)	306 (21)	45 (3)	-1 (17)	2 (7)	-13 (7)
C(14)	256 (23)	262 (21)	46 (3)	-1 (18)	3 (8)	-2 (7)
C(15)	101 (19)	395 (28)	94 (6)	-97 (19)	17 (9)	-14 (11)
C(16)	201 (20)	297 (21)	46 (4)	16 (19)	19 (7)	-3 (7)
C(17)	258 (25)	322 (24)	53 (4)	21 (20)	15 (8)	9 (8)
O(1)	213 (14)	304 (15)	53 (3)	-65 (13)	-1 (5)	-22 (5)
O(2)	185 (14)	411 (20)	88 (4)	-102 (14)	36 (6)	-64 (7)
O(3)	135 (12)	302 (14)	43 (2)	-37 (10)	4 (4)	-17 (5)
O(4)	252 (14)	245 (14)	57 (3)	-49 (12)	22 (6)	-22 (5)
O(5)	147 (12)	311 (15)	70 (3)	-70 (12)	33 (5)	-28 (5)
O(6)	273 (15)	351 (17)	45 (3)	-47 (14)	-3 (6)	-13 (5)

Table 5. Bond lengths and *e.s.d.*'s (Å) of the aflatoxin B₁ molecules

	Orthorhombic	Monoclinic		Orthorhombic	Monoclinic
C-C bonds					
<i>sp</i> ³ - <i>sp</i> ³					
C(2)-C(3)	1.534 (6)	1.554 (11)			
C(13)-C(14)	1.554 (6)	1.559 (11)			
<i>sp</i> ² - <i>sp</i> ³					
C(1)-C(2)	1.505 (6)	1.510 (12)			
C(3)-C(5)	1.497 (5)	1.517 (11)			
C(11)-C(13)	1.502 (5)	1.511 (11)			
C(13)-C(16)	1.504 (6)	1.508 (9)			
<i>sp</i> ² - <i>sp</i> ²					
C(1)-C(4)	1.469 (6)	1.453 (9)			
C(4)-C(6)	1.444 (6)	1.431 (11)			
C(5)-C(7)	1.426 (5)	1.417 (9)			
C=C bonds					
C(4)-C(5)	1.363 (6)	1.362 (11)			
C(16)-C(17)	1.307 (6)	1.298 (12)			
C...C bonds					
C(7)-C(8)	1.419 (6)	1.427 (11)			
C(7)-C(9)	1.419 (5)	1.400 (11)			
C(8)-C(10)	1.383 (6)	1.386 (10)			
C(9)-C(11)	1.391 (5)	1.369 (9)			
C(10)-C(12)	1.390 (6)	1.365 (12)			
C(11)-C(12)	1.370 (6)	1.389 (12)			
C=O bonds					
C(1)-O(1)	1.214 (6)	1.233 (10)			
C(6)-O(2)	1.195 (6)	1.206 (11)			
-C-O bonds					
C(14)-O(4)			1.445 (5)	1.436 (12)	
C(14)-O(6)			1.413 (5)	1.419 (8)	
C(15)-O(5)			1.435 (6)	1.441 (11)	
=C-O bonds					
C(6)-O(3)			1.402 (5)	1.405 (9)	
C(9)-O(3)			1.360 (5)	1.385 (9)	
C(8)-O(5)			1.349 (5)	1.347 (10)	
C(12)-O(4)			1.363 (5)	1.362 (8)	
C(17)-O(6)			1.387 (6)	1.412 (10)	
C-H bonds					
C(2)-H(1)			0.95 (4)	1.1 (1)	
C(2)-H(2)			1.01 (5)	1.0 (1)	
C(3)-H(3)			0.94 (4)	1.1 (1)	
C(3)-H(4)			1.02 (4)	1.0 (1)	
C(10)-H(8)			1.02 (5)	1.0 (1)	
C(13)-H(9)			1.01 (5)	1.1 (1)	
C(14)-H(10)			1.03 (5)	1.3 (1)	
C(15)-H(5)			1.07 (5)	1.3 (1)	
C(15)-H(6)			1.08 (5)	1.0 (1)	
C(15)-H(7)			0.96 (5)	0.9 (1)	
C(16)-H(11)			1.06 (5)	1.3 (1)	
C(17)-H(12)			1.04 (4)	1.1 (1)	

short CH...O contacts; these interactions would be due to hydrogen bonding.

Table 6. Bond angles and *e.s.d.*'s of the aflatoxin B₁ molecules

	Orthorhombic	Monoclinic
C(2)—C(1)—O(1)	125.9 (4)°	124.8 (7)°
C(4)—C(1)—O(1)	127.2 (4)	127.6 (7)
C(2)—C(1)—C(4)	106.9 (4)	107.6 (7)
C(1)—C(2)—C(3)	106.4 (3)	106.1 (7)
C(2)—C(3)—C(5)	104.2 (3)	103.1 (7)
C(1)—C(4)—C(5)	110.5 (3)	110.9 (7)
C(1)—C(4)—C(6)	125.9 (4)	126.6 (7)
C(5)—C(4)—C(6)	123.5 (3)	122.5 (7)
C(3)—C(5)—C(4)	111.8 (3)	111.9 (7)
C(3)—C(5)—C(7)	127.9 (3)	126.3 (7)
C(4)—C(6)—O(2)	128.9 (4)	129.5 (7)
C(4)—C(6)—O(3)	114.7 (4)	114.9 (7)
O(2)—C(6)—O(3)	116.4 (4)	115.5 (7)
C(5)—C(7)—C(8)	125.8 (3)	126.1 (7)
C(5)—C(7)—C(9)	116.2 (3)	116.3 (7)
C(8)—C(7)—C(9)	117.9 (3)	117.6 (7)
C(7)—C(8)—O(5)	114.5 (3)	114.1 (7)
C(7)—C(8)—C(10)	122.2 (3)	120.9 (7)
C(10)—C(8)—O(5)	123.3 (4)	125.0 (7)
C(8)—O(5)—C(15)	120.0 (3)	118.4 (7)
C(6)—O(3)—C(9)	122.5 (3)	122.6 (7)
C(7)—C(9)—O(3)	122.7 (3)	121.9 (7)
C(7)—C(9)—C(11)	120.6 (3)	122.5 (8)
O(3)—C(9)—C(11)	116.7 (3)	115.6 (7)
C(8)—C(10)—C(12)	116.2 (4)	117.3 (7)
C(9)—C(11)—C(12)	117.9 (3)	116.6 (8)
C(9)—C(11)—C(13)	131.8 (3)	133.5 (7)
C(12)—C(11)—C(13)	110.2 (3)	109.8 (6)
C(10)—C(12)—C(11)	125.1 (3)	125.0 (7)
C(10)—C(12)—O(4)	122.6 (3)	122.3 (8)
C(11)—C(12)—O(4)	112.3 (3)	112.7 (8)
C(11)—C(13)—C(14)	101.0 (3)	100.4 (7)
C(11)—C(13)—C(16)	114.3 (2)	113.8 (7)
C(14)—C(13)—C(16)	101.0 (3)	101.5 (6)
C(13)—C(14)—O(4)	107.1 (3)	108.2 (6)
C(13)—C(14)—O(6)	107.5 (3)	107.0 (6)
O(4)—C(14)—O(6)	107.8 (3)	106.8 (8)

Table 6 (cont.)

	Orthorhombic	Monoclinic
C(13)—C(16)—C(17)	109.3 (4)	109.9 (7)
C(16)—C(17)—O(6)	114.8 (4)	114.3 (7)
C(14)—O(6)—C(17)	107.2 (3)	107.3 (6)
C(12)—O(4)—C(14)	109.1 (3)	108.6 (7)
C(1)—C(2)—H(1)	107 (3)	96 (7)
C(1)—C(2)—H(2)	106 (3)	112 (7)
C(3)—C(2)—H(1)	116 (3)	112 (7)
C(3)—C(2)—H(2)	114 (3)	116 (7)
H(1)—C(2)—H(2)	106 (4)	112 (7)
C(2)—C(3)—H(3)	110 (3)	112 (7)
C(2)—C(3)—H(4)	115 (3)	114 (7)
C(5)—C(3)—H(3)	115 (3)	118 (7)
C(5)—C(3)—H(4)	109 (3)	111 (7)
H(3)—C(3)—H(4)	104 (4)	98 (7)
O(5)—C(15)—H(5)	111 (3)	106 (7)
O(5)—C(15)—H(6)	109 (3)	103 (7)
O(5)—C(15)—H(7)	107 (3)	116 (7)
H(5)—C(15)—H(6)	110 (4)	108 (7)
H(5)—C(15)—H(7)	116 (4)	105 (7)
H(6)—C(15)—H(7)	103 (4)	118 (7)
C(8)—C(10)—H(8)	116 (3)	122 (7)
C(12)—C(10)—H(8)	122 (3)	121 (7)
C(13)—C(14)—H(10)	114 (3)	115 (7)
O(4)—C(14)—H(10)	104 (3)	107 (7)
O(6)—C(14)—H(10)	116 (3)	112 (7)
C(11)—C(13)—H(9)	112 (3)	113 (7)
C(14)—C(13)—H(9)	114 (3)	120 (7)
C(16)—C(13)—H(9)	113 (3)	108 (7)
C(13)—C(16)—H(11)	122 (3)	113 (7)
C(17)—C(16)—H(11)	129 (3)	136 (7)
C(16)—C(17)—H(12)	132 (3)	133 (7)
O(6)—C(17)—H(12)	113 (3)	113 (7)

Thermal motion

The atomic vibration ellipsoids of the two molecules have been analysed in terms of rigid-body tensors of translation (**T**), libration (**L**) and screw motion (**S**) (Schomaker & Trueblood, 1968). All 23 heavy atoms were considered and the results of the analysis are given in Tables 8(a) and 8(b).

Table 7. Equations of the least-squares planes and the distances from the atoms to these planes

Orthorhombic modification				Monoclinic modification			
$-0.4219X + 0.5451Y + 0.7245Z - 10.8087 = 0$				$+0.4208X - 0.5550Y + 0.7176Z + 7.4222 = 0$			
C(1)	+0.016 Å	C(11)	+0.002 Å	C(1)	-0.032 Å	C(11)	-0.012 Å
C(2)	-0.036	C(12)	-0.031	C(2)	+0.072	C(12)	+0.024
C(3)	+0.011	C(13)	+0.114	C(3)	+0.012	C(13)	-0.117
C(4)	-0.019	C(14)	+0.026	C(4)	+0.020	C(14)	-0.018
C(5)	-0.007	C(15)	+0.053	C(5)	+0.015	C(15)	-0.023
C(6)	-0.031	O(1)	+0.082	C(6)	+0.038	O(1)	-0.161
C(7)	-0.014	O(2)	-0.083	C(7)	+0.006	O(2)	+0.140
C(8)	-0.013	O(3)	+0.020	C(8)	-0.004	O(3)	-0.011
C(9)	+0.008	O(4)	-0.069	C(9)	-0.007	O(4)	+0.051
C(10)	-0.029	O(5)	-0.001	C(10)	+0.028	O(5)	-0.022
$-0.8862X + 0.3716Y - 0.2768Z + 12.1932 = 0$				$+0.8803X - 0.3815Y - 0.2820Z - 7.1915 = 0$			
C(13)	+0.005	C(17)	+0.015	C(13)	+0.002	C(17)	-0.008
C(14)	+0.003	O(6)	-0.011	C(14)	-0.006	O(6)	+0.009
C(16)	-0.012			C(16)	+0.004		

Angle between the two planes
112.1°

112.3°

Table 8(a). Rigid-body thermal parameters

Orthorhombic modification

$$T = \begin{pmatrix} 360 & -39 & 26 \\ & 337 & -17 \\ & & 331 \end{pmatrix} \times 10^{-4} \text{ \AA}^2$$

$$\sigma(T) = \begin{pmatrix} 16 & 14 & 14 \\ & 15 & 14 \\ & & 15 \end{pmatrix} \times 10^{-4} \text{ \AA}^2$$

$$L = \begin{pmatrix} 52 & -29 & 48 \\ & 92 & -62 \\ & & 120 \end{pmatrix} \times 10^{-1} (\text{^\circ})^2$$

$$\sigma(L) = \begin{pmatrix} 6 & 5 & 6 \\ & 8 & 6 \\ & & 8 \end{pmatrix} \times 10^{-1} (\text{^\circ})^2$$

Unique origin (\AA)* 4.884 0.429 17.699

Principal axes of I†

Eigenvalue	Direction cosines ($\times 10^4$)		
1265 \AA ²	-775	7187	-6910
2738	-8458	-4143	-3360
3671	-5278	5584	6400

Principal axes of T‡

Eigenvalue	Direction cosines ($\times 10^4$)		
0.0402 \AA ²	-7421	5122	-4321
0.0310	6621	4608	-5908
0.0296	-1035	-7246	-6812

Table 8(a) (cont.)

Principal axes of L

Eigenvalue	Direction cosines ($\times 10^4$)		
19.2 (\text{^\circ}) ²	-3710	5657	-7363
4.5	-3604	-8185	-4472
2.7	-8558	994	5075

R.m.s. difference between 'observed' and calculated U_{ij} : $50 \times 10^{-4} \text{ \AA}^2$.

* This origin symmetrizes S.

† Calculated for the unique origin, using atomic weights instead of mass weights.

‡ Calculated after S had been symmetrized.

Table 8(b). Rigid-body thermal parameters

Monoclinic modification

$$T = \begin{pmatrix} 406 & -52 & -16 \\ & 498 & -38 \\ & & 386 \end{pmatrix} \times 10^{-4} \text{ \AA}^2$$

$$\sigma(T) = \begin{pmatrix} 19 & 16 & 17 \\ & 17 & 16 \\ & & 17 \end{pmatrix} \times 10^{-4} \text{ \AA}^2$$

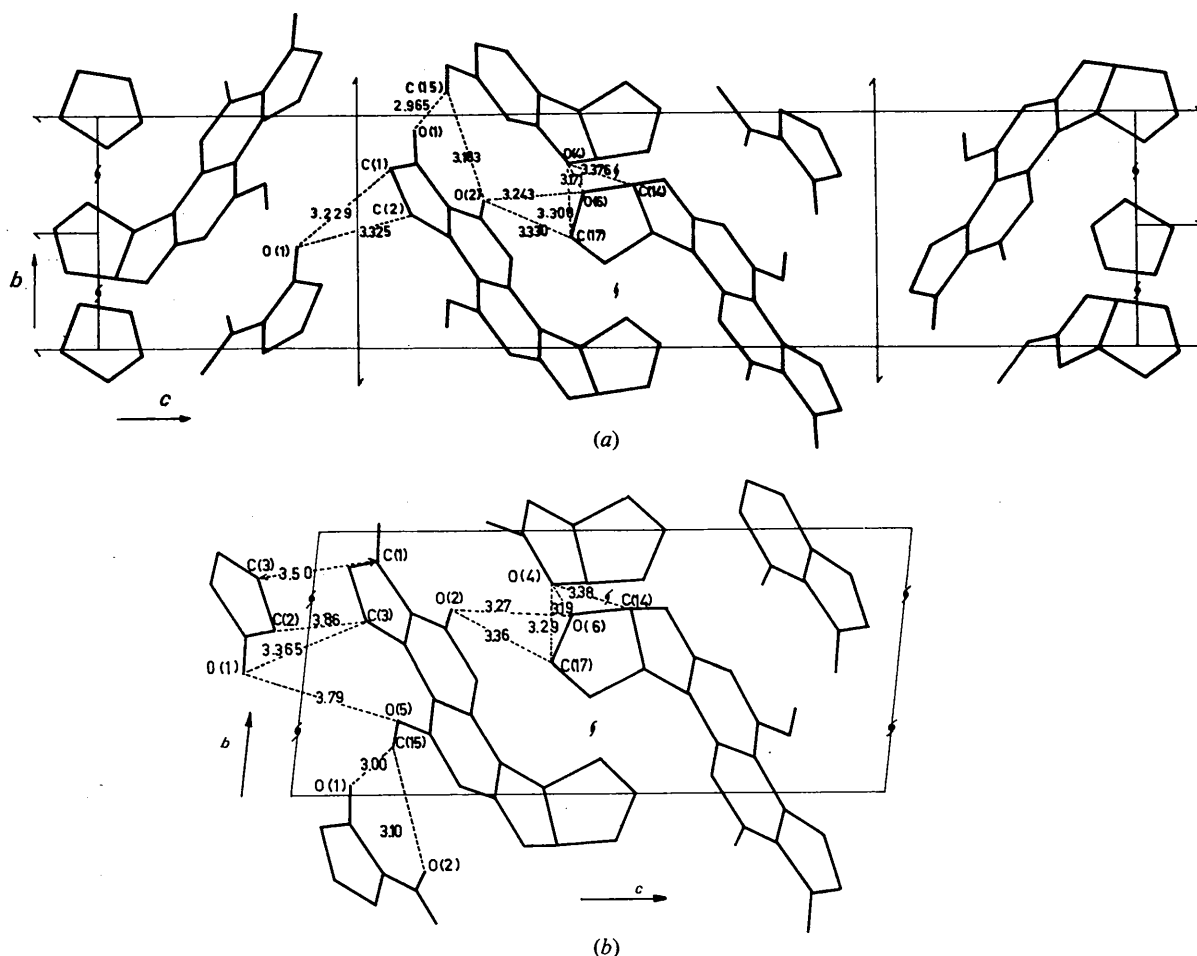


Fig. 2. Projection of the structure of aflatoxin B₁ on the (100) plane: (a) orthorhombic modification; (b) monoclinic modification.

Table 8(b) (cont.)

$$L = \begin{pmatrix} 26 & -17 & -20 \\ & 92 & 49 \\ & & 103 \end{pmatrix} \times 10^{-1} (^\circ)^2$$

$$\sigma(L) = \begin{pmatrix} 6 & 6 & 7 \\ & 9 & 8 \\ & & 10 \end{pmatrix} \times 10^{-1} (^\circ)^2$$

Unique origin (Å)*	2.292	2.134	-10.356
Principal axes of I†	Direction cosines ($\times 10^4$)		
Eigenvalue	-755	7130	6970
1217 Å ²	-8591	-4014	3176
2832	5063	5748	6428
3721	Direction cosines ($\times 10^4$)		
Eigenvalue	-3560	9137	-1930
0.0524 Å ²	-6827	-1141	7228
0.0405	6381	3907	6630
0.0346	Direction cosines ($\times 10^4$)		
Eigenvalue	2037	-6531	-7292
15.2 (°) ²	197	7475	-6638
4.8	9788	1228	1635
2.0	Direction cosines ($\times 10^4$)		

R.m.s. difference between 'observed' and calculated U_{ij} : 59×10^{-4} Å².

* This origin symmetrizes S.

† Calculated for the unique origin, using atomic weights instead of mass weights.

‡ Calculated after S had been symmetrized.

The r.m.s. deviation between the thermal parameters obtained by the least-squares refinement and those calculated from the rigid-body tensors is 0.0050 Å² for the orthorhombic and 0.0059 Å² for the monoclinic modification.

The translation tensors are slightly anisotropic; however, an explanation for the directions of their prin-

cipal axes could not be found. The libration tensors are clearly anisotropic in both cases: one of the principal axes is always appreciably longer than the other two.

The inertia tensors I (the principal axes and their directions with respect to an orthogonal axial system) for the two aflatoxin B₁ molecules were calculated using the unique origins obtained by symmetrizing the screw tensors S. The tensors I have one principal axis being appreciably shorter than the other two. The angle between the largest principal axis of the libration tensor and the smallest principal axis of the inertia tensor is 19° for the orthorhombic form and 8° for the monoclinic form.

The same anisotropy of the libration tensors has also been observed for the aflatoxin B₂ molecule and for the aflatoxin B₁ molecule of modification I. For both molecules, the axes showing the highest degree of libration are also approximately parallel to the axes, the moment of inertia of which is smallest; the angles between the corresponding axes are 3° and 11° respectively.

The conclusion seems justified that in all four structures, the libration of the aflatoxin molecule is influenced by its moment of inertia.

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