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1	Liquid Structure and Dynamics in the Choline Acetate:Urea 1:2 Deep Eutectic Solvent.
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4 5	Alessandro Triolo <sup>1,*</sup> , Maria Enrica Di Pietro <sup>2</sup> , Andrea Mele <sup>2</sup> , Fabrizio Lo Celso <sup>1,3</sup> , Martin Brehm <sup>4</sup> , Valerio Di Lisio <sup>5</sup> , Andrea Martinelli <sup>5</sup> , Philip Chater <sup>6</sup> , and Olga Russina <sup>1,5,*</sup> .
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7 8	<sup>1</sup> Laboratorio Liquidi Ionici, Istituto Struttura della Materia, Consiglio Nazionale delle Ricerche, (ISM- CNR) Rome, Italy
9	<sup>2</sup> Department of Chemistry, Materials and Chemical Engineering "G. Natta", Politecnico di
10	Milano, Milano, Italy.
11	<sup>3</sup> Department of Physics and Chemistry, Università di Palermo, Palermo, Italy.
12	<sup>4</sup> Institut für Chemie, Martin-Luther-Universität Halle–Wittenberg, Halle (Saale), Germany.
13	<sup>5</sup> Department of Chemistry, University of Rome Sapienza, Rome, Italy.
14	<sup>6</sup> Diamond House, Harwell Science & Innovation Campus, Diamond Light Source, Ltd.,
15	Didcot, Oxfordshire OX11 0DE, UK
16	
17	

Corresponding Authors: A. T. (triolo@ism.cnr.it); O.R. (olga.russina@uniroma1.it)

## 21 Abstract.

22 We report on the thermodynamic, structural and dynamic properties of a recently proposed Deep Eutectic 23 Solvent (DES), formed by choline acetate (ChAc) and urea (U) at the stoichiometric ratio 1:2, hereinafter 24 indicated as ChAc:U. Although the crystalline phase melts at 36-38 °C depending on heating rate, 25 ChAc:U can be easily supercooled at sub-ambient conditions, thus maintaining into the liquid state, with 26 a glass-liquid transition at about -50 °C. Synchrotron high energy X-ray scattering experiments provide 27 the experimental data for supporting a Reverse Monte Carlo analysis to extract structural information at 28 atomistic level. This exploration of ChAc:U's liquid structure reveals the major role played by hydrogen 29 bonding in determining interspecies correlations: both acetate and urea are strong hydrogen bond 30 acceptor sites, while both the choline hydroxyl and urea act as HB donors. All ChAc:U moieties are 31 involved in mutual interactions, with acetate and urea strongly interacting through hydrogen bonding, 32 while choline being involved mostly in van der Waals mediated interactions. Such a structural situation 33 is mirrored by the dynamic evidences obtained by means of <sup>1</sup>H NMR techniques, that show how urea 34 and acetate species experience higher translational activation energy than choline, fingerprinting their 35 stronger commitments into the extended hydrogen bonding network established in ChAc:U.

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#### 43 Introduction.

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In the last decade large interest has been growing around deep eutectic solvents (DES)<sup>1,2</sup> and their 45 applications in several fields<sup>3–8</sup>. After the classification proposed by Smith et al. of DES in terms of 46 four different types<sup>3</sup>, those belonging to type III are among the most commonly encountered ones. 47 48 These latter DES are composed by a mixture of a salt (e.g. choline (i.e. the (2-hydroxyethyl)-49 trimethylammonium cation) chloride) with a hydrogen bonding donor (such as urea, glycerol, etc.) 50 with, depending on the concentration ratio between the two components, a melting point depression 51 resulting from their mixing. The large interest on these compounds stems from several appealing 52 properties, not least their cheap production cost and easy preparation and purification. Most of them are 53 also characterised by nonflammability, bio-compatibility and low toxicity, thus turning out to be ideal 54 media for the development of a variety of processes. On the other hand, most of these appealing 55 features stem from the combination of chemical-physical properties of the different components. 56 Accordingly, by (even minor) changes to their chemical nature, one can efficiently modulate the resulting macroscopic performance, thus leading to the classification of DES as task-specific solvents.<sup>4</sup> 57 58 Among the most well-known DES, we recall the stoichiometric 1:2 mixture of choline chloride (CC) and urea (U), sometimes referred to as reline.<sup>9–16</sup> Dry reline melts at ca. 31  $^{\circ}C^{17}$  and has attracted huge 59 60 interest over the last few years. Other CC-based DES have been proposed, including CC-glycerol (Gly) 1:2 (glyceline)<sup>18–22</sup>, CC-ethylen glycole (EG) 1:2 (ethaline)<sup>22–24</sup> and, more recently, CC-water 1:3.3-4.2 61  $(aquoline)^{25-27}$ . The recent interest in DES stems from the opportunity that they provide to modulate 62 63 their solvating properties by changes in their chemical composition. Aiming at expanding the spectrum 64 of properties, other anions paired with choline have been explored as well. For example, choline acetate 65 (ChAc) has been recently considered as an interesting ionic liquid to be paired with an HB donor to 66 lead to a DES. ChAc is an ionic liquid with melting point at 51 °C, proposed by Fukaya et al., as an interesting example of an IL composed solely of biomaterials.<sup>28</sup> The opportunity to use it as a salt for 67 68 preparation of a DES was presented by Zhao et al., who showed the eutectic nature of mixtures of 69 ChAc with urea (1:2), Gly and EG; these DES showed low viscosity, high biodegradability and excellent compatibility with lipase.<sup>29</sup> More recently ChAc mixtures with different HBDs were probed 70 71 for their efficiency towards enzymatic reaction with β-galactosidase.<sup>30</sup> In 2020, some of us used ChAcbased DES in order to efficiently solubilise hemicellulose at mild conditions.<sup>31</sup> 72



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This intense applicative activity calls for deeper understanding of the chemical-physical properties of

dynamic properties of the DES composed by ChAc and urea at 1:2 molar ratio, hereinafter indicated as

ChAc-based DES that have so far received negligible attention compared e.g. to their CC-based

equivalents. Here we present a detailed experimental and computational study of structural and

ChAc:U. The structural properties of ChAc:U have been obtained by merging high-energy X-ray

structural details of the liquid organization in bulk. The sample has also been probed with NMR

and dynamic properties of a new, eco-sustainable DES, paving the way for its application as a

complementary medium to other related DES.

diffraction and a Reverse Monte Carlo computational approach, aiming at extracting atomistic level

techniques, aiming at extracting dynamic information related to rotational and translational processes,

occurring around room temperature. Overall, this study provides a careful characterization of structural

### 88 Experimental and Computational details.

- 89 Choline acetate (ChAc) used for DSC and X-ray scattering was a TCI product; urea was a Sigma
- 90 Aldrich product. ChAc and urea were dried under vacuum at ambient temperature for several days.
- 91 Eutectic mixtures at 1:2 ChAc:U ratio were prepared in a glovebox with an inert atmosphere to reduce
- 92 ambient moisture contamination, leading to ChAc:U formation (see Scheme 1). After mixing, the
- 93 sealed vials were kept at 40 °C under constant agitation for at least one hour, to lead to a transparent



Scheme 1. Schematic representation of choline (top, left), acetate (top, right) and urea (bottom) moieties of ChAc:U (choline acetate:urea=1:2). The nomenclature of the different atomic species is shown. homogeneous liquid. The sample could be maintained amorphous, when kept at ambient temperature (20 °C) in thin sealed capillaries; it would crystallise when kept inside large sealed vials.

DSC thermograms were acquired by a Mettler Toledo DSC 822e equipped with a FRS5 sensor and a liquid nitrogen cooler. The furnace was purged during the measurement with dry nitrogen at a flow rate of 30 ml min<sup>-1</sup>. A sample of about 5 mg was weighted in a 40  $\mu$ l aluminium pan and rapidly sealed. DSC scans comprised of a cooling

106 from 50 to -125 °C followed by a heating from -125 °C up to 50 °C, with a heating/cooling rate of 2/10107 °C min<sup>-1</sup>.

Warm, liquid ChAc:U was loaded into a borosilicate capillary of 1.5 mm outer diameter, which was glue-sealed. After this operation, the sample maintained liquid even at ambient temperature (ca.  $20^{\circ}$ C). The total high-resolution X-ray scattering data were collected on the I15-1 beamline at Diamond Light Source, UK, using X-rays of wavelength 0.309574 Å and a Perkin Elmer XRD 4343 CT detector. The total scattering data were integrated to 1D using DAWN<sup>32</sup> and then normalised and corrected to extract S(Q) using GudrunX<sup>33,34</sup>.

ChAc and U for NMR experiments were purchased from Iolitec and Sigma Aldrich, respectively, and
used without further purification. The DES at 1:2 molar ratio was prepared by the heating method, by

116 mixing the two constituents at 80 °C under stirring for 1h, until a homogeneous and transparent liquid

117 was formed. As the freshly prepared ChAc:U nor its starting components were dried, a residual amount

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118 of water is present in the sample (5.7 wt% by Karl Fischer titration). Controlled amounts of water are 119 beneficial to reduce the viscosity and allow for satisfactorily resolved NMR spectra. The sample was transferred to a 5 mm NMR tube, equipped with a capillary containing DMSO-d<sub>6</sub>. NMR measurements 120 121 were performed at 11.74 T NMR with a Bruker NEO 500 console equipped with a direct observe 122 BBFO (broadband including fluorine) iProbe (<sup>1</sup>H resonance frequency of 500.13 MHz). Measurements 123 were performed over a temperature range of 278 K to 358 K, in 5 K increments, and a minimum of 15 124 min allowed for thermal equilibration. The residual amount of water together with the liquid tendency 125 to remain in a supercooled state when slowly cooled (see Results & discussion) allowed for NMR 126 measurements at such temperatures.

127  $T_1$  relaxation measurements were carried out without sample spinning with the inversion recovery (IR) 128 pulse sequence, using relaxation delays at least five times the longest  $T_1$ , and the instrument was 129 carefully tuned, shimmed, and the 90° pulses calibrated before each measurement. The spin-lattice 130 relaxation rates were measured using data matrices of 16384 (t<sub>2</sub>)  $\times$  16 (t<sub>1</sub>), over a spectral width of 9 131 ppm for various delay times  $\tau$ , ranging from 0.05–5 to 0.05–12 s, according to the temperature. A total 132 of two transients per increment were collected for each  $T_1$  experiment. The baselines of all arrayed  $T_1$ 133 spectra were corrected prior to processing the data and integrals were used to calculate relaxation times. 134 A single exponential decay was observed for all samples over the entire temperature range investigated. 135 Relaxation times were computed from experimental raw data by means of the Bruker  $T_1/T_2$  relaxation 136 module using the manual integration option and applying the standard one-component fitting function. 137 Data were processed three times and errors were calculated from the maximum standard deviation 138 found at the lowest temperature. Maximum errors are estimated to be 1%. Fits to extract the correlation 139 times and rotational activation energies from the relaxation rates were performed with OriginPro 2018 140 using a user-defined function with the Levenberg–Marquardt algorithm. For the fit procedure, average 141 errors were estimated to be 5%

Self-diffusion coefficients were measured by pulsed field gradient (PFG) experiments by applying sineshaped pulsed magnetic field gradients along the z-direction up to a maximum strength of G = 53.5 G $cm^{-1}$ . All the diffusion experiments were performed using the bipolar pulse longitudinal eddy current delay (BPP-LED) pulse sequence. All experiments were carried out over a spectral width of 9 ppm, with a total of eight transients per increment. The relaxation delay was set to at least five times T<sub>1</sub>, and four dummy scans were programmed prior to acquisition. The pulse gradients were incremented from 2



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148 to 95% of the maximum gradient strength in a linear ramp with 32 steps. For each DOSY experiment, 149 the duration of the magnetic field pulse gradients ( $\delta$ ) and the diffusion times ( $\Delta$ ) were optimized to 150 obtain, where possible, 95% signal attenuation for the slowest diffusion species at the last step 151 experiment.  $\delta$  values were in the 2.4–6 ms range, while  $\Delta$  values were 0.4–0.8 s long. The baselines of 152 all arrayed spectra were corrected prior to processing the data. Data were processed using an 153 exponential filter in F2 dimension (LB = 0.3 Hz), and integrals were used in calculating relaxation 154 times. The determination of self-diffusion coefficients used the Bruker  $T_1/T_2$  module of TopSpin for 155 each peak. The precision of the measured diffusion coefficients is estimated to be within 3%.

156 2D <sup>1</sup>H-<sup>1</sup>H nuclear Overhauser enhancement (NOESY) experiments were recorded at 298 K by using 157 the phase-sensitive ge-2D NOESY pulse sequence using echo-antiecho (noesyetgp in the Bruker 158 library). Spectra were recorded using eight transients over 4096 (t<sub>2</sub>) × 256 (t<sub>1</sub>) complex data points. 32 159 dummy scans and mixing times in the range 20 – 500 ms were used. The relaxation delay was set to 4 160 s. The NOESY data sets were processed by applying a sine squared window function in both 161 dimensions (SSB = 2) prior to the Fourier transform.

The EPSR approach has been used to model the X-ray diffraction data.<sup>35</sup> This is a robust Reverse 162 163 Monte Carlo approach (using a NVT ensemble) that is based on the optimization of the empirically 164 proposed potential that leads to the best agreement with experimental diffraction data. 165 We used a simulation box containing 100 ChAc ion pairs and 200 urea moieties (ChAc:Urea=1:2) with a density of 1.17 g/cc<sup>30</sup> (cubic box size=35.3 Å) at 25 °C. The starting interatomic potential used 166 167 for choline and urea is the one that was successfully used by Hammond et al. in their study of reline.<sup>10,36</sup> The acetate interaction potential parameters are the same used by Bowron et al. in their study 168 of acetate based ionic liquids.<sup>37</sup> The used parameters are reported in the Supplementary Information. 169 170 After an equilibration of ca. 6,000 steps, the EPSR was activated and further 10,000 steps delivered a 171 good agreement of the calculated diffraction pattern with the experimental one. At this stage, further 172 7,000 steps were collected to achieve statistical accuracy on the structural observables (pair distribution 173 functions, angular distributions etc.). In order to evaluate structural properties from the resulting Monte 174 Carlo trajectories, the TRAVIS software was used.<sup>38–40</sup>

### 177 **Results & discussion.**

178 ChAc:U's DSC trace is shown in **Figure 1**, where two thermal traces are shown with heating/cooling

179 rates equal to 2 and 10°C/min, respectively. It appears that ChAc:U, if cooled from the melt state, can



Figure 1. Thermal traces of ChAc:U recorded at two different heating/cooling rates (2 and 10 °C min<sup>-1</sup>, respectively). Indications of the liquid-glass transition (Tg), cold-crystallization (Tcc) and crystal melting (Tm) are highlighted.

be easily supercooled, maintaining in the liquid state and eventually converting into a glass, without crystallization intervening. The liquid-glass transition (Tg) can be detected in a small temperature range between -48 and -50 °C in both cooling and heating stages. On the other hand, upon heating the glass, cold-crystallization (Tcc) occurs at 6 °C and 19 °C depending on the heating rate. Soon after, the crystalline phase of ChAc:U melts at Tm = 36 °C at  $2^{\circ}$ C/min or at Tm = 38 °C at 10 °C/min.

It is noteworthy that, upon cooling from the

193 melt, ChAc:U remains in the liquid supercooled state at 20 °C for long time (several days).

Accordingly, we determined the liquid structure of ChAc:U at ambient temperature, without incurring
 into sample crystallization during the experiment time duration. Synchrotron X-ray diffraction data
 collected in such a way are reported in Figure 2. It appears that ChAc:U is characterised by an X-ray
 diffraction pattern similar to the ones from other choline-based DES, such as reline, aquoline etc.
 <sup>10,11,21,24,27,41–43</sup>

The quality of the agreement of experimental X-ray scattering pattern and the corresponding EPSR computed quantity is shown in **Figure 2**. The EPSR-derived X-ray weighted scattering pattern nicely accounts for the experimentally observed features, thus providing a validation support to the structural information that can be extracted from the computed trajectories. It can be appreciated that similarly to other choline-based DES<sup>10,11,21,24,27,41–43</sup>, the experimental X-ray scattering pattern does not show appreciable features at low Q values, apart from the low Q peak at ca. 1.5 Å<sup>-1</sup>, thus suggesting that no large scale structural heterogeneities occur in this system, which could be related either to polar/apolar

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- 206 segregation <sup>44–47</sup> or to mesoscopic phase separation <sup>48–50</sup>. The EPSR-generated trajectories were further
- 207 interrogated to extract structural information on bulk ChAc:U.



Figure 2. Comparison between experimental (black) and EPSR-computed (red) X-ray scattering patterns from ChAc:U at ambient temperature.

Figures 3 shows the center of mass pair distributions functions (pdf) for the three moieties in ChAc:U, namely, choline cation (C), acetate anion (A) and urea (U). It emerges that strong correlations exist between differently charged ionic species and between urea and all the components. Correlations between ionic species with the same charge are instead weaker and less well defined. CC correlations are characterised by a weak broad peak centred at ca. 6.5 Å, building up a solvation shell containing ca. 3 moieties. This coordination number is substantially different from what is found in the case of reline,



Figure 3. Pair distribution function between centers of mass of ionic species (cation (C), anion (A)) (left) and urea (U) with A and C (right) in ChAc:U, as obtained from the EPSR modelling.

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214 where choline is surrounded by approx. 6 other choline cations. Such a situation likely stems from the 215 larger size, as well as the different shape and symmetry of acetate as compared to chloride anions. Each choline cation is on average surrounded by 3.4 acetate anions with a correlation peak at 5.3 Å. For 216 comparison in reline, 4.5 chloride anions where found in the first shell<sup>10</sup>, while 1 chloride anion was 217 found in the same shell in malicine<sup>51</sup>. Urea is characterised by strong correlations both with other urea 218 219 moieties and with both cations and anions. First solvation shells are detected around each ionic species, 220 with peaks centred at 5.1 Å and 4.5 Å and 6 and 4 nearest neighbour urea moieties for choline and acetate, 221 respectively.

Figure 4 reports a series of pdfs related to selected correlations between atomic species belonging to
 the different moieties building up bulk ChAc:U.



Figure 4. Selected pair distribution functions between different atomic species belonging to the three moieties in ChAc:U (choline, acetate and urea, respectively), after the EPSR modelling.

The selected pdfs indicate the existence of strong correlations between the different moieties. In particular, those pdfs involving acetate and either choline or urea, are characterised by strong peaks, fingerprinting hydrogen-bonding mediated interactions. Such interactions will be further explored later in the manuscript. Choline-choline correlations are rather weak and broadly distributed. The strongest correlation is between neighbour nitrogen atoms, with a peak centred at 6.5 Å, and a neighbour number of ca. 2.5 up to 7 Å. We also detect a relatively strong N1-COH correlation centred at ca. 5.3 Å with approximately 2.5 nearest neighbours (n.n.); however there is only weak interaction of the nitrogen

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with the hydroxyl group (weak peaks for N1-OH between 4 and 5 Å). Neighbour acetate anions are 231 232 only correlated through their methyl groups for which we detect a C1x-C1x peak at 4 Å, with one 233 methyl group directly correlated to the reference one. Urea-urea correlations look more structured: we 234 will see later that this is also because of the existence of hydrogen bonding interactions and accordingly 235 we find strong peak in the OU-NU pdf at ca. 3 Å, with a n.n. population of 2 NUs around the reference 236 OU. The other peaks reported in **Figure 4 c**) indicate the existence of strong correlations also between 237 other urea's moieties such as NU-NU (3 n.n.), CU-OU (2 n.n.) and, in particular, CU-CU (4 n.n.). Similar observations led Edler et al. to propose the existence of urea clustering in reline.<sup>10</sup> Inter-species 238 239 correlations are dominated, as we will see later in more detail, by HB correlations. Overall these 240 correlations look much stronger than correlations between similar species. The selected pdfs in **Figures** 241 4 d)-f) reflect in an indirect way the existence of such interactions. Choline-acetate correlations are characterised by a strong Ox-OH peak at 2.7 Å, fingerprinting the HB between the two species. The 242 243 broad peak related to the Cation-Anion pdf in Figure 3 is likely related to the existence of different 244 solvation scenarios of acetate around the reference choline: in particular, acetate will coordinate choline 245 both at the hydroxyl side and at the ammonium side. This latter scenario is fingerprinted in the Ox-N1 and C1x-N1 pdfs by the strong peaks centred at 4.2 and 5 Å, respectively. Choline and urea appear to 246 247 interact mostly through choline's ammonium: pdf peaks for N1 with CU, NU and OU are eminent at distances between 4 and 5.5 Å. Correlations mediated through choline's hydroxyl group look weaker. 248 249 The competition between acetate and urea in coordinating choline's N1 leads to ca. 5 urea and 3 acetate moieties surrounding N1 by a distance of ca. 7 Å. For comparison, the OH moiety of choline is 250 251 solvated by 0.6 acetate and 0.9 urea in the first shell (up to 4.5 Å) and ca. 2 choline in the first shell (up 252 to 7 Å). Acetate and urea interact through HB involving urea's hydrogen and the carboxyl group; such 253 an interaction, fingerprinted by the Ox-NU peak at ca 3 Å, is consistent with two different solvation environments indicated by the two peaks in the C1x-NU pdf (3.7 and 5 Å). 254

As mentioned, HB interactions are fundamental in driving structural correlations in ChAc:U. In **Figure** 5, the pair distribution functions associated to such correlations involving either the choline HOH or the urea HU1/2 donor groups. In particular, we specifically monitor the two hydrogens, HU1 and HU2, attached to the same nitrogen in urea (HU1 being the hydrogens in trans with the urea's oxygen and HU2 being the cis hydrogens), aiming at assessing differences in the HB features, due to steric hindrance. For these HB correlations the combined distribution functions accounting for the distance H··O and the angle D-H··O (where D is the HB donor atom) are reported in the supplementary



Figure 5. Pair distribution functions related to hydrogen bonding interactions in ChAc:U, as obtained from the EPSR modelling: (left) pdf related to the HOH donor agent in choline and (right) pdf related to the trans (HU1) and cis (HU2) hydrogens in urea.

by the shortest and strongest interaction, also the angular dependence of these HB reflects their
linearity. In terms of pdf peak amplitude, the next most intense peaks correspond to those involving

265 urea's oxygen (OU) and finally choline's oxygen (OH). Overall, all these HB interactions are found to



Figure 6. Linear Sankey diagram describing the hydrogen bonding topology in ChAc:U. Numbers correspond to the average hydrogen bond count per donor/acceptor. be characterised by a quite linear geometry, as shown in Figures **Figures S1-3.** In order to better illustrate the balance between HB donor and acceptor capabilities of the different moieties in ChAc:U, we exploit the linear Sankey diagram approach of **Figure 6**, introduced recently for this kind of analysis.<sup>39</sup> A wealth of information can be straightforwardly extracted from such a plot, on the nature of HB networking in ChAc:U. The hydrogen bond donated by choline OH (HOH) (upper left) is mainly involved with the acetate Ox (lower right). There is only a tiny amount of hydrogen bonding interaction between HOH and choline OH and negligible interaction with urea. The trans and cis protons of urea (HU1



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Figure 7. Spatial distribution functions around reference urea (top, left), choline (top, right) and acetate (bottom, left). The coloured lobes correspond to 20% distribution of choline (blue), acetate (red) and urea (yellow) in ChAc:U.

281 and HU2, respectively) behave differently. While the trans protons (HU1, middle left) do not form

282 hydrogen bonds to choline OH, but form strong hydrogen bonds to both urea OU and acetate Ox, the

283 cis protons (HU2, lower left) also form hydrogen bonds with choline OH. Now considering the

284 acceptors (right side), incoming hydrogen bonds at choline OH almost exclusively come from the urea

285 cis protons, HU2. The urea oxygen receives strong hydrogen bonds from both cis and trans urea's

286 protons, while it almost receives no hydrogen bonds from choline HOH. A similar picture arises for

287 acetate Ox, where the hydrogen bond received from the urea trans protons is most significant. Overall,



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the major role played by the acetate anion in establishing HB interactions is confirmed by this graph;analogously the minor role played by choline's OH acceptor site is also highlighted.

290 Additional understanding of the mutual spatial distribution of the different species with respect to each 291 other can be obtained by inspecting the spatial distribution functions reported in Figures 7. The first of 292 such plots refers to the distribution of the three different moieties surrounding a reference urea 293 molecule. Urea is strongly correlated with acetate anions (red lobes) at spatial locations corresponding 294 to its cis and trans hydrogens. Choline cations (blue lobes) distribute in a much more homogeneous 295 way around urea and correlations are not driven by HB, but rather by dispersive interactions. Finally, 296 urea (yellow lobes) competes with acetate to access the reference urea hydrogens; it moreover interacts 297 with reference urea oxygen. It also appears that choline tends to distribute around urea, aiming at 298 interacting also with the other species surrounding the reference one. In **Figure 7** the distributions 299 around a reference choline cation are also shown. The acetate anion is strongly interacting with the 300 hydroxyl group, with a weak competition on this site with urea; otherwise, both the choline cation and 301 urea are distributed rather homogeneously around the whole reference choline, with urea approaching 302 closer than choline the reference molecule. **Figure 7** also shows the distributions of cations and urea 303 around a reference acetate anion. The two species have similar distributions, although urea succeeds in 304 accessing closer to the anion, presumably due to its smaller size. Both moieties approach the anion 305 from the charged carboxyl part, thus reflecting the development of hydrogen bonding interactions. 306 Anions tend to approach the reference acetate from the opposite side, leading to methyl-methyl group 307 correlations (data not shown).

These pictures are consistent with the overwhelming role played by acetate in HB interacting with both urea's and choline' HB donor hydrogens. On the other hand, the HB donor and acceptor nature of urea and the possibility of choline to interact not only with coulombic forces, but also with dispersive ones, make these two moieties able to efficiently solvate any component in ChAc:U. Analogously to the case of reline, an intertwining of the different species occurs in delivering an intimate mixing of these components at atomic level.





Figure 8. <sup>1</sup>H relative shift observed for ChAc:U as a function of the temperature.

approach, variable-temperature NMR measurements were performed. As inter-species correlations appear to be dominated by HB interactions, the upfield or downfield movement of the temperature-dependent <sup>1</sup>H chemical shift was monitored to give a preliminary insight into the strength of the HB of the detected proton. **Figure 8** shows the relative shifts of the <sup>1</sup>H NMR signals of ChAc:U, which are defined as  $\Delta \delta = \delta - \delta_0$ , with  $\delta_0$  the chemical shift of a given proton in the pure DES and  $\delta$  the chemical shift of the same proton for increased temperature. <sup>52,53</sup>

The remarkable upfield shift of urea protons is compatible with a weakening of the H-bond strength at the urea site with temperature,<sup>54</sup> and points towards their strong involvement in the HB network of the mixture. No relevant changes are observed for the choline signals, including the N-methyl groups, which is in line with a minor role played by the cation in the intermolecular network. Only a tiny upfield shift emerges for the methyl group of acetate, as they do not directly participate in the HB interactions but most likely feel a pale indirect effect of the major role played by the acidic group of the anion.

334 The NMR experiments of choice to probe spatial intermolecular networks are typically based on the 335 nuclear Overhauser enhancement (nOe). In extensively connected systems like DES it is however quite common to observe intra- and inter-correlations between all sites/species in the mixtures.<sup>55,56</sup> This is 336 337 the case for ChAc:U too, as displayed in **Figure S4** in the Supporting Information. Due to spin 338 diffusion and/or exchange (facilitated by the residual water), all signals are positive. Choline shows 339 intramolecular NOE signals, and intermolecular NOE are observed between all the three species, 340 choline, acetate and urea. As expected, intense correlations are observed between the hydroxyl group 341 proton of choline and urea, and the N-methyl groups of choline and urea. The methyl group of acetate 342 shows the strongest correlations with the N-methyl protons of choline and with urea. This confirms the 343 major role of these protons in the interactions holding the DES components together.

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The NOESY data provide then support to the scenario of an extended HB network in the DES, which is the root of its peculiar macroscopic properties. We also exploited relaxation and diffusion NMR experiments to shed more light on the system. Intermolecular interactions and dynamics are indeed intertwined, as strong correlations reduce motion – as one can intuitively envisage. T<sub>1</sub> relaxation times and self-diffusion coefficients were measured over an 80 °C temperature interval and analyzed to get quantitative descriptors of the motion(s).

As displayed in **Figure S5** in the Supporting Information, all temperature-dependent T<sub>1</sub> curves, but that corresponding to methyl protons of acetate, pass through a minimum. This indicates that the protons of choline and urea undergo a transition from the extreme narrowing ( $\omega_0 \tau_C < 1$ ) to the diffusion limit ( $\omega_0 \tau_C > 1$ ) relaxation regime between ~25 °C and ~50 °C. Contrarily, the methyl protons of the anion fail to undergo this transition in the studied temperature range due to their higher mobility. In the case of <sup>1</sup>H T<sub>1</sub>, where the predominant relaxation mechanism is the homonuclear dipole–dipole interaction, the relaxation rate R<sub>1</sub> is defined by the Bloembergen, Purcell, and Pound (BPP) approach as:<sup>57–59</sup>

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$$R_1 = \frac{1}{T_1} = C \left( \frac{\tau_C}{1 + \omega_0^2 \tau_C^2} + \frac{4\tau_C}{1 + 4\omega_0^2 \tau_C^2} \right)$$
(1)

with  $\omega_0$  the observe frequency (rad s<sup>-1</sup>) and C a term evaluated separately for each nucleus. The 358 359 correlation time of the dipolar interaction  $\tau_c$  can be thought of as the time required for the vector 360 connecting the interacting nuclei to rotate through the angle of one radian, and for small rigid molecules it commonly reflects the molecular reorientational time constant.<sup>59</sup> As for flexible ionic 361 liquids<sup>60,61</sup>, the  $\tau_c$  observed for ChAc:U have to be rather considered as a combination of molecular 362 363 reorientation and internal motions of each given segment. From the term in brackets in Eq. (1), it follows that T<sub>1</sub> is minimum when  $\omega_0 \tau_c = 2\pi \nu_0 \tau_c = 0.616^{-63}$ , which means here  $\tau_c = 0.616/(2\pi \cdot 10^{-63})$ 364  $500.13 \cdot 10^6$  Hz) = 196 ps. Such minimum T<sub>1</sub> value can be used to calculate C from Eq. (1), then 365 366 enabling the calculations of  $\tau_c$  values from the T<sub>1</sub> values observed at any temperature. The 367 temperature-dependent correlation times can be then used in an Arrhenius-type equation to calculate the "apparent" activation energy  $E_a^{rot}$  (averaged over several types of movements).<sup>61,64</sup> Alternatively, 368 369 by substituting the function of the correlation time approximated as an Arrhenius expression into the 370 BPP equation (Eq. (1)), and assuming C temperature insensitive, the combined equation can be directly solved yielding the same outputs within the experimental error. <sup>61,65</sup> Although the two methods are 371 372 essentially the same from the theoretical standpoint, the latter nonlinear least squares method is useful



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373 in cases where an exact minimum is not reached in the examined temperature range, and is 374 recommended even for protons where a T<sub>1</sub> minimum can be distinctly observed as it needs less steps with a reduced margin of error.<sup>61</sup> The nonlinear least squares method was used here to fit all T<sub>1</sub> data 375 376 obtaining the correlation times and activation energies reported in **Figure 9**. All temperature-dependent 377 curves followed perfectly the BPP model, which means that a single basic motion occurs in the studied temperature range.<sup>62</sup> The best-fit parameters are given in **Table S1** in the Supporting Information, 378 379 together with those obtained by applying the most widely used method based on the T<sub>1</sub> minimum 380 followed by Arrhenius plot of the activation energies, to confirm that comparable results are obtained. Urea protons show the longest  $\tau_c$  values (slowest rotational motion), and the methyl protons of acetate 381 382 the shortest ones (fastest rotational motion), while the three methylene and methyl sites of choline



Figure 9. (left) <sup>1</sup>H correlation times  $\tau_c$  vs temperature and (right) rotational activation energy  $E_a^{rot}$  (kJ mol<sup>-1</sup>) obtained for the different proton sites of ChAc:U.

383 exhibited all close, intermediate  $\tau_c$  values. A direct comparison between the correlation times of the 384 different sites and species is complicated due to the contribution of different relaxation mechanisms. 385 More informative are the rotational activation energies, which mark a significant difference between acetate from the one side, with  $E_a^{rot}$  of ca. 12 kJ mol<sup>-1</sup>, and choline and urea from the other, all with 386  $E_a^{rot}$  above 20 kJ mol<sup>-1</sup>. Hence, the rotational motion of the acetate protons is not only the fastest, also 387 388 due to the intramolecular rotation around the symmetry axis of the methyl group, but it also requires 389 less energy to occur. For the sake of completeness, we also report the correlation times and rotational 390 activation energy obtained from the BPP analysis of the temperature-dependent T<sub>1</sub> data of the peak 391 corresponding to the residual water and the hydroxyl proton of choline (Figures S5 and 9). All T<sub>1</sub>,  $\tau_c$ 



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and  $E_a^{rot}$  values essentially overlap those corresponding to urea protons, pointing towards a strong correlation between the rotational motion of the two species. Despite its relevance, the role of water in the intermolecular network of ChAc:U is beyond the scope of the present paper and will be deepened in a separate work on hydrated ChAc:U. Here the focus is on the role of the DES constituents - choline, acetate and urea - and we can safely assume that the residual water molecules will participate in the intermolecular network without drastic alterations of the mutual relationships among them.

398 In order to monitor the translational mobility and gather a more complete overview of the system, the 399 self-diffusion coefficients of the different ChAc:U moieties were measured by PFG NMR. The 400 diffusivities, D, probed in the range 278 - 358 K are given in **Figure S6** and **Table S2** in the 401 Supporting Information. As expected, the diffusion coefficients measured for the methylene protons of 402 choline yielded the same value as  $CH_3$ , hence only the latter is presented. The temperature dependence 403 of the diffusion coefficients over the whole probed temperature range was modelled in terms of an 404 Arrhenius-activated process. Translational activation energies are reported in **Figure 10** and fit 405 parameters in **Table S3** in the Supporting Information. While the activation energies associated with relaxation data are in the range 10-30 kJ mol<sup>-1</sup>, the activation energies associated with diffusion data 406 407 are larger  $(40-50 \text{ kJ mol}^{-1})$ . This is due to the different molecular motion affecting these apparent 408 activation energies, rotational versus translational, and is in agreement with behaviours found for instance in ionic liquids. <sup>66,67</sup> Noteworthy is the order of  $E_a^{transl}$ : urea  $\approx$  H<sub>2</sub>O + OH > acetate > choline. 409

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Figure 10. Translational activation energy  $E_a^{transl}$  (kJmol<sup>-1</sup>) obtained for all species in ChAc:U.

This is unrelated to the molecular size of the species and can be explained only by admitting that the translational motion of urea and acetate is slowed down by their strong involvement in the HB network. The major role of urea and acetate in the intermolecular network, inferred here from a dynamic parameter, fits the molecular picture outlined by means of more common techniques for structure elucidation, such as X-ray and NOESY. Note, also, that this prominent role is maintained here even in the presence of residual amounts of water (5.7 wt%). Contrarily, the activation energy of choline is the lowest one 423 regardless of its higher size due to its less fundamental role in the intermolecular connections. As urea 424 has proven to strongly connect with other constituents in several DES using both the oxygen and proton 425 nuclei (see also the linear Sankey diagram in Figure 6), its reduced rotational and translational mobility (high  $E_a^{rot}$  and  $E_a^{transl}$ ) is quite expected. The peculiar role of acetate is instead not a foregone 426 427 conclusion. The key role of this small anion in the HB network keeps it on a tight leash, strongly affecting its translational mobility and increasing its  $E_a^{transl}$ , which is a dynamic indicator of the whole 428 429 molecule. Contrarily, the rotational mobility of the methyl protons of acetate does not suffer from a 430 strong effect, as they are not directly participating in the HB network. Hence the corresponding  $E_a^{rot}$  - a 431 local dynamic parameter - is still smaller than the rotational activation energy of all other proton sites 432 of both choline and urea.

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437 Choline acetate mixtures with urea at a stoichiometric composition of 1:2 are deep eutectic media, 438 whose melting point is ca. 40 °C, but it can be easily supercooled into the liquid state at sub-ambient 439 conditions. Liquid ChAc:U structure at atomistic level has been investigated by means of synchrotron 440 high energy X-ray diffraction, supported by the EPSR Reverse Monte Carlo analysis approach that 441 allows extracting detailed information on the mutual interactions between ChAc:U's moieties. 442 Hydrogen bonding plays a major role in determining structure in liquid ChAc:U. Radial distribution 443 functions shows how acetate-mediated HB are among the strongest in the system; urea plays also a 444 major role as HB donor and these correlations are straightforwardly described by the use of a Sankey 445 diagram illustrating HB flow among the different donor and acceptor moieties. A complex intertwining 446 of different moieties is observed with coulombic interactions (via HB correlations) mostly involving 447 acetate and urea, while choline is involved mostly in dispersive interactions. This peculiar situation is 448 mirrored in the dynamics monitored in ChAc:U. While acetate's methyl group shows the lowest 449 correlation times and activation energy considering <sup>1</sup>H rotational motion, the anion diffuses slower than 450 expected from its size, thus confirming its strong role in the HB network. Choline turns out to be the 451 moiety with the lowest activation energy concerning diffusive dynamics, reflecting its secondary 452 involvement into the HB interactions network.

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# 454 Supplementary Material.

455 Combined distribution functions accounting for the hydrogen bonding geometries; NMR plots and456 tables; EPSR force field parameters.

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## 471 DATA AVAILABILITY.

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The data that support the findings of this study are available from the corresponding authors uponreasonable request.

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