

PRF Award Number: 58158-DNI6

Project Title: Computational design of deep eutectic solvents for natural gas sweetening applications

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Our research progress this year consists of: (1) simulating the physical properties of deep eutectic solvents using polarizable force fields, and (2) developing software tools to improve the accuracy of these simulations.

Our simulations used the polarizable AMOEBA force field, whose hallmark is the use of point multipoles and polarizable dipoles for accurate descriptions of molecular electrostatics. The force field for choline and urea was parameterized using the standard workflow, with additional refinement of the intramolecular valence and torsion parameters (*vide infra*). The simulations were run using the TINKER and OpenMM software packages. TINKER is used as a front-end to set up and run the simulations, and uses OpenMM to accelerate the simulations dramatically on graphics processing units (GPUs). Using Tinker-OpenMM, we are able to simulate a 25 ns molecular dynamics trajectory in a single day for a system consisting of 128 choline chloride molecules and 256 urea molecules (4864 atoms total). These simulation lengths were previously found to be sufficient for calculating the equilibrium properties of deep eutectic solvents. From these simulations, we are able to compute thermodynamic, structural, and dynamic properties, and validate simulation results by comparison to experimental data where available. The ACS-PRF award enabled the training of a graduate student in setting up these advanced molecular simulations.

Our simulations were carried out at 303 K to match an experimental study that derived RDFs using neutron diffraction data and empirical potential structural refinement.¹ We also compared results with a 2013 simulation study that used a non-polarizable force field in the popular OPLS-AA/AMBER paradigm.² Our preliminary results for structural data are shown in Figure 1 and Table 1. The simulated density is 1.06 g/cm³, which differs by ~12% from the experimental measurement of 1.19 g/cm³. The radial distribution functions show similar agreement with experiment compared to the non-polarizable study with one major exception: our simulations are much more accurate for hydrogen bonding of the choline hydroxyl group to chloride ion (Figure 1 bottom). One promising result is that the coordination numbers, computed by integrating the RDFs up to the first trough, are all in agreement with experiment to within the experimental error. Calculations of key kinetic properties, such as viscosity, are planned for the near future.

These results show that polarizable simulations using the AMOEBA model have the potential to make accurate predictions for deep eutectic solvents, because these simulations were not parameterized from experimental data. However, additional data from high-level quantum chemistry calculations may further improve the model accuracy. This motivated us to develop software tools to automate the computation of quantum chemical data for refining these force fields that we describe in the next section.

	AMOEBA	Exp
Urea – Cl ⁻	1.6	2.1 ± 1.0
Choline – Cl ⁻	3.8	4.3 ± 1.3
Choline – Urea	4.5	5.9 ± 2.8
Choline – Choline	6.5	6.7 ± 2.2
Urea – Urea	5.9	6.8 ± 3.0

Table 1: Simulated coordination numbers compared with experimental data taken from Ref. 1.

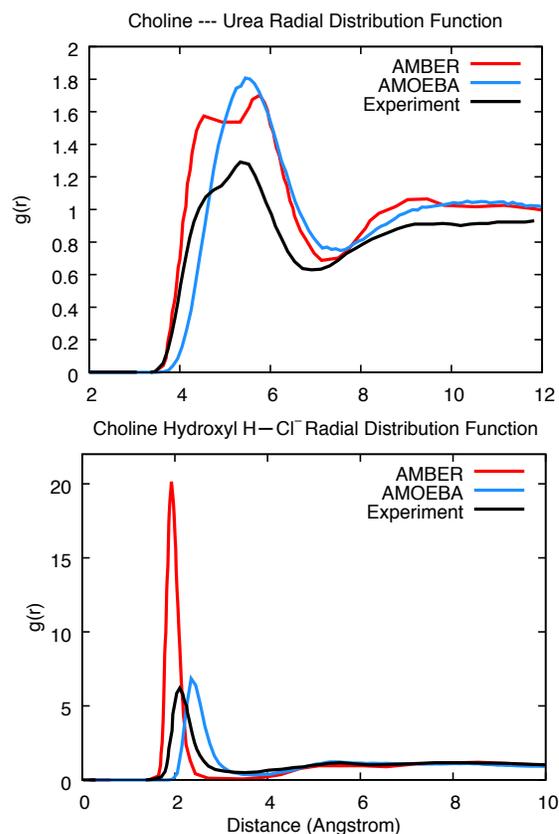


Figure 1: Radial distribution functions (RDF) for a 2:1 choline chloride:urea deep eutectic solvent. *Black:* RDF derived from experimental data from Ref. 1. *Red:* AMBER-OPLS simulations from Ref. 2. *Blue:* Polarizable simulations using AMOEBA model in this work. Top panel: RDF of choline and urea using molecular centers of mass. Bottom panel: RDF of choline hydroxyl hydrogen and chloride ion.

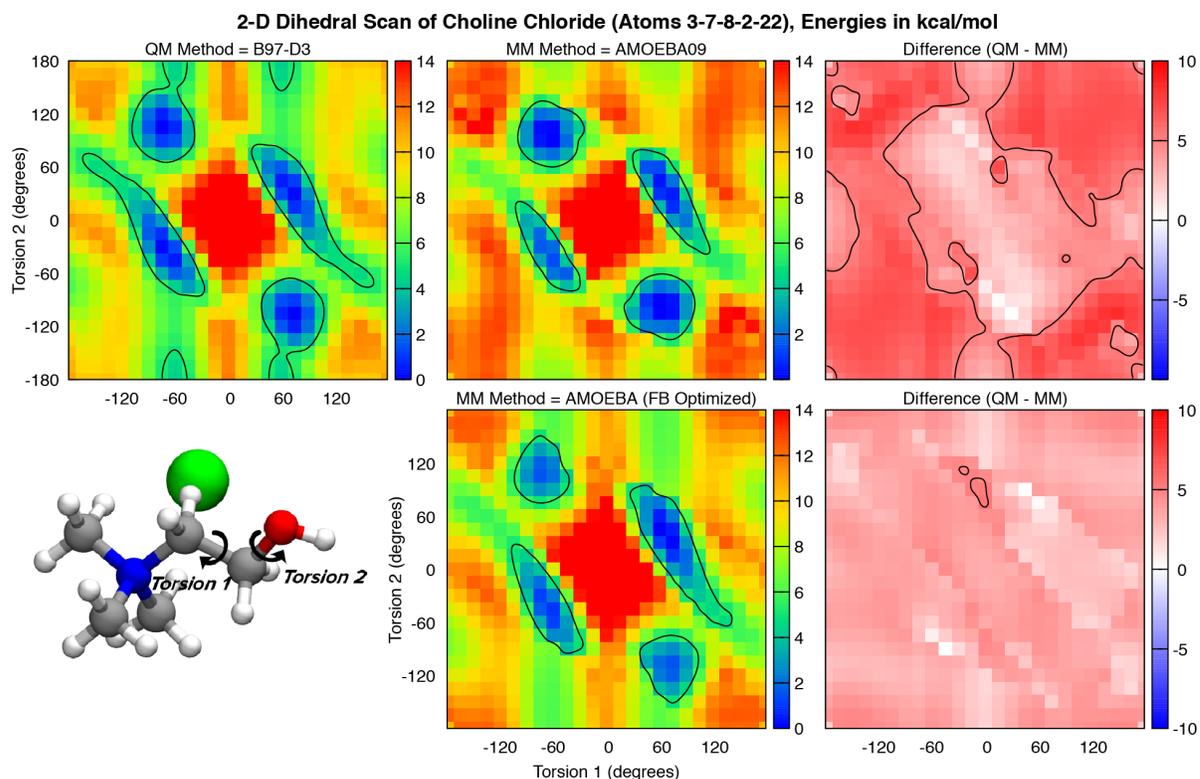


Figure 2: Torsional energy profiles for choline chloride. *Top left:* Reference energy from *ab initio* calculations using B97-D3/TZVP method. Contours are drawn at 5 kcal/mol. Structures are optimized with torsions constrained to values shown on grid. *Top middle:* Single-point energies computed using AMOEBA force field. *Top right:* Energy difference plot showing bias towards higher energies. *Bottom middle:* Single-point energies from AMOEBA force field after ForceBalance optimization. *Bottom right:* Energy difference plot showing improved agreement with *ab initio* method.

This ACS-PRF award supported a postdoc and the PI to develop software to improve force field accuracy. The standard parameterization tools do not include the computation of torsional energy profiles, which are important for flexible organic molecules. These calculations are made challenging by the many local minima on the potential energy surface, such as the formation of intramolecular hydrogen bonds. We developed the *torsiondrive* code that computes torsional energy profiles; a key innovation is the launching of new calculations where needed to reduce energy discontinuities from disparate local minima. The open-source code is available via GitHub.³ The energy profiles, and the use of the ForceBalance code to improve the accuracy of the intramolecular parameters, are summarized in Figure 2. We developed procedures to compute quantum mechanical intermolecular interaction energies,⁴ which we expect will be important for further improving the accuracy of simulating deep eutectic solvents. We also published a method to directly target the radial distribution function in ForceBalance.⁵ Fitting the choline chloride:urea RDF could provide simple empirical corrections to AMOEBA van der Waals parameters for other deep eutectic solvents.

REFERENCES CITED

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