Co-operative and Competitive Hydrogen Bonding in Sucrose determined by SIMPLE ¹H N.M.R. Spectroscopy

John C. Christofides and David B. Davies*

Department of Chemistry, Birkbeck College, Malet Street, London WC1E 7HX, U.K.

SIMPLE ¹H n.m.r. measurements of isotope-shifted resonances for hydroxy groups in sucrose show that hydrogen bonding in solution is different from that observed in the solid state *viz*. there are two inter-residue hydrogen bonds in competition for one acceptor group (*i.e.* OH1' \cdots O2 *vs*. OH3' \cdots O2) and an intramolecular hydrogen-bond network that is nucleated by the inter-residue hydrogen bonds.

Observations of carbohydrate crystals by neutron diffraction have shown that most hydroxy groups are involved in intermolecular hydrogen bond interactions with other hydroxy groups, with ring oxygen atoms, or with water of crystallisation to form infinite chains of hydrogen bonds through the crystal lattice.¹ In some crystal structures of oligosaccharides intramolecular hydrogen bonds are also observed between hydroxy groups (e.g. $OH1' \cdots OH2$ in sucrose²) or between hydroxy groups and ring oxygen atoms (e.g. $OH6' \cdots O5$ in sucrose²). Such detailed information about hydrogen bonds is generally not available for molecules in solution, though a number of n.m.r. methods have been used to indicate the presence of hydrogen bonds e.g. chemical shifts, temperature and solvent dependence of chemical shifts, H/D exchange rates.³ Recently high field ¹H n.m.r. observations of H/D isotopomers in the slow exchange condition (*i.e.* (i.e.)SIMPLE n.m.r.; Secondary Isotope Multiplet n.m.r. spectroscopy of Partially Labelled Entities⁴) have shown that



Figure 1. 500 MHz ¹H n.m.r. spectrum of the hydroxy proton resonances of sucrose in $[{}^{2}H_{6}]Me_{2}SO$ solution at a deuteriation ratio of OH : OD *ca*. 1 : 1; *T* = 305 K. Chemical shifts given with respect to δ ($[{}^{2}H_{5}]Me_{2}SO$) = 2.49.

hydrogen bonds between hydroxy groups are manifested by isotope-shifted signals *e.g.* cyclodextrin,⁵ sucrose,⁶ and some sucrose derivatives.^{7,8}

In the present work the 500 MHz SIMPLE ¹H n.m.r. spectrum of sucrose (Figure 1, OH: OD *ca.* 1:1) shows that the negative isotope effect observed for OH1' is similar to that observed previously by Lemieux and Bock⁶ but the number of isotope effects on other hydroxy signals is quite different, *viz.* three effects for OH3 (++-) and two resolved effects for OH2 (++) and OH3' (+-). Small isotope effects that lead to line broadening are also observed for the OH2, OH4, OH3', OH6, and OH6' signals by comparison with the sharp lines of the other signals or by comparison with the normal spectrum of sucrose.

The large positive isotope effect on OH2 (+70 \times 10⁻⁴ p.p.m., acceptor) and the negative isotope effect on OH1' $(-43 \times 10^{-4} \text{ p.p.m., donor})$ correspond to the presence of the OH1' · · · O2 inter-residue hydrogen bond previously found in [2H6]Me2SO solutions of sucrose⁶ and a 3'-sucrose derivative (3,3',4',6'-tetra-O-acetylsucrose).⁷ The medium-sized isotope effect on OH2 (+32 × 10^{-4} p.p.m., acceptor) and the isotope effect on OH3' (-22 × 10^{-4} p.p.m.) correspond to the presence of the novel inter-residue $OH3' \cdots O2$ hydrogen bond recently observed for 1'-sucrose derivatives.9 Observation of these isotope effects is consistent with either a bifurcated hydrogen bond in which OH2 simultaneously acts as acceptor for both the OH1' and OH3' donors (excluded because of unfavourable steric interactions as shown by molecular models) or, more likely, the two inter-residue hydrogen bonds exist in competitive equilibrium, as shown in Figure 2. Assuming that the magnitudes of isotope shifts reflect the relative 'strengths' of hydrogen bonds, it is found that the equilibrium favours the $OH1' \cdots O2$ compared to the OH3' $\cdot \cdot \cdot$ O2 hydrogen bond. The smaller isotope effects observed for most hydroxy signals correspond to very weak hydrogen bonds between neighbouring hydroxy groups which are nucleated by the presence of a relatively strong and predominantly unidirectional inter-residue hydrogen bond; such isotope effects are not observed for the corresponding



Figure 2. Conformational equilibrium of sucrose showing two inter-residue hydrogen-bonded forms in solution and the hydrogen-bond network in the glucose residue nucleated by the inter-residue hydrogen bonds. Hydrogen bonds in the fructose residue have not been characterised completely.

hydroxy resonances of the monomer units of sucrose. The hydrogen-bond network in the glucose residue is similar to that observed previously for 1'- and for 3'-sucrose derivatives.^{8,9}

Despite the conformational flexibility of the molecule and the exocyclic carbinol and hydroxy groups, it is found that hydrogen-bond interactions between hydroxy groups are sufficiently stable to be manifested as isotope shifts. The number and magnitudes of the isotope shifts observed for sucrose in solution can be understood in terms of an intramolecular hydrogen-bond network between hydroxy groups that is quite different from the intermolecular hydrogen-bond network observed in the solid state. For molecules dissolved in $[{}^{2}H_{6}]Me_{2}SO$ solution it is likely that the solvent acts as a hydrogen-bond acceptor for each hydroxy group¹⁰ whereas crystal packing is likely to be dominant for molecules in the solid state. Crystal packing constraints may also account for the different glycosidic bond conformations observed for sucrose (with its $OH1' \cdots O2$ hydrogen bond)² and the sucrose unit in raffinose (with no inter-residue hydrogen bond)11 whereas, in solution, our SIMPLE 1H n.m.r. studies show that the two competitive inter-residue hydrogen bonds (OH1' \cdots O2 vs. OH3' \cdots O2) found for sucrose are also observed for the sucrose residue in the trimer raffinose and the tetramer stachyose.

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