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HEPTITOL CONFORMATIONS REVISITED: C,O *versus* O,O PARALLEL 1,3-INTERACTIONS*†

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ABSTRACT

The molecular and crystal structure of D-*glycero*-L-*allo*-heptitol has been determined. It crystallises in the orthorhombic space-group $P2_12_12$ with a = 8.399(2), b = 23.484(8), c = 4.664(2) Å, $\alpha = \beta = \gamma = 90°$, and Z = 4. The heptitol was found to be in the $_3G^-$ form, which has a 1,3-parallel interaction between C-2 and O-5. In solution, as determined by ^{1}H-n.m.r. spectroscopy, the heptitol and its hepta-acetate also assume conformations which have a C,O parallel interaction. Such an interaction has also been found to occur in several other heptitols and in hexose dialkyl acetals. Because conformers with such an interaction had been disregarded in the past, the conformations of several heptitols had been wrongly assigned.

INTRODUCTION

In an important but seldom quoted paper, Mills[2] discussed the conformations of the higher alditols in solution. He realised that, for a chain of more than six carbon atoms, there will be diastereomers which can have no conformation free from 1,3-parallel interactions. He defined the circumstances under which such a condition would occur; thus, no alditol having a sequence of three consecutive centres of *ribo* configuration that is separated from each end of the chain by at least

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one asymmetric centre can avoid having some 1,3-parallel interaction. By the study of stereomodels, and from theoretical considerations, he predicted the most probable conformation for each of the ten heptitols; on the basis of their ^{13}C-n.m.r. spectra, we concluded that these predictions were correct[1].

Mills's definition can be slightly extended. It is not necessary that each carbon atom adjacent to the *ribo* sequence be asymmetrical; it is sufficient that it be bonded to three atoms larger than hydrogen. With this extension, the definition also embraces the aldose dimethyl acetals and diethyl dithioacetals, the conformations of which have been extensively studied[3–6]. The *allo* and the *talo* diastereomers can have no conformation free from 1,3-parallel interactions.

The conformations of the alditols, up to the hexitols, have been successfully interpreted by the postulate that 1,3-parallel interactions between substituents are avoided[7]. In the study of those heptitols for which such interactions are unavoidable, conformations were postulated having 1,3-parallel interactions between oxygen atoms. Mills[2], as well as Horton and co-workers[3–7] and the present authors[1,8,9], assumed, tacitly or explicitly, that conformations with 1,3-parallel interactions between an oxygen atom and the carbon chain need not be considered because they would be too unstable. This reasonable assumption was based on the well documented fact that the *syn*-axial interaction (which is a special case of 1,3-interaction) in cyclohexanes and pyranoses between carbon and oxygen atoms is greater than that between two oxygen atoms*.

We now show that conformations containing C,O parallel interactions (usually designated as C//O) not only occur in solutions of several heptitols but also are frequently more stable than those containing O,O parallel interactions (O//O). Consequently, some of Mills's predicted conformations, though apparently confirmed by us[1], proved to be wrong.

RESULTS

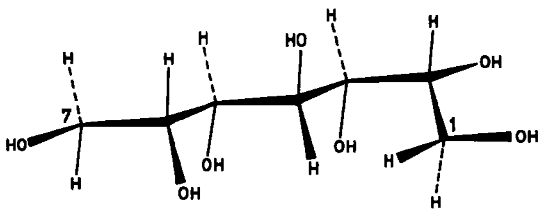
It was concluded by Mills[2] and by Angyal and Le Fur[1] that D-*glycero*-L-*allo*-heptitol is preponderantly in the $_2G^+$ conformation (**1a**) which has two hydroxyl groups in the O//O arrangement. In the crystalline state, the repulsive interactions between the two hydroxyl groups could be reduced by an intramolecular hydrogen-bond; although such a bond is rare in acyclic polyols[15], it has been found in the crystals of one form of potassium D-gluconate[16] and of D-talose diethyl dithioacetal[17]. It was of interest therefore to determine whether it also occurred in

*An interaction energy of 10.5–10.9 kJ.mol^{-1} (2.5–2.6 kcal.mol^{-1}) was found between a methyl group on C-5 and HO-1 of a pyranose in aqueous solution[10]; this value is likely to be too high because C-1 and C-5 are closer to each other than carbon atoms in a cyclohexane ring. For a 2-propanol solution, a value of 10.0 kJ.mol^{-1} (2.4 kcal.mol^{-1}) was obtained[11] and the same value was also derived from kinetic data for an ethanol solution[12]. A much lower value of 6.7 kJ.mol^{-1} (1.6 kcal.mol^{-1}) was derived for cyclitols in aqueous solution by Angyal *et al.*[13]. The accepted value[14] for the *syn*-axial OH–OH interaction in aqueous solution is 8.0 kJ.mol^{-1} (1.9 kcal.mol^{-1}).

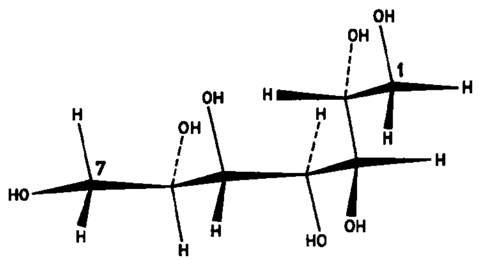
the crystals of D-*glycero*-L-*allo*-heptitol. An X-ray crystal structure determination was carried out and is fully described below; it showed, however, that the alditol does not assume the $_2G^+$ form (**1a**) in the crystal but the $_3G^-$ form (**1b**). This conformation has a C//O interaction between C-2 and O-5, rather than an O//O interaction.

Although Jeffrey and Kim[18] found that the preponderant conformation of hexitols in solution also occurs in their crystal form, this is not necessarily true for all alditols. Hence, we thought it advisable to confirm the conformation in solution by the use of ^{1}H-n.m.r. spectroscopy. In the past, this would have been a very difficult proposition, all signals in the spectra of the alditols being close to each other (usually between δ 3.6 and 4.0). Recently, however, the ^{1}H-n.m.r. spectra of all of the hexitols have been assigned[19] at 400 MHz; even at this high field, extensive computer simulation and deuterium labelling were required because the spectra were still very second order.

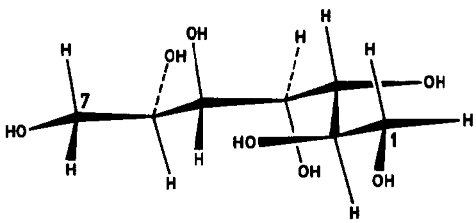
In the 300-MHz ^{1}H-n.m.r. spectrum of D-*glycero*-L-*allo*-heptitol, several signals could not be identified and assigned. One part of the spectrum that could be analysed is the upfield multiplet that contains three protons, all of which were assigned to methylene protons since each possesses a coupling constant of ~12 Hz. One pair of coupled protons has couplings of 4.95 and 7.72 Hz. These values, and



1a



1b



1c

the small difference in the chemical shifts, are typical[19] of a methylene group adjacent to a *threo*-diol; hence, they were assigned to H-7,7, and the third signal to one of the H-1 protons. The rest of the spectrum was assigned by using two-dimensional techniques[20]. Analysis of the 2D-COSY spectrum in the light of the above assignments led to the assignments of H-1, H-2, and H-6, the latter being the most deshielded proton. The assignment of H-5 followed, since it is coupled to H-6. The remaining two protons have obviously very similar chemical shifts and are slightly shielded relative to H-2. Close inspection of the 1D spectrum, in conjunction with the COSY, led to the assignment of a number of lines in the 1D spectrum to a specific proton. It was evident that a number of lines are the result of a tightly coupled system. The 2D J-resolved spectrum reinforced the assignments already made, but did not help in the identification of the last two protons; it was useful for determining a number of apparent coupling constants. At this stage, approximate chemical shifts were known for each proton, as were all apparent coupling constants with the exception of $J_{3,4}$. Therefore, a theoretical spectrum was calculated using the Bruker program PANIC. This spectrum, calculated with the values given in Tables I and II, was essentially identical with that obtained experimentally (the difference between calculated and experimental values being <0.15 Hz for each resonance). The calculated difference between the chemical shifts of H-3 and H-4 is 0.01 p.p.m. (3 Hz). The final experiment was a 2D C–H shift-correlated spectrum, which confirmed the proton assignments and gave a shift difference of 4 Hz between H-3 and H-4. The results are shown in Tables I and II.

From consideration of its ^{13}C-n.m.r. spectrum, Angyal and Le Fur[1] concluded that D-*glycero*-L-*allo*-heptitol is mainly in the $_2G^+$ (**1a**) conformation but that some of the $_3G^+$ and the $_3G^-$ forms may also be present. The $^3J_{H,H}$ coupling constants now show that the $_3G$ forms are, in fact, preponderant, and the $_2G^+$ form is only a minor component (~40%). The C-3–C-7 segment of the molecule is clearly a planar zigzag. For the $_2G^+$ form, the expected values[19,21] of $J_{2,3}$ and $J_{3,4}$ are 2.3 and 9.6 Hz, respectively, and for the $_3G$ forms, 9.6 and 2.3 Hz, respectively. The experimental values are closer to the latter.

Coupling constants, alone, do not always define the conformation of an alditol in solution. A large coupling (~9 Hz) shows that the two hydrogen atoms are antiperiplanar, a small one (~2 Hz) that they are *gauche*. Intermediate values usually indicate that more than one conformation is present in substantial amounts, but may also indicate a conformation in which the torsional angles deviate from the usual staggered geometry.

Whereas a large $^3J_{H,H}$ value defines an antiperiplanar relationship, a small one allows for two possible *gauche* forms; hence, the coupling constants do not differentiate between the $_3G^+$ and the $_3G^-$ forms. In such cases, in the past, a choice was often made on the basis that one of the *gauche* forms contained a 1,3-parallel interaction and was therefore regarded as less stable[22]. In the present instance, both the $_3G^+$ and the $_3G^-$ form have one C//O interaction. A choice is possibly provided by the ^{13}C-n.m.r. spectrum. It was pointed out[1] that the position of the C-4 signal is diagnostic. In the spectrum of D-*glycero*-L-*allo*-heptitol, this signal is at lower field than that for any other heptitol. This finding is explained by the presence of one H//O interaction and a *gauche* arrangement in the $_3G^+$ form (**1c**); in the $_3G^-$ form (**1b**), with two H//O interactions, this signal would be at higher field.

Confirmation of the preponderance of the $_3G^+$ form is provided by a comparison of the ^{1}H-n.m.r. data for H-7 to H-3 of the heptitol with those for H-1 to H-5 of altritol[19]. In these segments, the hydrogen atoms of the two alditols have the same environments if the heptitol is in the $_3G^+$ form, altritol being in the $_4G^+$ form[8,19]. The good agreement shows that the two conformations are similar; if the heptitol were in the $_3G^-$ form, H-4 and H-5 would resonate at higher field (being in 1,3-parallel relation to O-2 and O-3, respectively), and H-3 would resonate at lower field (not now being in 1,3-parallel relation to O-5).

The $_3G^+$ (**1c**) and the $_3G^-$ (**1b**) form have the same number of *gauche* and 1,3-parallel interactions. It is not clear why one should be favoured. Calculation by group interactions derived from six-membered rings[11,23], when applied to this heptitol, gives the same free energy for the two $_3G$ forms and a slightly lower one for the $_2G^+$ form (**1a**); it is apparent that these values are not readily applicable to acyclic systems.

Conformations of the heptitol acetates. — In view of these anomalies, it appeared worthwhile to reinvestigate also the conformation of the hepta-acetate of D-*glycero*-L-*allo*-heptitol in solution (together with that of three other acetates). Analysis of the ^{1}H-n.m.r. spectra again proved to be difficult, but was solved by the use of heteronuclear ^{13}C–^{1}H correlation by the Reverse DEPT method[24] and simulation by the PANIC program. Details of these analyses will be published elsewhere[25]. The results are given in Tables I and II.

The coupling constants of D-*glycero*-L-*allo*-heptitol hepta-acetate are similar to those of the free heptitol. Again, the $_2G^+$ form is a minor component; the $_3G^+$ and/or the $_3G^-$ forms are preponderant. The observation of a coupling of −0.4 Hz between H-3 and H-5 indicates *anti-gauche* bonds between these two hydrogen atoms (analogous to a $^4J_{e,a}$ coupling in a six-membered ring[26]), in accordance with the $_3G^-$ form. On the other hand, comparison with the chemical shifts of D-altritol hexa-acetate (which are also shown in Table I) favours the $_3G^+$ form. Whichever $_3G$ form it is, it will have a C//O interaction.

The opportunity was taken to look again at the conformation of those heptitol acetates which showed a poor agreement of their ^{13}C shifts with those of the homologous hexitol acetates[1]. The coupling constants of D-*glycero*-L-*galacto*-heptitol hepta-acetate* (Table II) show that it is in the $_5G^+$ form, confirming the

*A recent paper[27] lists the ^{1}H-n.m.r. data of D-*glycero*-D-*gluco*- and L-*glycero*-D-*galacto*-heptitol hepta-acetates. However, inspection of their formulae and perusal of their methods of preparation show that both compounds were wrongly named. In fact, the published data refer to *meso-glycero-gulo*- and D-*glycero*-D-*manno*-heptitol, respectively. The data in this paper confirm the planar zigzag conformation proposed[1] for D-*glycero*-D-*galacto*-heptitol hepta-acetate and the $_5G^+$ conformation for D-*glycero*-D-*manno*-heptitol hepta-acetate, and show that *meso-glycero-gulo*-heptitol hepta-acetate is mainly in the $_2G^+$,$_3G^+$ and the enantiomeric $_2G^-$,$_3G^-$ forms.

TABLE I

PROTON CHEMICAL SHIFTS (P.P.M.) FOR SOME HEPTITOLS AND THEIR ACETATES[a]

Heptitol	*H-1*$_R$	*H-1*$_S$	*H-2*	*H-3*	*H-4*	*H-5*	*H-6*	*H-7*$_R$	*H-7*$_S$
D-*glycero*-L-*allo*-Heptitol	3.66	3.82	3.94	3.88	3.87	3.80	3.97	3.66	3.67
—, hepta-acetate	4.09	4.39	5.21	5.29	5.29	5.43	5.33	3.93	4.29
D-*glycero*-L-*galacto*-Heptitol, hepta-acetate	3.84	4.29	5.25	5.25	5.36	5.34	5.10	4.14	4.39
D-*glycero*-D-*gluco*-Heptitol, hepta-acetate	4.32	3.96	5.39	5.46	5.43	5.12	5.21	4.19	4.37
D-*glycero*-L-*gulo*-Heptitol, hepta-acetate	4.13	4.24	4.99	5.41	5.35	5.22	5.47	4.02	4.19
meso-glycero-altro-Heptitol	3.61	3.61	3.93	~3.73	~3.77				
D-Altritol, hexa-acetate	3.97	4.28	5.34	5.38	5.30	5.22	4.35	4.17 (H-6$_R$)	

[a]Free heptitols in deuterium oxide; acetates in deuteriochloroform.

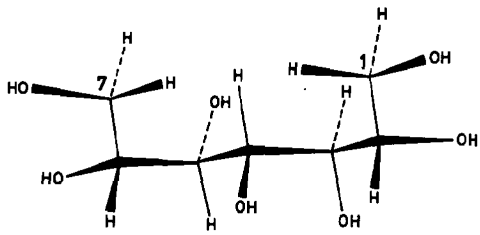
TABLE II

PROTON-PROTON COUPLING CONSTANTS (Hz) FOR SOME HEPTITOLS AND THEIR ACETATES

Heptitol	$J_{1R,1S}$	$J_{1R,2}$	$J_{1S,2}$	$J_{2,3}$	$J_{3,4}$	$J_{3,5}$	$J_{4,5}$	$J_{5,6}$	$J_{6,7R}$	$J_{6,7S}$	$J_{7R,7S}$
D-*glycero*-L-*allo*-Heptitol	−11.88	7.10	3.30	6.43	4.99		7.60	1.77	7.72	4.95	−11.49
—, hepta-acetate	−12.3	6.0	2.85	6.5	3.3	−0.4	8.65	2.95	7.0	4.95	−11.7
D-*glycero*-L-*galacto*-Heptitol, hepta-acetate	−11.8	7.4	4.9	2.0	9.2		2.3	7.8	5.6	3.3	−12.4
D-*glycero*-D-*gluco*-Heptitol, hepta-acetate	−11.7	5.2	6.4	4.5	6.35		4.35	7.0	4.8	2.65	−12.45
D-*glycero*-L-*gulo*-Heptitol, hepta-acetate	−12.6	4.75	2.9	7.65	2.7		8.0	3.3	6.55	4.9	−11.7
meso-glycero-altro-Heptitol	−11.0	6.8	5.0	1.8	~7						
D-Altritol, hexa-acetate	−11.8	6.75	4.9	3.3	8.0		3.6	3.4		7.3 ($J_{5,6R}$)	−12.1 ($J_{6R,6S}$)

explanation advanced for this discrepancy[1]. The coupling constants of D-*glycero*-L-*gulo*-heptitol hepta-acetate (which were obtained without the need to use heteronuclear ^{13}C-^{1}H correlation) show that it is in the $_4G^-$ form, as postulated for the free heptitol[1].

The hepta-acetate of D-*glycero*-D-*gluco*-heptitol*, however, is clearly *not* in the $_2G^-$,$_5G^+$ form (**2**) observed for the parent heptitol; the coupling constants for this form would be[19,21] 9.6, 0.5, 9.6, and 2.3 Hz, respectively, from $J_{2,3}$ to $J_{5,6}$. The coupling constants indicate the presence of more than one form, but the preponderant one (~2/3) appears to be $_3G^+$,$_4G^+$ (**3**), for which the expected J values are 0.5, 9.6, 2.3, and 9.6 Hz, respectively. This conformation has a 1,3-parallel interaction between C-3 and O-6. Hence, the poor agreement of the ^{13}C-n.m.r.



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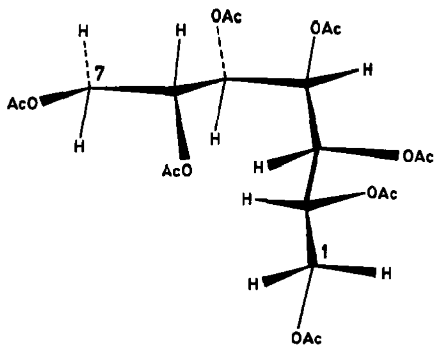

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data between this compound and the homologous hexitol acetates[1] correctly showed that the conformations are different. There is no reason, however, to doubt that the free heptitol is in the $_2G^-$,$_5G^+$ form (**2**) as shown by the excellent agreement of its ^{13}C-n.m.r. data with those of the corresponding hexitols and with the C-5–C-7 segment of D-*glycero*-D-*manno*-heptitol in the $_5G^+$ conformation.

DISCUSSION

D-*glycero*-L-*allo*-Heptitol, its hepta-acetate, and D-*glycero*-D-*gluco*-heptitol hepta-acetate represent three cases in which the preponderant conformation in solution has a C//O interaction. A search of the literature disclosed several other such instances.

Less than half of hexa-*O*-acetylallitol is in the $_2G^-,_4G^+$ form[9] which is free from 1,3-parallel interactions. This form would have $J_{2,3}$ 2.3, $J_{3,4}$ 9.6, and $J_{4,5}$ 2.3 Hz; the values found were 5.6, 4.3, and 5.6 Hz, respectively. The main components of the conformational equilibrium are therefore forms which have large $J_{2,3}$ and $J_{4,5}$ and small $J_{3,4}$ values, namely, $_3G^+$ and $_3G^-$ (which are enantiomers). Both of these forms have a C//O interaction.

It has not been realised until quite recently, owing to lack of accurate n.m.r. data[28], that free allitol in deuterium oxide also constitutes a conformational mixture[19]. Although the proportion of the $_3G^+$ and $_3G^-$ forms is somewhat less than in the equilibrium mixture of the acetate, it is still considerable (~43% according to Hawkes and Lewis[19]). This case, therefore, is closely similar to that of D-*glycero*-L-*allo*-heptitol, except that here the alternative to the $_3G$ forms, namely, the $_2G^-,_4G^+$ form, has no parallel interaction. Apparently, the two "unfavourable" *gauche* interactions[1] in the latter are of similar magnitude to the C//O interaction in the former forms.

Among the dimethyl acetals and diethyl dithioacetals studied by Blanc-Muesser *et al.*[3], there are four which cannot be free from 1,3-parallel interactions. D-Talose dimethyl acetal penta-acetate is in a conformation ($_2G^+$) which has a C//O interaction between one O-1 and C-4. The corresponding diethyl dithioacetal penta-acetate is a conformational mixture in which no single form can be clearly defined. D-Allose diethyl dithioacetal penta-acetate is mainly in the $_3G^-$ form, with a C//O interaction between C-5 and O-2 (or possibly in the $_3G^+$ form, with such an interaction between C-2 and O-5). This compound is analogous to D-*glycero*-L-*allo*-heptitol and assumes the same conformation. D-Allose dimethyl acetal is mainly in the $_2G^-,_4G^+$ form, with a C//O interaction between C-4 and one of the methoxyl groups. In all of these cases, conformations would be possible which have an O//O interaction rather than a C//O interaction.

Even more clear-cut are the data for two 4,5,6-tri-*O*-benzoyl-2,3-di-*S*-ethyl-2,3-dithio-D-allose dithioacetals and for the corresponding dimethyl acetal[29]. The former are almost completely in the $_3G^-$ form, which has a C//O interaction between C-5 and O-2; the latter is in the $_2G^-,_4G^+$ form, which has a C//O interaction between C-4 and one of the O-1 atoms.

In addition to 1,3-parallel interactions, another factor controls the conformation of the dimethyl acetals of aldoses, namely, a pronounced tendency to avoid the conformation in which O-2 is *gauche* to both oxygen atoms on C-1. This is clearly seen from the $J_{1,2}$ values[3] of the hexose acetals which are all close to ($\not>$1.7 Hz below) the value found in this series for the antiperiplanar arrangement of H-1 and H-2. This tendency is not found in the dithioacetals: the $J_{1,2}$ values have a much larger range. This explains why the acetals and the dithioacetals sometimes assume quite different conformations[3]. If O-2 and O-3 are *erythro*, maintenance of the antiperiplanar H-1,H-2 arrangement in the acetals introduces a 1,3-parallel interaction into the planar chain form; this can be relieved by rotation to a sickle form which, however, may introduce another unfavourable interaction. Thus, the acetate of L-gulose dimethyl acetal is in the $_2G^-,_3G^-$ form[3], with a C//O interaction between C-4 and one O-1. (The alternative $_4G^+$ form, which would have been expected to be more stable, would have an O//O interaction.)

There are, thus, numerous examples among heptitols and hexose acetals of conformations which have a C//O interaction. Most of them are fully acetylated compounds, and the configuration of the acetoxyl groups contributes to the conformational preferences. It has been pointed out[1] that acetyl groups on O-3 and O-4 of the hexitol acetates, and those on O-3, O-4, and O-5 of the heptitol acetates, inevitably have 1,3-parallel interactions in the planar zigzag form unless they are antiperiplanar to the acetoxyl groups on both neighbouring carbon atoms (in which case, there is such an interaction between those two acetoxyl groups). Sometimes these interactions can be relieved by rotation around the carbon–carbon bond. Thus, in the $_3G^+$ form of allitol hexa-acetate, AcO-4 is free of such interaction. In the surprising $_3G^+,_4G^+$ form (**3**) of hepta-*O*-acetyl-D-*glycero*-D-*gluco*-heptitol, AcO-5 is free of such interaction, whereas it would be affected in the (previously assumed) $_2G^-,_5G^+$ form.

In acyclic compounds, apparently, the C//O interaction is not as prohibitive as had been thought. In fact, this interaction may be quite small. In the crystal structure of D-*glycero*-L-*allo*-heptitol, the distance between C-2 and O-5 is 3.06 Å, larger than any that occurs between *syn*-axial groups in cyclohexane. The C-5–O-5 and the C-3–C-2 bonds are not truly parallel (Fig. 1). This is the result of a widening of the bond angles on C-3 and C-4, and of an alteration by about 15° from the fully staggered arrangement along the C-3–C-4 bond. Evidently, such deviations from the normal angles are less likely to occur in six-membered ring systems; hence, the interactions observed in the latter are not necessarily applicable to acyclic compounds. It is not uncommon to find differences in interaction energies between cyclohexane and aliphatics (see, for example, refs. 30 and 31); it is not clear, however, why such deviations would favour C//O interactions over O//O interactions.

From these considerations, it now appears that the conformation assigned[1] to *meso-glycero-allo*-heptitol is incorrect. The excellent agreement of its ^{13}C chemical shifts with those of allitol was taken to indicate the $_2G^-,_5G^+$ form (which has an O//O interaction) because allitol was thought to be in the $_2G^-,_4G^+$ conformation[8,9]. Now that it is known[19] that allitol is a mixture of the $_2G^-,_4G^+$ and the $_3G$ forms, the agreement in ^{13}C shifts shows that there is a *gauche* arrangement both in the middle of the chain and at a penultimate bond; that is, the conformations present are the $_2G^-,_4G^+$ (and the enantiomeric $_3G^+,_5G^-$ form) and/or the $_2G^-,_4G^-$ (and the enantiomeric $_3G^-,_5G^-$) forms, all of which have C//O interactions. The former has the same conformation as the *allo* segment of the preponderant $_3G^+$ form of D-*glycero*-L-*allo*-heptitol; the two heptitols, and their conformations, are closely analogous.

These revisions of the assigned conformations leave us with only one heptitol, *meso-glycero-altro*-heptitol, which has an O//O interaction if it is, as previously postulated[1], in the planar zigzag form. It now appears that this assignment is correct; the n.m.r. data are listed in Tables I and II. The signals of H-3, H-4, and H-5 are close together, forming the tightly coupled AB_2 part of an AB_2X_2 system, which has not been fully analysed. Hence, the value of $J_{3,4} = J_{4,5}$ (7 Hz) is only approximate, but it indicates that the planar form is preponderant; possibly, this form is slightly distorted by a change of the dihedral angles on C-3, C-4, and C-5 to reduce the O//O interaction. The good agreement of the n.m.r. data with those of D-altritol[19] also supports the preponderance of the planar conformation. All other possible conformations seem to be less stable.

The discovery of C//O interactions in the alditols enriches our knowledge of their conformations, but makes their prediction much more difficult.

Attention is drawn to the numerous n.m.r. spectra described by Moore *et al.*[27], which include those of the partially acetylated derivatives of three heptitols. They show that the partially acetylated alditols often assume conformations quite different from those of the fully acetylated, or of the free, alditols; *e.g.*, 1,2,4,6,7-penta-*O*-acetyl-*meso-glycero-gulo*-heptitol is in the planar zigzag form, presumably because of an intramolecular hydrogen-bond between the two free hydroxyl groups.

CRYSTAL STRUCTURE DETERMINATION

A needle-shaped crystal (0.40 × 0.14 × 0.14 mm) of D-*glycero*-L-*allo*-heptitol was irradiated with graphite-monochromated CuKα radiation on a CAD-4 diffractometer. The cell parameters were found at 22(2)°, using 17 reflections with θ between 66 and 70°, and taking $\lambda_{CuK\alpha_1}$ as 1.54056 Å, to be a = 8.399(2), b = 23.484(8), c = 4.664(2) Å, $\alpha = \beta = \gamma = 90°$.

Intensities to $(\sin \theta)/\lambda = 0.61$ of 1067 unique reflections were measured to a programmed 2% accuracy, of which 1010 are "observed" [$I > 3\sigma(I)$]. Absorption corrections were applied, using $\mu = 1152\ m^{-1}$ and a 6 × 6 × 6 point grid: correction factors ranged from 1.12 to 1.45, the mean being 1.17. Systematic absences uniquely determined the space group to be $P2_12_12$ with $Z = 4$.

The structure was solved automatically by the MULTAN-80 set of programs[32], which found all the 14 non-hydrogen atoms in the first run from a phase set with outstanding figures of merit. After preliminary least-squares refinement, all of the H atoms were detected on Fourier difference maps. At this stage, the chirality of the molecule was changed to agree with its known configuration.

In subsequent refinement by full-matrix least squares, a scale factor, an isotropic extinction parameter, positional parameters for all atoms, and anisotropic thermal parameters for non-hydrogen atoms were refined. The hydrogen atoms were all given isotropic thermal parameters equivalent to those atoms to which they were bonded, after it was found that some of them (all those bonded to carbon atoms) refined to very low or negative values if allowed to refine freely as independent isotropic parameters. The function minimised was $\Sigma w(|F_o| - |F_c|)^2$, where w $= [\sigma(F_o)]^{-2}$. The variance of the raw intensities I was taken as the variance based on counting statistics plus 0.0016 I^2.

After the final cycle, the crystallographic agreement indices R and R_w were, respectively, 0.026 and 0.037 for the 1010 observed data, and 0.029 and 0.037 for all data, with $S = [\Sigma w(|F_o| - |F_c|)^2/(n_o - n_v)]^{1/2} = 1.38$. The mean and maximum values of the shift-to-error ratio in the final cycle were 0.015 and 0.17, respectively. The final Fourier difference synthesis showed no residual electron density peaks above 0.25 eA^{-3}. Of the 7 highest peaks (0.16 eA^{-3} and above), 6 are at the centres of the C–C bonds. Of the remaining 8 peaks above 0.12 eA^{-3}, 7 are situated near H atoms bonded to C atoms, which is consistent with the behaviour noted above of the thermal parameters of these atoms.

The final value of the extinction parameter R was 1.18×10^{-3}, where the corrected value is given[33] by

$$|F_c|^* = k\,|F_c|\,[1 + 2R\bar{T}\gamma\,|F_c|^2]^{-1/4},$$

where

$$\gamma = \frac{1 + \cos^4 2\theta}{\sin 2\theta(1 + \cos^2 2\theta)},$$

$\bar{T}$ = effective path-length (cm), k = scale factor, and $|F_c|$ is the uncorrected value.

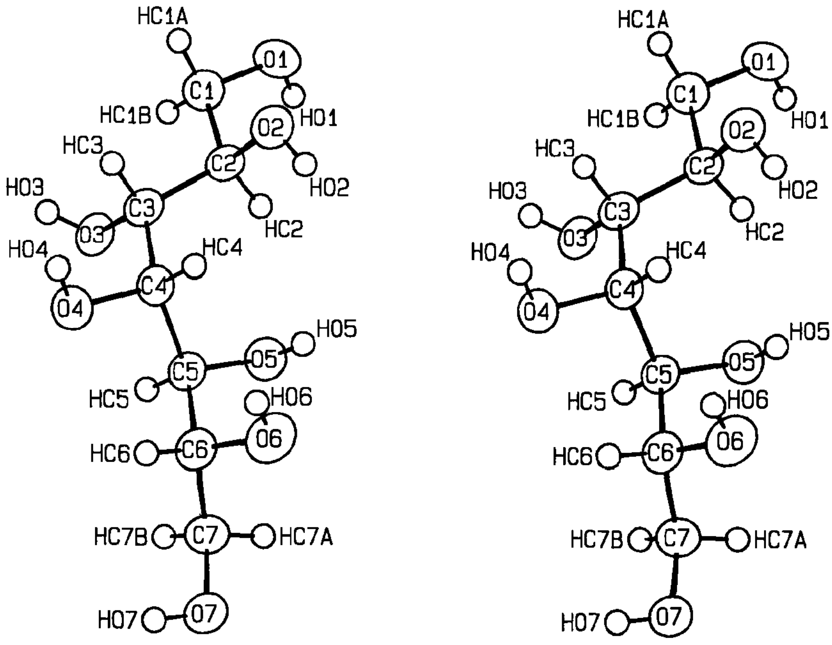

Fig. 1. Stereoview and atomic notation for D-*glycero*-L-*allo*-heptitol. The hydrogen atoms are depicted by spheres of arbitrary radius.

TABLE III

FINAL ATOMIC COORDINATES AND THERMAL PARAMETERS, WITH ESTIMATED STANDARD DEVIATIONS IN PARENTHESES[a]

Atom	x/a	y/b	z/c	B_{eq}
C-1	−0.0524(2)	0.1952(1)	−0.0915(5)	2.1
C-2	0.1092(2)	0.1868(1)	0.0473(4)	1.7
C-3	0.1220(2)	0.1268(1)	0.1787(4)	1.6
C-4	0.2801(2)	0.1130(1)	0.3291(4)	1.5
C-5	0.4223(2)	0.1016(1)	0.1297(4)	1.6
C-6	0.5738(2)	0.0864(1)	0.2954(4)	1.9
C-7	0.6979(2)	0.0625(1)	0.0914(5)	2.2
O-1	−0.0585(2)	0.2473(1)	−0.2523(3)	2.2
O-2	0.1257(2)	0.2286(1)	0.2684(3)	2.2
O-3	0.0895(2)	0.0851(0)	−0.0356(3)	1.8
O-4	0.2593(2)	0.0610(1)	0.4871(3)	1.9
O-5	0.4526(2)	0.1484(1)	−0.0578(3)	1.8
O-6	0.6382(2)	0.1356(1)	0.4319(3)	2.4
O-7	0.8361(2)	0.0413(1)	0.2344(4)	2.7
HC1A	−0.1361(38)	0.1980(11)	0.0616(72)	
HC1B	−0.0715(35)	0.1649(12)	−0.2177(70)	
HC2	0.1949(38)	0.1926(11)	−0.0820(67)	
HC3	0.0430(33)	0.1243(11)	0.3250(64)	
HC4	0.3023(31)	0.1473(11)	0.4544(64)	
HC5	0.3978(35)	0.0695(11)	0.0106(61)	
HC6	0.5497(35)	0.0593(12)	0.4329(72)	
HC7A	0.7380(37)	0.0923(11)	−0.0431(71)	
HC7B	0.6483(36)	0.0334(12)	−0.0369(68)	
HO1	−0.0022(42)	0.2439(12)	−0.4017(75)	
HO2	0.2193(42)	0.2358(13)	0.2826(77)	
HO3	0.0163(40)	0.0652(11)	0.0322(68)	
HO4	0.2052(38)	0.0681(13)	0.6383(74)	
HO5	0.4763(36)	0.1764(13)	0.0527(70)	
HO6	0.5874(36)	0.1407(13)	0.5788(73)	
HO7	0.8078(37)	0.0116(13)	0.3258(70)	

[a]$B_{eq} = {}^4/_3 \sum_i a_i^2 \beta_{ii}$.

The scattering factors for C, H, and O were those given in The International Tables for X-Ray Crystallography[34] ("HF" values for C) with corrections $\Delta f'$ 0.017 and 0.047 for C and O, respectively.

The principal computer programs used were MULTAN-80[32]; FANDEB, derived from ORFFE[35]; BLOCKLS, a much-modified ORFLS[36]; and ORTEP[37].

Description of the structure. — The labelling scheme is shown in Fig. 1. Tables III and IV list the atomic coordinates and selected bond lengths, bond angles, and torsional angles*. The *gauche* arrangement is at C-3–C-4; the C-1–C-4 and the C-3–C-7 segments of the molecule are almost planar.

*The Tables of observed and calculated structure factors and of anisotropic, thermal parameters may be obtained from Elsevier Science Publishers B.V., BBA Data Deposition, P.O. Box 1527, Amsterdam, The Netherlands. Reference should be made to No. BBA/DD/342/*Carbohydr. Res.*, 150 (1986) 7–21.

TABLE IV

BOND LENGTHS (Å), BOND ANGLES (DEGREES), AND TORSION ANGLES (DEGREES) IN D-*glycero*-L-*allo*-HEPTITOL

Bond	*Bond distance*	*Bond*	*Bond distance*
C-1–C-2	1.516(3)	C-6–O-6	1.426(2)
C-2–C-3	1.540(2)	C-7–O-7	1.428(2)
C-3–C-4	1.536(2)	C-1–HC1A	1.003(34)
C-4–C-5	1.537(2)	C-1–HC1B	0.940(31)
C-5–C-6	1.531(2)	C-2–HC2	0.950(32)
C-6–C-7	1.519(3)	C-3–HC3	0.953(29)
C-1–O-1	1.435(2)	C-4–HC4	0.944(28)
C-2–O-2	1.431(2)	C-5–HC5	0.958(27)
C-3–O-3	1.426(2)	C-6–HC6	0.927(31)
C-4–O-4	1.436(2)	C-7–HC7A	0.995(40)
C-5–O-5	1.427(2)	C-7–HC7B	1.001(31)
Bonds	*Bond angle*	*Bonds*	*Bond angle*
C-2–C-1–O-1	111.5(1)	C-5–C-4–O-4	104.9(1)
C-1–C-2–C-3	110.7(1)	C-4–C-5–C-6	112.4(1)
C-1–C-2–O-2	107.7(1)	C-4–C-5–O-5	112.1(1)
C-3–C-2–O-2	109.5(1)	C-6–C-5–O-5	109.9(1)
C-2–C-3–C-4	115.8(1)	C-5–C-6–C-7	109.9(2)
C-2–C-3–O-3	109.6(1)	C-5–C-6–O-6	110.6(1)
C-4–C-3–O-3	109.9(1)	C-7–C-6–O-6	108.5(1)
C-3–C-4–C-5	115.6(1)	C-6–C-7–O-7	113.2(2)
C-3–C-4–O-4	108.0(1)		
Bonds	*Torsion angle*	*Bonds*	*Torsion angle*
O-1–C-1–C-2–C-3	−171.2(1)	C-3–C-4–C-5–C-6	−178.2(1)
O-1–C-1–C-2–O-2	69.1(2)	C-3–C-4–C-5–O-5	57.4(2)
C-1–C-2–C-3–C-4	−179.4(2)	O-4–C-4–C-5–C-6	−59.4(2)
C-1–C-2–C-3–O-3	55.6(2)	O-4–C-4–C-5–O-5	176.2(1)
O-2–C-2–C-3–C-4	−60.8(2)	C-4–C-5–C-6–C-7	167.0(1)
O-2–C-2–C-3–O-3	174.1(1)	C-4–C-5–C-6–O-6	−73.2(2)
C-2–C-3–C-4–C-5	−74.6(2)	O-5–C-5–C-6–C-7	−67.5(2)
C-2–C-3–C-4–O-4	168.3(1)	O-5–C-5–C-6–O-6	52.3(2)
O-3–C-3–C-4–C-5	50.3(2)	C-5–C-6–C-7–O-7	−173.3(1)
O-3–C-3–C-4–O-4	−66.8(2)	O-6–C-6–C-7–O-7	65.7(2)

The C–C bond lengths range from 1.516 to 1.540, the C–O lengths from 1.426 to 1.436, the C–H lengths from 0.93 to 1.00, and the O–H lengths from 0.81 to 0.86 Å. Bond angles involving only non-hydrogen atoms range from 107.7 to 113.2°, except for C-5–C-4–O-4, C-3–C-4–C-5, and C-2–C-3–C-4 (all in the vicinity of the *gauche* arrangement in the chain) which are 104.9, 115.6, and 115.8°, respectively, indicating some strain. If hydrogen atoms are included, the overall range of bond angles is 104.1 to 115.8°.

Hydrogen bonding is entirely intermolecular, there being 14 such bonds between each molecule and 7 of its neighbours (Table V). Atom O-1 acts as a

TABLE V

HYDROGEN-BOND DISTANCES (Å) AND ANGLES (DEGREES)

Atom	*As donor O-H···O*	*O-H*	*O···O*	*H···O*	*O-H···O*	*As acceptor Donor atoms*
O-1	O-1–HO-1···O-2[h]	0.85(4)	2.754(2)	1.91(4)	174(3)	O-2[g], O-5[g]
O-2	O-2–HO-2···O-1[b]	0.81(4)	2.714(2)	1.91(4)	171(4)	O-1[d]
O-3	O-3–HO-3···O-7[i]	0.83(3)	2.678(2)	1.87(3)	163(3)	O-4[h]
O-4	O-4–HO-4···O-3[d]	0.86(4)	2.703(2)	1.85(4)	179(3)	O-7[f]
O-5	O-5–HO-5···O-1[b]	0.86(3)	2.847(2)	2.04(3)	156(3)	O-6[h]
O-6	O-6–HO-6···O-5[d]	0.82(3)	2.861(2)	2.05(3)	176(3)	—
O-7	O-7–HO-7···O-4[f]	0.85(3)	2.793(2)	1.95(3)	173(3)	O-3[e]

[a]Symmetry code, −x, −y, z; [b]½ + x, ½ − y, −z; [c]½ − x, ½ + y, −z; [d]x, y, 1 + z; [e]1 + x, y, z; [f]1 − x, −y, z; [g]−½ + x, ½ −y, −z; [h]x, y, −1 + z; [i]−1 + x, y, z.

single donor and double acceptor, atoms O-2, O-3, O-4, O-5, and O-7 as single donors and single acceptors, while O-6 acts only as a single donor. Most of these hydrogen bonds are classified as strong bonds, as the O–O distances range from 2.678 to 2.861 Å.

EXPERIMENTAL

The proton spectra of the two heptitols were recorded on a Bruker CXP-300 spectrometer operating at 300 MHz. Chemical shifts were measured relative to acetone and corrected relative to Me_4Si (δ 2.234). The 1D spectrum was measured by using a sweep width of 1000 Hz and 8K memory. The resulting FID was resolution-enhanced using a Gaussian multiplication, zero filled to 32K, and transformed. For the COSY, 256 files of 1K each were obtained by using sweep widths of 1000 Hz in each direction. Window functions of sinebell were used in both directions and the spectra were zero filled to give a 2K × 1K matrix. Similar conditions were employed for the 2D *J*-resolved spectra, except that 32 files were recorded and zero filled to 0.5K with a sweep of 61.5 Hz. The carbon spectrum was recorded at 75.446 MHz, using a sweep width of 4000 Hz.

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