Molecular docking simulations to determine organic cation sorption to organic matter

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Development of an environmental sorption model for charged contaminants to organic matter is challenged by the lack of knowledge on the extent of electrostatic binding mechanisms driving sorption. Current approaches to predicting sorption coefficients (K_d values) to environmental solids have largely been developed using empirical sorption data of neutral compound systems and, as such, largely underestimates electrostatic sorption contributions for charged systems. Thus, there is still a need to determine the extent of electrostatic and non-ionic contributions driving organic cation sorption to organic matter to improve prediction of K_d values.

Computational binding simulations are commonly used in the Pharmaceutical Sciences to account for ionic interactions in protein-ligand systems. Molecular docking techniques allow for prediction of sorbent/sorbate interaction mechanisms as well as calculated binding affinities arising from atom-atom interaction energy contributions (i.e. hydrogen bonding, electrostatic, and van der Waals energies). These simulations account for unique molecular charge distributions arising from polar sorbent and sorbate atoms in the form of partial charges. The Schulten humic acid model was used as a representative organic matter structure organic matter in the docking simulations. Experimental K_d values were obtained for organic cation sorption to Pahokee Peat.

Molecular docking outputs using AutoDock 4.2 suggest that increasing cation N-substitutions may lead to a shift in the underlying binding mechanisms due to amine increasing charge delocalization. Primary, secondary, and some tertiary amines interact with organic matter carboxylic groups via hydrogen bonds while positive charges on quaternary amine hydrogens were too weak to participate. Quaternary amines partition into hydrophobic organic matter pockets rather than participate in electrostatic interactions with organic matter functional sites. Differences in sorption within amine orders appear to be driven largely by the extent of van der Waals energy contributions. Calculated binding energies for 70+ cationic compounds correlated strongly with experimental sorption data further validating the representativeness of the Schulten humic acid model. Our work shows that molecular docking tools provide an straight-forward approach to studying binding mechanisms and calculating K_d values for cationic contaminants to organic matter.