

Comment on “NMR spectroscopic studies of cellobiose solvation in EmimAc aimed to understand the dissolution mechanism of cellulose in ionic liquids” by J. Zhang, H. Zhang, J. Wu, J. Zhang, J. He and J. Xiang, *Phys. Chem. Chem. Phys.*, 2010, 12, 1941

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In a manuscript recently published in this journal,¹ Zhang and co-workers studied the solvation of cellobiose in the ionic liquid (IL) 1-ethyl-3-methylimidazolium acetate ([C₂mim]OAc) using chemical shift perturbation ($\Delta\delta$) measurements. According to the authors, their analysis of the IL and sugar ¹H and ¹³C $\Delta\delta$ s as a function of concentration provides direct evidence for the formation of hydrogen bonds (H-bonds) between the hydroxyl group of the sugar and both ions of the imidazolium salt. Based on this, they conclude that the anion and cation of [C₂mim]OAc and related ILs have similar roles in the mechanism of cellulose dissolution. In this comment we wish to point out serious flaws in the design of the study and in the interpretation of the data that, in our opinion, led the authors to erroneous conclusions.

To begin with, the study was carried out exclusively *via* the measurement and analysis of $\Delta\delta$ data. While $\Delta\delta$ data are good general indicators of changes in the chemical environment of nuclei, they are in this case too vague to be attributed to specific interactions between the IL and the sugar with any confidence. For example, in one section of the manuscript, the authors claim that as the concentration of [C₂mim]OAc in the system increases, the cellobiose hydroxyl proton signals become deshielded due to H-bonding with the IL acetate ions. Interestingly, they also attribute the *upfield* shift observed for the proton on the C2-position of [C₂mim]OAc as a function of cellobiose concentration to its participation in H-bonds with the oxygen atoms of the sugar hydroxyl groups. The authors note this discrepancy (*i.e.*, shielding instead of deshielding), and reason that it is due to the disruption of the strong H-bonds between the C2-position protons and acetate ions, and the formation of weaker bonds involving these protons and the sugar hydroxyl group oxygens. This is a pretty lofty and speculative conclusion that cannot be unambiguously derived from simple analysis of $\Delta\delta$ data. Indeed, one could interpret the same results to indicate only a disruption of intraionic H-bonds and a lack of specific interactions between the imidazolium cation and the solvated carbohydrate. Given

the complexity of the IL/sugar system, and since $\Delta\delta$ s alone do not represent “direct evidence” of the presence or absence of H-bonding interactions, this seems to be a speculative conclusion stemming from overinterpretation of the data.

Similarly, it is not clear how the $\Delta\delta$ data are employed to estimate the interaction stoichiometries between cellobiose and [C₂mim]OAc. While it is not mentioned in the experimental section, it appears that the authors simply use the concentration of the IL at which some of the cellobiose ¹³C $\Delta\delta$ s reach a plateau to determine these values. Even if an accurate analysis of the titration curves had been carried out, the system used is inadequate for performing this type of study. Firstly, all measurements were carried out in DMSO-d₆ solution, and thus H-bonding between the sugar and/or IL with the sulfoxide oxygen should be expected. These interactions will interfere with those occurring between the sugar and the IL, therefore affecting the estimation of H-bonding stoichiometries. Secondly, the ¹³C signal of the solvent was used as an internal reference for $\Delta\delta$ estimations. Taking into account the high concentration of [C₂mim]OAc in some of the samples, which according to the data presented in the experimental section can reach up to 5 M, considerable variations in the chemical shift of the reference signal are likely to occur between different samples. NMR-based investigations of IL–solute interactions should only be carried out in the absence of a cosolvent, and the study of $\Delta\delta$ s should always be done using external references.

In addition, the authors overlook some of the results reported previously for this and other related systems. Although they indicate that their conclusions regarding the formation of H-bonds between the imidazolium C2-position proton and the oxygen atoms of the sugar hydroxyl groups agree with molecular dynamics (MD) simulation data from Youngs *et al.*,^{2,3} they fail to discuss that these claims disagree with results from the experimental ¹³C and ^{35/37}Cl NMR relaxation studies which are cited in their manuscript.^{4,5} It is important to indicate that Youngs *et al.* propose that these interactions exist, but do not provide strong evidence to support their presence or absence. On the other hand, although our relaxation studies do not explain the solvation phenomena at the atomic level, they clearly indicate a lack of specific interaction between the carbohydrate and the imidazolium cation. There are, however, other documented studies regarding sugar solvation in ILs that should have been cited in the manuscript. Systems consisting of [C₄mim]Cl and glucose, [C₄mim]Cl and cellobiose, and [C₂mim]OAc and cellobiose have been

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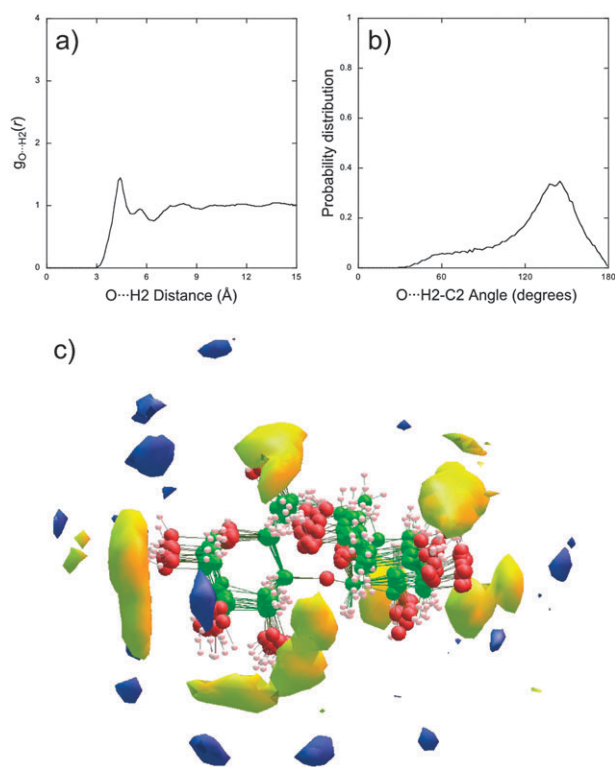


Fig. 1 O...H2 RDFs (a), O...H2-C2 ADFs (b), and spatial distribution of OAc⁻ (yellow) and [C₂mim]⁺ ions (blue) around cellobiose (c) obtained from MD simulations of the [C₂mim]OAc/cellobiose system.⁷ The most stable conformations of the sugar sampled in the simulation are shown.

investigated in detail by means of MD simulations.^{6,7} As described in these reports, the solvation mechanism is based on the interaction of the IL anion with the hydroxyl group protons of the sugar solute. More importantly, these studies also demonstrate that the IL cation does not play a primary role in the dissolution process.

As an example, we show in Fig. 1 the radial and angular distribution functions (RDF and ADF) between the sugar hydroxyl group oxygen and the imidazolium C2-position proton obtained from MD simulations of the [C₂mim]OAc/cellobiose system.⁷ It is clear that based on standard geometric definitions,⁸ neither the distance nor angular requirements for H-bond formation are fulfilled. This is depicted visually by spatial distribution plots (Fig. 1c), which show that although the acetate anions are in close proximity to the carbohydrate hydroxyl groups, the imidazolium cations lie on the periphery. These results not only corroborate NMR measurements, but they also agree with data from computational studies recently published by Liu and co-workers.⁹ Furthermore, this solvation model is

consistent with a number of reports which recognize the anion H-bonding basicity as the primary parameter governing the dissolution of cellulose in ILs.^{10–13}

In summary, we believe that the data presented by Zhang and co-workers does not support their claims. In addition, the conclusions are speculative and biased due to the partial interpretation of results from the literature. As we and others have shown, both experimental and theoretical studies indicate that the imidazolium ion is not involved in H-bonding with the sugar solute as proposed in the manuscript. It is worth noting, however, that the structure of the IL cation is known to have an effect on cellulose solubility.^{10–13} Further studies are thus necessary to properly address this issue.

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