DFT Conformational Studies of α-Maltotriose

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Abstract: Recent DFT optimization studies on α-maltose improved our understanding of the preferred conformations of α-maltose. The present study extends these studies to α-maltotriose with three α-D-glucopyranose residues linked by two α-[1→4] bridges, denoted herein as DP-3’s. Combinations of gg, gt, and tg hydroxymethyl groups are included for both “c” and “r” hydroxyl rotamers. When the hydroxymethyl groups are for example, gg-gg-gg, and the hydroxyl groups are rotated from all clockwise, “c”, to all counterclockwise, “r”, the minimum energy positions of the bridging dihedral angles ($\phi_H$ and $\psi_H$) move from the region of conformational space of $(+, -)$, to a new position defined by $(+, +)$. Further, it was found previously that the relative energies of α-maltose gg-gg-c and “r” conformations were very close to one another; however, the DP-3’s relative energies between hydroxyl “c” or “r” rotamers differ by more than one kcal/mol, in favor of the “c” form, even though the lowest energy DP-3 conformations have glycosidic dihedral angles similar to those found in the α-maltose study. Preliminary solvation studies using COSMO, a dielectric solvation method, point to important solvent contributions that reverse the energy profiles, showing an energy preference for the “r” forms. Only structures in which the rings are in the chair conformation are presented here.

Key words: conformation; DFT; B3LYP/6-311+G**; α-maltotriose; COSMO

Introduction

α-maltotriose is the second most abundant fermentable sugar in brewer’s wort and, due to incomplete fermentation, causes quality and economic problems in the beer and wine industry.1–3 This sugar is of structural interest, being a repeating unit of pullulan, a linear homopoly saccharide of glucose made up of α-(1→6) linked maltotriose units. Many uses for this carbohydrate or its derivatives can be found, for example in the inhibition of specific enzymes,3 as well as use in spectroscopic examination of size effects as the carbohydrate chain length increases.4

Although many empirical computational structural studies have been carried out on the conformational properties of carbohydrates, in particular starch and model amylose fragments (see ref. 7 for lists of earlier computational studies), DFT studies on carbohydrates are recent additions to this extensive list of studies.4–7,19 To date, high quality computational DFT studies have not, to our knowledge, been applied to linear amylose fragments larger than maltose outside of our laboratory. Further, there have been few accounts outside of our DFT work7,8 on the direction of the hydroxyl groups and their role in determining the dihedral angles at the glycosidic bridge between residues. Our recent α-maltose7 studies examined the orientation of the hydroxymethyl groups relative to the ring hydroxyl group’s direction and found these factors to be important in determining the preferred conformation at the glycosidic bonds. Because of this, it becomes important to study larger systems to note how the dihedral angles ($\phi_H$, $\psi_H$) of the optimized conformers, which direct the overall three-dimensional structure, change with chain length.

In the work presented here, rigorous DFT optimization studies at the B3LYP/6-311+G** level of theory have been carried out on α-maltotriose (with a degree of polymerization of three residues, denoted as DP-3) conformers in vacuo and with solvent contributions, looking specifically at the question of the effect of “c” (clockwise) and “r” (reverse clockwise) hydroxyl rotamers and hydroxymethyl conformations on glycosidic ($\phi_H$, $\psi_H$) dihedral angle values. Applying a dielectric solvation

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Names are necessary to report factually on available data; however, the USDA neither guarantees nor warrants the standard of the product, and the use of the name by USDA implies no approval of the product to the exclusion of others that may also be suitable

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method, COSMO,\(^{20}\) to selected DP-3 conformations, is found to reverse the energy preference by favoring the “r” conformers over the “c” forms. It is of further interest to examine the differences between maltose\(^7,8\) conformations and larger amylose fragments, in order to examine longer range contributions to the energetic stability and favored conformations. Optimized DP-3 structures in which the central residue is in a boat or skew conformation will be presented elsewhere.

### Computational Methodology

#### Generation of Starting Conformations

Starting conformations are generated using in-house empirical potentials\(^{21}\) and InsightII/Discover software.\(^{22}\) To obtain coverage of the many different conformations, we have chosen to include all of the low energy combinations of the gg and gt

<table>
<thead>
<tr>
<th>Structure</th>
<th>(\Delta E) (kcal/mol)(^a)</th>
<th>Dipole moment</th>
<th>(\phi_{II}^b)</th>
<th>(\psi_{II}^b)</th>
<th>(\phi_{II}^c)</th>
<th>(\psi_{II}^c)</th>
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<td>0.27</td>
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<td>-8.0</td>
<td>-18.1</td>
<td>-8.0</td>
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<td>0.9</td>
<td>15.2</td>
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<td>16.1</td>
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<td>7.3</td>
<td>3.3</td>
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<td>14.1</td>
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<td>-17.9</td>
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<tr>
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<td>10.0</td>
<td>0.9</td>
<td>15.4</td>
<td>4.3</td>
<td>12.9</td>
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</tbody>
</table>

\(\Delta E\) (kcal/mol)\(^a\) = G** electronic energy of lowest energy conformer. (tg(t)-gt(g)\(\rightarrow\)gg(g)+c) = \(-1198104\) kcal/mol.

### Table 2

Glycosidic Dihedral Angles (\(\phi_{II}^b\), \(\psi_{II}^b\)) and (\(\phi_{II}^c\), \(\psi_{II}^c\)), Relative Dipole Moments (Debye), and Relative Energies (kcal/mol) of DP-3 Amylose Fragments Optimized with COSMO.

<table>
<thead>
<tr>
<th>Structure</th>
<th>(\Delta E) (kcal/mol)(^a)</th>
<th>Dipole moment</th>
<th>(\phi_{II}^b)</th>
<th>(\psi_{II}^b)</th>
<th>(\phi_{II}^c)</th>
<th>(\psi_{II}^c)</th>
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<td>-3.1</td>
<td>12.2</td>
<td>-4.0</td>
<td>11.0</td>
</tr>
<tr>
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<td>9.4</td>
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<td>-11.4</td>
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<td>8.3</td>
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<td>9.6</td>
<td>-2.8</td>
<td>6.2</td>
<td>2.4</td>
<td>7.8</td>
</tr>
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<td>3.37</td>
<td>7.0</td>
<td>1.5</td>
<td>14.1</td>
<td>2.0</td>
<td>14.0</td>
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</tbody>
</table>

\(\Delta E\) (kcal/mol)\(^a\) = G** electronic energy of lowest energy conformer. (tg(t)-gt(g)\(\rightarrow\)gg(g)+c) = \(-1198139\) kcal/mol.
hydroxymethyl groups for both the all "c" (clockwise) and all "r" (counterclockwise) hydroxyl groups found for α-maltose. Conformations in which the primary residue hydroxymethyl groups are tg are examined and the indication is that this conformation could be favorable as an end effect at the nonreducing end. Placing the hydroxymethyl group in the tg conformation in the second or third residue was found to have unfavorable high energy in maltose and for that reason these types of conformations are not studied here in detail, only those with all three residues in the tg form are examined. Band-flip and kinked conformers are not included in this work but have been described in detail in the α-maltose work.7

**Basis Set and Hardware**

DFT calculations are carried out using the B3LYP nonlocal exchange functionals23 with preliminary optimization using the 6-31+G* basis set, followed by optimization at the larger, 6-311++G**, basis set. This methodology has proven to be very useful for carbohydrates where hydrogen bonding is important for determining the conformational and structural parameters of carbohydrates.7–19 Parallel Quantum Solutions24 (PQS) software and hardware (QS8-2800S, and QS16-2800S) were utilized throughout and results are reported for the larger basis set. A comparison of the small and large basis sets applied to carbohydrates can be found elsewhere.7,16 Convergence criteria were analogous to those used for the mono- and disaccharides7–16 with an energy change of less than $3 \times 10^{-6}$ a.u. The Hessians created and used during the optimization process did not show negative eigenvalues, which ensures that the geometry optimized conformations are at local minima. Results have been displayed using HyperChem v7.5.25

The COSMO20 solvation method used is that distributed by PQS, using parameters that are default in the software.

**Definition of Conformations**

We define the ring hydroxyl groups to be clockwise, “c”, relative to the numbered glucose ring starting at the anomeric carbon atom #1 and counting clockwise, and the reverse or counter-clockwise direction is denoted, “r”. Because of the extended hydrogen bond network around the rings, “c” and “r” conformations are not normally mixed on the same residue or between residues. Mixed hydroxyl directions were examined in the α-maltose study7 and were found to be of high relative energy. The hydroxymethyl groups were started in the gg, gt, or tg conformation, using the standard nomenclature for hydroxymethyl rotation around the C5-C6 bond (that is, the first term is relative to the ether ring O5 oxygen while the second term is relative to atom C4). The orientation of the hydroxyl hydrogen on the O6 atom is described by \((g-, g+, o, t)\), to designate the O6-H direction, i.e. pointing toward a potential hydrogen bond acceptor (O4 for g-; O5 for g+) and trans (t) which does not point toward an acceptor.16 The glycosidic dihedral angles...
between rings a and b, and rings b and c, are denoted as, (\(\phi_{ab}, \psi_{ab}\)) and (\(\phi_{bc}, \psi_{bc}\)), labeling from the nonreducing end (residue a) and defining the dihedral angles relative to the hydrogen atoms on the anomeric or C1a-carbon and the C4b-carbon atom of ring b, and similarly for rings b to c. The dihedral angles \(\phi_{ab}, \psi_{ab}\) are defined by the atoms, H1a-C1a-O1a-C4b and C1a-O1a-C4b-H4b respectively, with the second set defined accordingly between the b and c residues.

### Selecting DP-3 Starting Conformations

DP-3 is composed of three \(\alpha\)-D-glucopyranose rings joined by two \(\alpha\-(1\rightarrow4)\) glycosidic linkages. Structures were generated with all the glucose rings in the \(4C_1\) chair conformation and different conformations of “r” and “c” and gg, gt, or tg were modeled using the InsightII/Discover program, in house empirical potentials, and partial optimization using the PM3 semiempirical method. When a unique structure of interest is found to be stable using the preliminary methods, the coordinates are transferred to the PQS programs for geometry optimization at the B3LYP/6-31++G** level of theory, and the structures resulting from this minimization are re-optimized at the B3LYP/6-311++G** level of theory.

### Results

Tables 1 and 2 lists the conformational and energetic details for the DP-3 conformers studied herein. Table 2 results were calculated using COSMO. The relative energies are given, as are the glycosidic dihedral angles and dipole moment as calculated from the B3LYP/6-311++G** optimized geometry. The relationship between hydroxyl conformations, hydroxymethyl conformations, and glycosidic bridge conformation, becomes more complex as more residues are included. In particular, although the glycosidic dihedral angles are similar in some cases to the \(\alpha\)-maltose results, there are examples where no obvious relationship appears. It has become obvious that maltose may not be a good model for larger amylase fragments, a result of the relative energies changing from “r” slightly preferred to “c” preferred by \(~1\) kcal/mol with addition of a third residue. The energy difference becomes more pronounced when 4-residue fragments, DP-4’s, are studied using the same basis sets.

The glycosidic dihedral angles (Table 1, Fig. 1) are similar to those obtained from \(\alpha\)-maltose for the all gg-gg conformers, with the “c” form having \(\phi_{ab} \approx -8^\circ, \psi_{ab} \approx -18^\circ\) for both sets of dihedral angles, and the “r” form having \(\phi_{ab} \approx 1^\circ, \psi_{ab} \approx 15^\circ\) for both, in agreement with results from the recent \(\alpha\)-maltose study. However, the relative energy of the two DP-3s, is not consistent with \(\alpha\)-maltose, with the “r” form of the DP-3s \(~1\) kcal/mol higher in energy than the “c” form, in contrast to \(\alpha\)-maltose where the relative energy “c” and “r” difference for the gg-gg case is a few tenths of kcal/mol. The addition of a
third residue in vacuo stabilized the energy of the “c” form, and destabilized the “r” form, relative to the lowest energy DP-3 conformer.

Optimization of these two all-gg conformers using the solvation method, COSMO, results in a reversal of the relative energies, with the “c” form now 1.7 kcal/mol higher in energy than the “r” form, see Table 2. This energy difference amounts to a relative change in energy of 3.0 kcal/mol upon application of the solvent model. The glycosidic dihedral angles are also modified with the “c” conformer $\phi_{H}^{ab}, \psi_{H}^{ab}$ values changing by more than 12° (see Tables 1 and 2). The reversal in relative energy is consistent with results presented previously on α-maltotriose, where the “r” form with solvent was 1 kcal/mol lower in relative energy than the “c” form, and the “c” form converted into the “r” form after several picoseconds of dynamics.

The experimental X-ray structure (gg-gg-gg) of methyl-α-maltotriose produced dihedral angles ($\phi_{H}^{ab} = -36°, \psi_{H}^{ab} = -27°$) and ($\phi_{H}^{ab} = -35°, \psi_{H}^{ab} = -30°$) that are similar to those calculated here (see Table 1), with a complex network of hydrogen bonding in the crystal. They found four water molecules per molecule of α-maltotriose and these waters play a role in the crystal packing arrangement and conformation. A second X-ray structure of a hexasaccharide complex (p-Nitrophenyl α-maltohexaoside)-Ba(II)$_2$27H$_2$O resulted in two molecules per unit cell with average glycosidic dihedral angles of ($\phi_{H}^{ab} = -8°, \psi_{H}^{ab} = -8°$) and ($\phi_{H}^{ab} = -24°, \psi_{H}^{ab} = -6°$) respectively, in excellent agreement with the COSMO results presented here in Table 2. This structure is of interest as the hydroxymethyl groups were almost all in the gg conformation. Another relative X-ray result is that of the maltoheptaose, where glycosidic dihedral angles of ($\phi_{H}^{ab} \approx -15°, \psi_{H}^{ab} \approx -15°$) were found for most of the residues where a hydroxymethyl conformation could be deduced. The early work depended upon modeling in order to achieve a fit of the electron density.

When α-maltose in the gg-gg’ form is totally solvated using COSMO during DFT molecular dynamics the average dihedral angles oscillate closely around (0°, 0°). This set of conformers, “r/c”, shows the beginning of conformational effects found upon lengthening the chain, with the “c” form dihedral angles ($\phi_{H}^{ab} \approx -8°, \psi_{H}^{ab} \approx -24°$) being different to those in the gt-gt form of α-maltose, but the “r” form showing (Fig. 2) more typical “r” form conformation in both sets of glycosidic dihedral angles ($\phi_{H}^{ab} \approx 3°, \psi_{H}^{ab} \approx 16°; \phi_{H}^{bc} \approx 1°, \psi_{H}^{bc} \approx 14°$). The (±,+) form was also found in the α-maltose gt-gt conformers. It is of interest to mention that for the “r” form an energetically similar (−,−) form (in the first set of glycosidic dihedral angles) was observed, not previously seen in the case of α-maltose. The “r” form is also higher in relative energy, ~4.15 kcal/mol, than the “c” form, ~3.09 kcal/mol, just the opposite of that found in the case of α-maltose, where the “c” form was also found in the α-maltose gt-gt conformers.7 It is of interest to mention that for the “r” form an energetically similar (−,−) form (in the first set of glycosidic dihedral angles) was observed, not previously seen in the case of α-maltose. The “r” form is also higher in relative energy, ~4.15 kcal/mol, than the “c” form, ~3.09 kcal/mol, just the opposite of that found in the case of α-maltose, where the “c” form was also found in the α-maltose gt-gt conformers.7
One of the lowest energy DP-3 conformers (Table 1, Fig. 3), with relative energy of ~0.1 kcal/mol, is the “c” form of this set, with the “r” form ~1.9 kcal/mol higher in relative energy. The glycosidic dihedral angles are similar to the all gg-c conformer, but the “r” form appears as a mix of favored dihedral angles, being negative in $\phi_H$ and positive in $\psi_H$. This is similar to that found for the gg-gt and gt-gg $\alpha$-maltose conformations. One is tempted to suggest that the favored conformation of the DP-3 amylose fragment is just the paired form of the similarly paired maltose conformers, but that would be too simplistic since the relative energy terms are very different.

The “c” and “r” forms are of nearly equal energy (Table 1, Fig. 4) and the glycosidic dihedral angles of the “c” form are similar to those found for the previous pairings of the $\alpha$-maltose sequence gt-gg. The “r” form shows some preference for the gg-gt-gg sequence, with the second set of dihedral angles very nearly the same as in the all gg conformer. It appears that when the gt conformation is in the primary position it neutralizes the dipole enhancement. However, in the next section where the gt is in the last position in the sequence, this neutralization is not sufficient to bring the energies closer.

Figure 7. B3LYP/6-311++G** geometry optimized gt-gg-gt $\alpha$-maltotriose structures. [Color figure can be viewed in the online issue, which is available at www.interscience.wiley.com.]
The relative energy of the “c” form (~0.6 kcal/mol) is considerably lower than the “r” form (~2.3 kcal/mol) in this sequence of hydroxymethyl conformations. The “c” form glycosidic bonds dihedral angles are similar (Table 1, Fig. 5) to those for the all gg-c and all gt-c conformers described above, while the “r” form is again a mix of values ($\phi_{12}^x \approx -8^\circ$, $\psi_{12}^x \approx -3^\circ$, $\phi_{12}^{bc} \approx +13^\circ$, $\psi_{12}^{bc} \approx +15^\circ$). The (−, +) region of conformational space is only found in the “r” form, never in the “c” form.

The “r” form (~3.6 kcal/mol) is again significantly higher in relative energy than the “c” form (~1.4 kcal/mol). The glycosidic dihedral angles of the “c” form are close to those found previously (Table 1, Fig. 6) and the relative energy is not so different from the gt-gg-gg-c form. The dihedral angles for the “r” form are however, quite different, being ($\phi_{12}^x \approx -4^\circ$, $\psi_{12}^x \approx +3^\circ$, $\phi_{12}^{bc} \approx +13^\circ$, $\psi_{12}^{bc} \approx +15^\circ$), similar to the gg-gt-gg-r conformer but with considerably higher relative energy (~3.7 kcal/mol).

The “c” conformer has dihedral angles (Table 1, Fig. 7) that are combinations of other all gt-c or all gg-c sequences. The “r” form appears similar to the gg-gt-gg-r conformer in dihedral angles. The relative energy difference of both the “c” and “r” forms is similar to the other double gt conformers.

The dihedral angles for the “c” conformer (Table 1, Fig. 8) are similar to those noted previously, while the “r” dihedral angles are more similar to the all gt-r conformer. The relative energy difference between the two forms of ~0.5 kcal/mol is smaller than most of the above combinations with two gt conformers, the relative energies to the lowest energy conformation being ~2 kcal/mol.

Series in which tg conformations are included were examined in the DP-3 group, even though these conformations were of relatively high energy in α-maltose when the tg is in the second position. However, since tg-gg is the lowest energy α-maltose conformer found previously, it was important to test this in the DP-3 series. In the case of the all-tg form (Table 1, Fig. 9), the relative energy is quite high, ~4.6 kcal/mol for the “c” form, and similarly, ~4.2 kcal/mol for the “r” form. Even though the relative energies are similar, the dihedral angles differ significantly between the two forms ($\phi_{12}^x \approx -8^\circ$, $\psi_{12}^x \approx -3^\circ$, $\phi_{12}^{bc} \approx +13^\circ$, $\psi_{12}^{bc} \approx +15^\circ$) for the “c” form and ($\phi_{12}^x \approx +2^\circ$, $\psi_{12}^x \approx -6^\circ$, $\phi_{12}^{bc} \approx 0.2^\circ$) for the “r” form.

The “r” conformer has dihedral angles (Table 1, Fig. 7) that are combinations of other all gt-c or all gg-c sequences. The “r” form appears similar to the gg-gt-gg-r conformer in dihedral angles. The relative energy difference of both the “c” and “r” forms is similar to the other double gt conformers.

The dihedral angles for the “c” conformer (Table 1, Fig. 8) are similar to those noted previously, while the “r” dihedral angles are more similar to the all gt-r conformer. The relative energy difference between the two forms of ~0.5 kcal/mol is smaller than most of the above combinations with two gt conformers, the relative energies to the lowest energy conformation being ~2 kcal/mol.

Series in which tg conformations are included were examined in the DP-3 group, even though these conformations were of relatively high energy in α-maltose when the tg is in the second position. However, since tg-gg is the lowest energy α-maltose conformer found previously, it was important to test this in the DP-3 series. In the case of the all-tg form (Table 1, Fig. 9), the relative energy is quite high, ~4.6 kcal/mol for the “c” form, and similarly, ~4.2 kcal/mol for the “r” form. Even though the relative energies are similar, the dihedral angles differ significantly between the two forms ($\phi_{12}^x \approx -8^\circ$, $\psi_{12}^x \approx -3^\circ$, $\phi_{12}^{bc} \approx +13^\circ$, $\psi_{12}^{bc} \approx +15^\circ$) for the “c” form and ($\phi_{12}^x \approx +2^\circ$, $\psi_{12}^x \approx -6^\circ$, $\phi_{12}^{bc} \approx 0.2^\circ$) for the “r” form.

The “r” conformer has dihedral angles (Table 1, Fig. 7) that are combinations of other all gt-c or all gg-c sequences. The “r” form appears similar to the gg-gt-gg-r conformer in dihedral angles. The relative energy difference of both the “c” and “r” forms is similar to the other double gt conformers.
Application of COSMO20 (see Table 2) to these conformers was undertaken to determine if the tg rotamers were less or more favored with solvent. As we found above, the "r" form is energy favored over the "c" form, and only very small variations in glycosidic dihedral angles were found, unlike the all gg and all gt conformations, suggesting that the tg forms are more tightly held although remaining of higher relative energy (C24 3 6 kcal/mol).

This combination of hydroxymethyl group conformations with the "c" form is the lowest energy structure found in this study (Table 1, Fig. 10). The "r" form is C24 1.9 kcal/mol higher in energy. The dihedral angles of the glycosidic bridge are nearly the same as those found for the gg-gg-gg-c and gg-gt-gg-c forms, suggesting that the first residue in the fragment does not influence the conformation of the bridging regions very significantly, while in each of the three cases, the energy is low, being only C 0.1 - 0.2 kcal/mol higher in the two forms above. On the other hand, the "r" form of this combination is C 1.9 kcal/mol higher in energy and this is also consistent with the relative energies of the "r" forms of the two combinations noted above, so the relative energies of the "r" forms are not changed by moving the first residue to the tg conformation.

This combination is also of very low energy in the "c" form (Table 1, Fig. 11), with the "r" form being C 1.1 kcal/mol higher in relative energy. The dihedral angles are similar to those found for the all-gg-c and all-gg-r forms, and again it appears that the tg conformation on the first residue is not strongly influencing the glycosidic bonds.

This structure is also of relatively low energy (Table 1, Fig. 12) for the "c" form, and of higher energy in the "r" case. The dihedral angles are consistent with those described above for each form.

It is intriguing that in this combination, the relative energies are significantly different, with the "c" form now C 1.3 kcal/mol and the "r" form C 3.8 kcal/mol higher than the lowest energy conformation. The dihedral angles in the "c" and "r" form (Table 1, Fig. 13) are very similar to those found previously.

Geometry Variances in Middle Residue

Structural parameters from our DFT study of C-maltose7 and glucose13 give a base structure around which one may look for...
long range effects as a result of adding residues on both ends of the central glucose residue in DP-3. To that end it is of interest to examine the overall chair shape of the ring to observe if adding residues on each end have flattened or puckered the ring in any way. To this end several parameters such as the C1 to C4 distances across the ring of glucose, two rings of maltose, and three rings of DP-3 were calculated from all the optimized conformations of each. The results can be summarized by the statement "no difference". That is, within a small variance, there is no deviation from the average value for all the glucose rings independent of the molecule they are in. Similarly there are only slight deviations in the chair conformations across a large database of DFT structures. When we examine the three atom plane at the O5-C1-C2 end relative in orientation to the C3-C4-C5 end, we find no significant differences between the single glucose molecule and the di- and tri-saccharides. One might consider a small deviation in the reducing ring vs. the nonreducing ring in the DP-3 structures, but it is not of significance if molecular motion is included from molecular dynamics simulations using the DFT method.  

Because of the very slight deviations that were found we do not include more details on the molecular internal coordinates. A detailed listing of glucose/maltose residue internal coordinates can be found in ref. 7.

Conclusions

The most important take home lesson of this study is that α-maltose is not a particularly good model for larger fragments of amylose. The reason is that the relative energies of the “c” and “r” forms are reversed in the DP-3 segments, suggesting that in solution, the “c” form could have an energetic preference, unless the solvent plays a significant role. The second take home message is that solvent does play a role in both the relative energy values and in the conformational preferences around the glycosidic bridge.

Clearly, the fact that several different combinations of hydroxymethyl groups with the first residue tg are of low energy is important. It may very well be that in amylose fragments the tg form exists, primarily at the α-position in the chain. However, the all-gg and all-gt forms are also of low relative energy and so have high probability of being occupied in the α-position. One would expect that the all-gg conformations would predominate in solution from the results presented here, and that appears to be generally true.

To examine the effect that solvent could play on the conformations of the DP-3 structures, a preliminary study using COSMO, a dielectric solvation method, was made comparing relative energies of the all-gg, all-gt, and all-tg conformations in the “c” and “r” forms. The result was a decided shift in relative energies to favor the fully solvated “r” forms in every case. This work and other solvated carbohydrate studies will be reported in detail elsewhere. However, it is important to note that the study of in vacuo structures remains important, there being a question of low hydration amylose materials, where the in vacuo environment is more like the amylose residues environment than they would be in the fully solvated molecules. With this in mind, it is interesting to speculate that the best conformational features of amorphous amylose materials will be a mix of “c” and “r” hydroxyl conformations, with possible band-flip conformations acting to help neutralize the buildup of large dipole moments.

The experimental NMR studies, for amylose fragments larger than maltose, show average dihedral angles in the range of ϕH1 ~ -22° and ψH1 ~ -27° for the maltotriose. Although these dihedral angles are close to the values obtained here, the trend is toward dihedral angles that are larger than our DFT ab initio molecular dynamics values for maltose. The NMR maltose average dihedral angles31 were much larger than the DFT studies predict.27

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