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Solution Chemistry and Structure

Roger Davey

Content: Studying and defining solute-solute interactions in the liquid phase. Techniques available. Speciation in solution. Do these (thermodynamic features have) an impact on nucleation rate or outcome? Examples – glycine/saccharin/benzoic acid/tetrollic acid/mandelic acid/paminobenzoic acid/co-crystals.

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The context - making clusters

$A + A \rightleftharpoons A_2$
 $K = [A_2] / [A]^2$

Equilibria in supersaturated homogeneous solution

monomers → dimers → Critical nucleus → crystal

Are the dimers created by thermodynamically driven self association present in the nucleation clusters – The link hypothesis.

Thermodynamics | Kinetics

Are these equilibria and quasi equilibria in anyway related?

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First a note about ideal solutions

The usual way: dissolve solid in solvent

The ideal way: melt solid and mix with solvent.

composition vs time graph

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A macroscopic view - 'ideal solubility' and why I use it.

Enthalpy changes: $\Delta H_{\text{solution}} = \Delta H_{\text{sublimation}} + \Delta H_{\text{solvation}}$
 $\Delta H_{\text{solution}} = \Delta H_{\text{fusion}} + \Delta H_{\text{mixing}}$

In an ideal solution $\Delta H_{\text{mixing}} = 0$.
 This means that $(E_{s-s} + E_{\text{sol-solv}})/2 = E_{s-solv}$
 Real solutions don't have this exact balance and in a non-ideal solution ΔH_{mixing} is thus non zero.

And the ideal solubility is given by a very familiar equation:
 $\ln(x_{\text{ideal}}) = \{\Delta H_f(1/T_m - 1/T) + \Delta C_p[T_m/T - \ln(T_m/T) - 1]\}/R$

If $x > x_{\text{ideal}}$ then negative deviationsolvation
 If $x < x_{\text{ideal}}$ then positive deviation.....aggregation.

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(102) plane

Untwinned

Twinned

A macroscopic link between solution chemistry and a crystallographic event that occurs at the point of nucleation.

Graph: 0 saccharin per mol solvent vs T (°C)

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Macroscopic picture: polymorphism of dihydroxybenzoic acid.

Form 1. Toluene

Form 2. Chloroform

Lower solubility in toluene – self association in toluene – self association gives dimer structure.

Solubility (mol/m³) vs T (°C) graph

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Solution chemistry - the path to more direct insights.

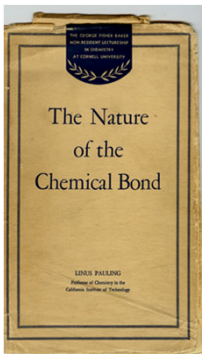
Year 1945 : page 307

'Benzoic acid and other carboxylic acids have been shown to associate to double molecules in solution in certain solvents such as benzene, chloroform, carbon tet and carbon disulphide. Benzoic acid exists in monomeric form in solution in acetone, acetic acid, ethyl ether, ethyl acetate and phenol; in these solutions single molecules are stabilised by hydrogen bond formation with the solvent.'

These data came from freezing point depression but could we now observe it directly using spectroscopy?

The Nature of the Chemical Bond

LINUS PAULING
Professor of Chemistry at the California Institute of Technology

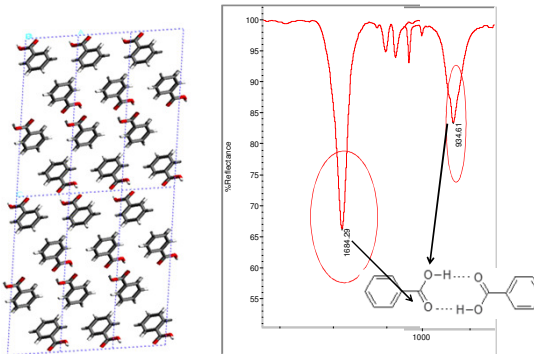


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FTIR Spectroscopy - crystalline benzoic acid.



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Saturated benzoic acid in toluene

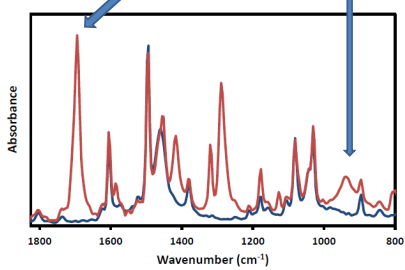


Figure 5.15: C=O region of the solution state FTIR spectra for toluene (dark blue) and saturated benzoic acid in toluene (red) (0.67M) at 25°C.

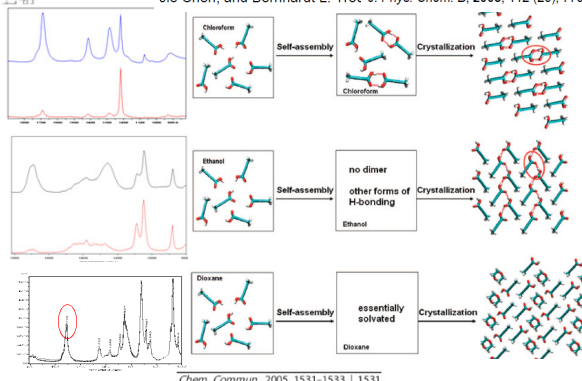
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Tetrolc acid and the link.

Jie Chen, and Bernhardt L. Trout *J. Phys. Chem. B*, 2008, 112 (26), 7794

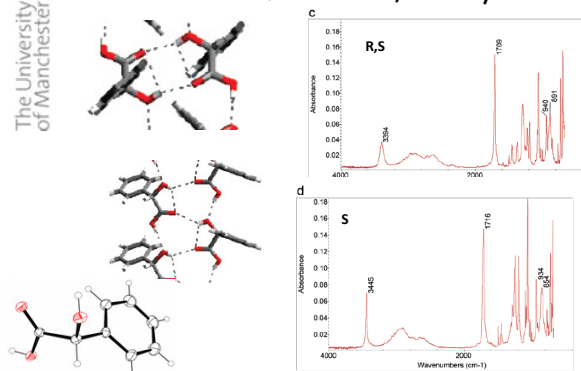


S. Parsons, R. J. Davis, G. Dent and R. G. Pritchard *Chem. Commun.*, 2005, 1531-1533 | 1531

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Some times there is no link - mandelic acid, chirality.

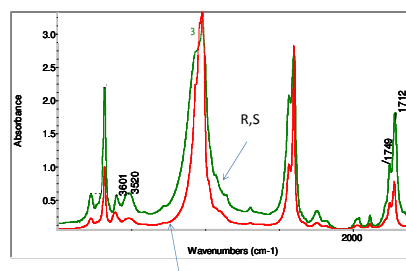


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Saturated solutions in CHCl₃ identical νc=O .



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Data analysis - C.A Hunter and M. J. Packer,
Chem Eur. J., 1999, 5, 1891- 1897

NMRDi_Dimer which use a Simplex procedure to fit the experimental data and determine the optimum solutions for the association constant, and the limiting bound and free chemical shifts. Thus, for example, *NMRDi_Dimer* fits the data to a dimerisation isotherm by solving the following equations.

$$[AA] = \frac{1 + 4K_d[A]_0 - \sqrt{(1 + 8K_d[A]_0)}}{8K_d}$$

$$[A] = [A]_0 - 2[AA]$$

$$d_{obs} = 2[AA]/[A]_0 d_d + [A]/[A]_0 d_f$$

In which $[A]_0$ is the total concentration, $[A]$ is the concentration of unbound free species, $[AA]$ is the concentration of dimer, K_d is the dimerisation constant and d_f and d_d are the chemical shifts of the free and limiting bound dimer respectively.

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NMR - visualisation using SHIFTY.

The method used to determine and visualise three-dimensional structures from the measured complexation-induced changes in the chemical shifts (CIS), *SHIFTY*, CIS values are calculated by building the molecules in XED 2.8 using standard bond lengths and angles.

The anisotropy parameters used for the base were taken from *ab-initio* calculations. The representation used treats the five-membered ring as aromatic with a ring current factor of 1.03, and the six-membered ring as non-aromatic.

A genetic algorithm was used to optimise the structure of the dimeric complex, so that the calculated CIS values matched the experimental values as closely as possible. The conformational search was divided into five steps, each with population size of 750 and 2000 generations. In the first step, the intermolecular distance was set to 10 Å, the range of allowed rotations of one molecule relative to the other was set to 360°. Intramolecular torsions were allowed to change within the full range of 360° for both molecules. In subsequent steps, each search space parameter was reduced to half of its previous value.

The self-association constant (K_f) was varied by a factor of 10, to scale the experimental values to allow for errors in the isotherm curve fitting.

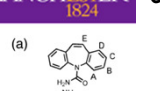
All the solutions showed a root mean square difference between the experimental and calculated chemical shifts of less than 0.002 ppm.

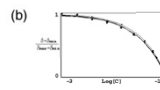
The scaling factor applied to the self association constant was close to one in all cases with an average value of 1.2, suggesting that the experimental value is reasonably accurate. The final structure predicted using *SHIFTY* may be compared with the actual crystal structures of the associated polymorph.

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Carbamazepine - solvent dependence

(a) 

(b) 

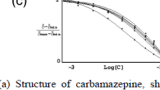
(c) 

Figure 2. (a) Structure of carbamazepine, showing the proton labeling scheme. (b) Normalised changes in chemical shift observed for all protons of carbamazepine as a function of concentration in CD₃OH solution at 295 K. The lines represent the best fit to a dimerization isotherm. (c) Normalised changes in chemical shift observed for all protons of carbamazepine as a function of concentration in CDCl₃ solution at 295 K. The lines represent the best fit to a dimerization isotherm.

Figure 4. Comparison of carbamazepine dimer motifs found in the X-ray crystal structure (grey) with solution phase NMR structures of carbamazepine dimers (red) determined in CD₃OH (a) and in CDCl₃ (b). The mismatch between the solution and solid state structures is 1.0 Å in CD₃OH and 1.8 Å in CDCl₃.

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The co-crystal BZP-DPA - solvent dependence of dimer

In methanol

In toluene

Figure 4. Comparison of carbamazepine dimer motifs found in the X-ray crystal structure (grey) with solution phase NMR structures of carbamazepine dimers (red) determined in CD₃OH (a) and in CDCl₃ (b). The mismatch between the solution and solid state structures is 1.0 Å in CD₃OH and 1.8 Å in CDCl₃.

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Using UV/vis - conc dependence of ϵ .

species. By measuring UV absorbance at different concentrations, the molar absorptivity was calculated and plotted as a function of concentration (Fig. 11). Hypochromic deviation from the Beer-Lambert law is evident, suggesting self-association of solute molecules (43,60). The total absorbance may be regarded as a sum of individual species in the solution:

$$\epsilon C_T = \epsilon_m C_m + \epsilon_n n K_{1,n} (C_m)^n \quad (1)$$

where ϵ is the apparent molar absorptivity determined from the experimental absorbance; ϵ_m and ϵ_n are the molar absorption coefficients of monomers and n -mer aggregates of solute molecules, respectively. In addition, n is the size of

Alessandra Mattei • Tonglei Li

Pharm Res (2012) 29:460-470

Polymorph Formation and Nucleation Mechanism of Tofenamic Acid in Solution: An Investigation of Pre-nucleation Solute Association

Figure 11. Concentration dependence of the apparent molar absorptivity of TR at $\lambda_{max} = 246 \text{ nm}$. The solid line is a fit of the data according to Eq. 1; the dimer fraction is also shown as dash line versus the total TR concentration.

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Probing the radial distribution function - Neutron Scattering

$g(r)$

short range

intermediate range

long range

r

Figure 1. A two-dimensional liquid and its corresponding pair correlation function, showing the relation between the liquid structure and its pair correlation function description.

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Neutron scattering is isotope specific.

oxygen For a simpler two-component liquid system AB, we can describe the liquid mixture in terms of three *partial* pair correlations, $g_{AA}(r)$, $g_{AB}(r)$, $g_{BB}(r)$ where $g_{AA}(r)$ describes the probability of finding an A atom at a distance r from another A atom and so on. Now, if we can change the neutron scattering power of, for example, component A by isotope substitution, we can make neutron scattering measurements on both (chemically similar) liquids. Although the structures of the two liquid samples are essentially the same, the neutron scattering pattern is different, and this difference is caused by the different neutron scattering powers in the two cases of the atom which has been isotope substituted. Taking the difference of these scattering patterns and then performing a Fourier transform results in a pair correlation function, *but one which is centred on the A atom*. In essence, by using isotope substitution on a given atom, we can in effect 'sit on the substituted atom and survey our environment from the vantage point of that atom'. By performing a further substitution of the B atom, we can discriminate also the identity of the neighbouring atoms.

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J. Phys. Chem. B 2008, 112, 8007-8016

The Relationship between Solution Structure and Crystal Nucleation: A Neutron Scattering Study of Supersaturated Methanolic Solutions of Benzoic Acid

R. C. Barton,¹ E. S. Farnes,¹ R. J. Davey,^{2*} J. L. Flannery¹ and D. T. Brown¹

(Left) Experimentally measured $F(Q)$ s (blue circles), EPSR fits (red lines) and fit residuals (green dotted lines) for 0.60 mole fraction of benzoic acid in methanol at 25°C. (Right) Composite $g(r)$ s determined by Fourier Transform of the experimental $F(Q)$ s (blue circles) and EPSR fits (red lines).

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Benzoic acid partial radial distributions.

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Hydrogen bonded interactions in solution: saturated pink, supersaturated blue. 0.16 mole fraction

0.7 on supersaturation
0.6 methanol molecules
1 methanol molecule: no change on supersaturation
0.1 benzoic acid molecules
No change on supersaturation
No acid dimers
C-H...O in solution 0.2 sat 0.3 supersat

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Spatial density functions

solvation
OH
C5-C5 no dimers
Ring-ring self assembly, saturated and supersaturated solutions.

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Solution vs crystal structure

Again the solution has all the elements of the crystal structure but methanol is in the way. Absence of dimers means these must form in the cluster.

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A general picture - concerted desolvation and densification? Or is it a stepwise process?

Solute densified Solvent rejected

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Nucleation of Organic Crystals—A Molecular Perspective

Roger J. Davey,* Sven L. M. Schroeder, and Joop H. ter Horst

Angew. Chem. Int. Ed. 2013, 52, 2166–2179

Self association - link hypothesis summary.

There are cases which show a clear correspondence between solution and crystal synthon but also cases that do not.

Solute (Solvent)	Technique employed	Correspondence between solution associate and crystal synthon?	Ref.
benzoic acid (methanol, chloroform, dioxane)	FTR	yes (exp. and computation), polymorph and solute	[86,88]
5-fluorouracil (nitro-methane/water)	molecular modelling	yes (exp. and computation), polymorph	[104]
sulfonamides (acetone)	NMR	yes	[79]
BZSDPA cocrystal (methanol, toluene)	NMR	yes	[81]
α-insosine (water)	NMR	yes	[80]
inosine diphosphate (water)	NMR	no	[80]
(R,S)-mandelic acid (nitromethane, acetonitrile)	FTR	no	[81]
benzoic acid (methanol)	neutron scattering	no	[83]
3-substituted [1,2,3]triazine-2,4-dione	FTR	yes, monomers in solution, catemers in the solid.	[84]
benzophenone (methanol, toluene)	NMR	yes	[81]
diphenylamine (methanol, toluene)	NMR	yes	[81]
p-acetamidide (chloroform)	NMR	yes	[84]
isonicotinamide (methanol, nitromethane)	FTR, Raman	yes	[89]
carbamazepine (methanol, chloroform)	NMR	yes	[104, 108]

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Finally some words about speciation.

Polymorphism of anthranilic acid

Form I contains zwitterion Form II - no zwitterion

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Anthranilic Acid: equilibria

Defining a crystallisation process means having the right molecular species.

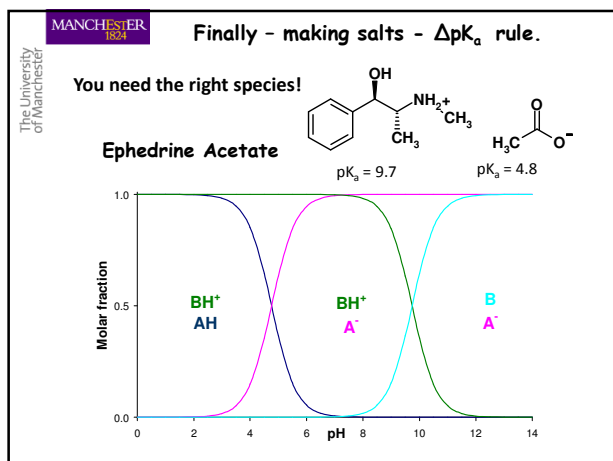
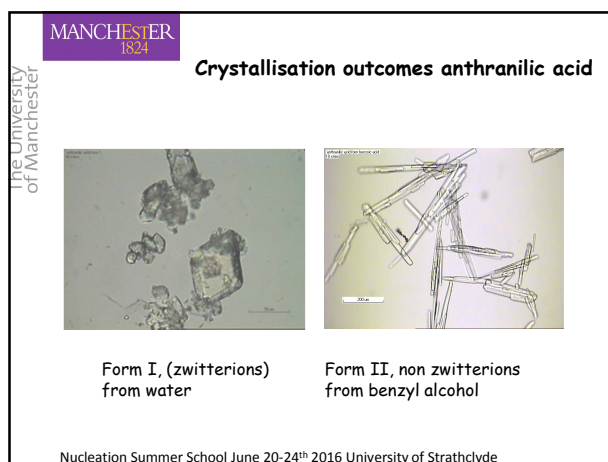
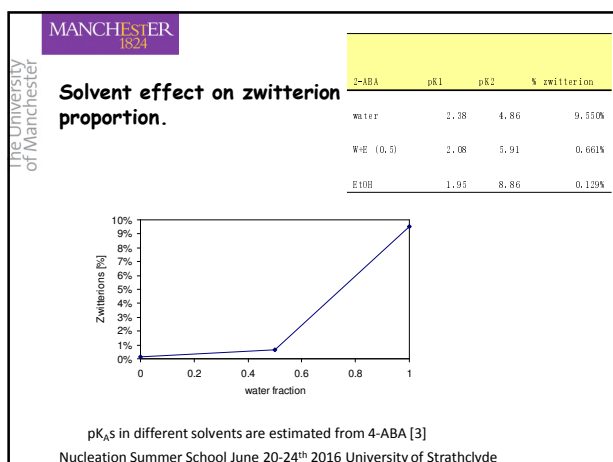
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Speciation vs pH for anthranilic acid in water

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