Use of Molecular Dynamics Simulations to Investigate the Molecular Association of Dihydroxybenzoic Acids in Solution

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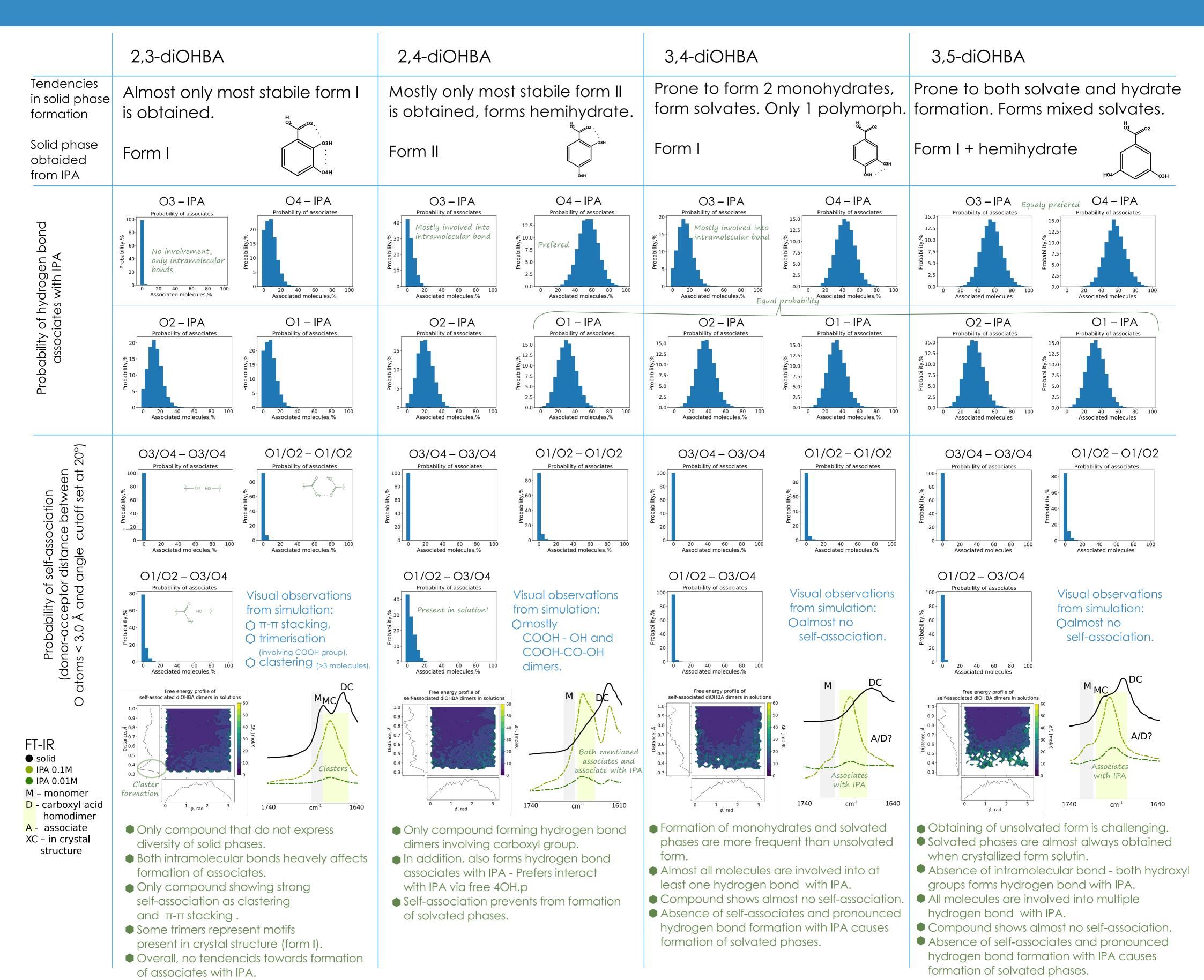


Molecular dynamics (MD) is a very versatile method that can depict the motion of the molecular system. It can be used in association studies in solution^{1,2} for small organic molecules such as dihydroxybenzoic acids (diOHBA) – six isomeric molecules with mutually different ability to form solvated and polymorphic forms³⁻⁶.

In the previous computational studies no distinctive tendencies for formation of carboxyl acid homodimer (present in almost all crystal structures) in solution was observed. However, calculations indicated towards existence of possible stable hydrogen bond associates with solvent molecules.

In this study, diOHBA isomers having different diversity of obtainable crystalline phases (2,3-, 2,4-, 3,4- and 3,5-diOHBA) and 2-propanol (IPA) as a solvent that can act both as hydrogen bond donor and acceptor and did not form solvate were used.

MD simulations for diOHBA IPA solutions were used to investigate molecular association processes and rationalize how these processes differed for each diOHBA and could influence obtainable crystalline phase. In addition, FT-IR spectroscopy (C=O antisymmetric stretch region) was used to experimentally confirm/deny the formation of associates observed in the simulations.



Conclusions

- Presence of intramolecular bonds (as in orhto-substituted diOHBA and with neighboring hydroxyl groups) hinders association with IPA (solvent) molecules thus also hinders formation of solvated forms.
- Pronounced self-association promotes formation of unsolvated phases. Furthermore, if hydrogen bond motif in solution resemble those present in crystal structure, more likely formation of specific will be observed.
- •The more freely molecule can form hydrogen bonds with IPA (solvent) molecules the more pronounced solvate former the compound is.

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