



Thermodynamic Interactions Due to Transfer of Amino Acids, Glycine and DL-Alanine from Water to Aqueous Mixture of Cationophilic Dipolar Aprotic *N,N*-Dimethyl Formamide

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In this paper, the standard free energies ($\Delta G_t^0(i)$) and entropies ($\Delta S_t^0(i)$) of transfer of homologous α -amino acids *viz.* glycine (gly), DL-alanine (ala), from water to aqueous mixture of cationophilic dipolar aprotic *N,N*-dimethyl formamide (DMF) have been calculated from solubility measurements at five equidistant temperatures *i.e.*, from 15–35 °C. The observed $\Delta G_t^0(i)$ and $T\Delta S_t^0(i)$ *versus* composition profiles are complicated because of the various interactional effects. The chemical transfer Gibbs energies ($\Delta G_{t, ch}^0(i)$) and entropies ($T\Delta S_{t, ch}^0(i)$) have been determined after elimination of cavity effect, estimated by the scaled particle theory and dipole-dipole interaction effects, estimated by the use of Keesom-orientation expression. The chemical contributions of transfer energetics of glycine and DL-alanine are guided by the composite effects of increased dispersion interaction, basicity and decreased acidity, hydrogen bonding, hydrophobic and hydrophilic interaction effects of aqueous DMF as compared to that of reference solvent, water.

Key Words: Transfer energetics, α -Amino acids, Aqueous solvent system, Dispersion interaction.

INTRODUCTION

Amino acids play an important role in our body. They play central roles both as building blocks of proteins and as intermediates in metabolism. The different chemical properties of the amino acids determine the biological activity of the protein. Proteins not only catalyze all (or most) of the reactions in living cells, they also control virtually all cellular process. The native state of a protein is determined by the nature and sequence of its constituent's amino acids as well as by the solvent environment.

From these points of view many researchers had drawn their attention¹⁻⁵ to determine the various thermodynamic properties of amino acids in aqua-organic mixed solvent system.

The aims of such studies were to gain the various aspects of protein folding and unfolding process and protein hydration⁶⁻⁹. In this regard Tanford¹⁰, and Lyyah and Shehabuddin¹¹ reported free energies of some amino acids from water to urea from solubility measurements. Transfer free energies and entropies data of some amino acids, dipeptides, tripeptides and other biomolecules in aqueous ethylene glycol^{12,13}, glycerol^{14,15} and *N,N*-dimethyl formamide¹⁶ are also available.

All these experiments tried to give an explanation about the relative stabilization of these amino acids and other

biomolecules in aqua-organic media with respect to water and the complex solute-solvent and solvent-solvent interactions therein.

Here we have used two simple α -amino amino acids like glycine and DL-alanine. The α -carbon of DL-alanine is bound with a $-\text{CH}_3$ group whereas in glycine no such group is present. So the aqua-organic chemistry regarding thermodynamic solvation of these two α -amino amino acids may be different in various aspects. In our experiments here we have used amide like solvent *N,N*-dimethyl formamide in particular. This will be very much useful for better understanding of the biological processes because the environment in which the different biological activities occur may be much more 'amide like' than 'water like'¹⁷.

In the present article we are reporting the transfer free energies [$\Delta G_t^0(i)$] and entropies [$\Delta S_t^0(i)$] of these α -amino acids, namely glycine(gly), DL-alanine (ala), from water to aqueous mixture of dipolar aprotic *N,N*-dimethyl formamide at 25 °C, as determined from solubility measurements using 'formol titrimetry' at five equidistant temperatures ranging from 15 to 35 °C.

After eliminating effects due to cavity formation and dipole-dipole interactions and neglecting dipole-induced dipole interactions the results have been discussed in terms of

dispersion interaction, acidity-basicity, hydrophilic and hydrophobic hydration and in the case of transfer entropies in terms of relative structuredness as well.

EXPERIMENTAL

Amino acids like glycine (E Merck) and DL-alanine (E-Merck) are used after drying as described earlier^{12,13}. N,N-Dimethyl formamide (LR, BDH) and water are purified by the usual method¹⁸. Aqueous mixtures of co-solvent (H₂O + DMF) that have been used were 20, 40, 60, 80 and 100 wt %. The solubility of these amino acids was measured by formol titrimetry method. These measurements were taken at 15, 20, 25, 30 and 35 °C temperatures. The low-cum-high temperature thermostat used for all measurements was capable of registering temperatures having an accuracy of ± 0.1 °C. Four sets of measurements were made for all the solutes by equilibrating the solutions from both above and below the required temperatures and at least three sets of measurements were made for all the solvents and the solubilities were found to agree to within ± 1.0 -1.5 %.

RESULTS AND DISCUSSION

The solubilities (m) of the α -amino acids, glycine and DL-alanine on molal scale are listed in the Table-1. In the previous studies by Bates and coworkers on Tris¹⁹ and by Kundu and coworkers^{19,20} on non-electrolyte like pNA, HBz and amino acids²¹, glycine (G), diglycine (DG) and triglycine

(TG), the Gibbs energies of solutions (ΔG_s^0) on molal scale were calculated for each solvent using eqn. 1.

$$\Delta G_s^0(i) = -RT \ln C\gamma = -RT \ln C = -RT \ln m \quad (1)$$

where γ is the molar activity coefficient of the solutes but taken tentatively to be unity in each solvent. Since α -amino acids, glycine and DL-alanine likely to be mostly in zwitterionic forms as in non-aqueous solvent mixtures^{22,23}. The involved activity coefficient factor $-RT \ln C\gamma$ arising from interactions of dipolar solutes (here α -amino acids) with large dipole moments may not be so small. But as there is neither the required experimental data nor any appropriate theoretical correlations for computing the same, these have been tacitly taken to be negligibly small, as is usually done for non-electrolytes²⁴. This is because the effective contribution of activity coefficient factor $-RT \ln \gamma_s/\gamma_R$ in the transfer free energetics; $\Delta G_t^0(i) = \Delta G_s^0(i) - \Delta G_R^0(i)$ in particular which is our main concern likely to be hardly significant.

The free energies, at different temperatures are fitted by the method of least squares to an equation of the form[2],

$$\Delta G_s^0 = a + bT + cT \ln T \quad (2)$$

where T is the temperature in Kelvin scale. The values of the coefficients a, b, c are presented in Table-2. These are found to reproduce the experimental data within ± 0.04 kJ mol⁻¹. Transfer Gibbs energies and entropies of the amino acids from water to N,N-dimethyl formamide mixtures were calculated at 25 °C on mole fraction scale by using the following eqns. 3 and 4:

Wt % solvent	Glycine					DL-alanine				
	15 °C	20 °C	25 °C	30 °C	35 °C	15 °C	20 °C	25 °C	30 °C	35
Water	2.720	3.060	3.340	3.720	4.060	1.634	1.720	1.800	2.300	2.400
–	(2.690) ^a	–	(3.330) ^a	–	(4.040) ^a	(1.650) ^a	–	(1.850)	–	(2.390) ^a
20 % DMF	0.103	0.110	0.118	0.120	0.128	0.111	0.124	0.138	0.147	0.157
40 % DMF	0.086	0.098	0.109	0.112	0.114	0.085	0.106	0.126	0.132	0.138
60 % DMF	0.069	0.081	0.091	0.095	0.099	0.068	0.079	0.089	0.094	0.098
80 % DMF	0.058	0.066	0.074	0.077	0.079	0.058	0.065	0.072	0.077	0.080
100 % DMF	0.038	0.042	0.045	0.049	0.053	0.041	0.044 ^b	0.047	0.052 ^b	0.056
–	(0.038) ^b	–	(0.046) ^b	–	(0.052) ^b	–	(0.041) ^b	(0.048) ^b	–	(0.055) ^b

^aRef.^{24,28}, ^bRef.¹⁸.

Solvents	a (kJmol ⁻¹)	b (kJ mol ⁻¹ K ⁻¹)	c (kJ mol ⁻¹ K ⁻¹)	ΔG_t^0 (kJ mol ⁻¹)	$T\Delta S_t^0$ (kJ mol ⁻¹)
Glycine					
Water	36.54	-0.5500	0.07326	0	0
20 % DMF	62.53	-1.2402	0.18400	7.921	-14.948
40 % DMF	373.32	-8.1742	1.21816	7.264	-11.836
60 % DMF	378.06	-8.2274	1.22497	7.469	-9.332
80 % DMF	342.94	-7.4672	1.11253	7.197	-10.655
100 % DMF	124.76	-2.5575	0.37993	7.164	-10.378
dl-Alanine					
Water	-239.99	5.6871	-0.85782	0	0
20 % DMF	155.27	-3.2290	0.47823	6.119	-9.203
40 % DMF	584.07	-12.7728	1.90100	5.508	-3.991
60 % DMF	313.77	-6.7700	1.00707	6.148	-8.405
80 % DMF	159.82	-3.3262	0.49357	5.865	-8.972
100 % DMF	30.18	-0.4409	0.06406	5.668	-10.356

$$\Delta G_t^0(i) = {}_s\Delta G_s^0 - {}_R\Delta G_s^0(i)$$

$$i.e. \quad \Delta G_t^0(i) = (a_s - a_R) + (b_s - b_R)T + (c_s - c_R)T \ln T - RT \ln \left(\frac{M_s}{M_R} \right) \quad (3)$$

$$\text{and } \Delta S_t^0(i) = (b_R - b_s) + (c_R - c_s)(1 + \ln T) + R \ln \left(\frac{M_s}{M_R} \right) \quad (4)$$

here the subscript 's' and 'R' refer to the co-solvent (H₂O + DMF) mixtures and reference solvent (H₂O), respectively and M_R and M_s are the molar mass of the pure and mixed solvent, respectively. $\Delta G_t^0(i)$ and $\Delta S_t^0(i)$ values of amino acids, glycine and DL-alanine thus obtained and presented in the Table-2. The involved uncertainties in $\Delta G_t^0(i)$ and $\Delta S_t^0(i)$ are *ca.* ± 0.05 kJ mol⁻¹ and $2 \text{ JK}^{-1} \text{ mol}^{-1}$, respectively.

Now ΔP_t^0 (where P = G or S) may be ascribed as the sum of the following terms (assuming dipole induced dipole term to be negligibly small).

$$i.e. \quad \Delta P_t^0(i) = \Delta P_{t,cav}^0(i) + \Delta P_{t,d-d}^0(i) + \Delta P_{t,ch}^0(i) \quad (5)$$

here, $\Delta P_{t,cav}^0$ indicates the transfer energy contribution of the cavity effect which is involved due to creation of cavities for the species in H₂O and H₂O + DMF mixed solvent system and $\Delta P_{t,d-d}^0(i)$ stands for the dipole-dipole interaction effect involving interaction between dipolar-zwitter-ionic amino acids and the solvent molecules. On the other hand, $\Delta P_{t,ch}^0(i)$ includes all other effects such as those arising from acid-base or short-range dispersion interaction, hydrophilic or hydrophobic hydration and structural effects *etc.* Here $\Delta P_{t,cav}^0(i)$ values were computed by using scaled particle theory (SPT)^{13,25,18}, assuming the solutes and solvent molecules as equivalent to hard-sphere models as dictated by their respective diameter (Table-3).

$\Delta G_{t,d-d}^0(i) = ({}_s\Delta G_{d-d}^0(i) - {}_R\Delta G_{d-d}^0(i))$ and $\Delta S_{t,d-d}^0(i) = ({}_s\Delta S_{d-d}^0(i) - {}_R\Delta S_{d-d}^0(i))$ are calculated by means of the

Keesom-orientation expression²⁷ for ${}_s\Delta G_{d-d}^0(i)$ in a solvent S, as given below

$${}_s\Delta G_{d-d}^0(i) = -\left(\frac{8\pi}{9}\right)N^2\mu_s^2\mu_x^2\sigma_{sx}^{-3}(kT)^{-1}v_s^{-1} = \frac{A}{TV_s} \quad (6)$$

where $A = -\left(\frac{8\pi}{9}\right)N^2\mu_s^2\mu_x^2\sigma_{sx}^{-3}(k)^{-1}$ and $V_s = \frac{M_s}{d_s}$ and that

of $\Delta S_{d-d}^0(i)$ as follow-

$${}_s\Delta S_{d-d}^0(i) = \left\{ \frac{\delta_s \Delta G_{d-d}^0(i)}{\delta T} \right\}_p \quad (7)$$

i.e., $T_s\Delta S_{d-d}^0(i) = {}_s\Delta G_{d-d}^0(i)[1 + T\alpha]$, where N stands for Avogadro's number, μ_s , μ_x are the dipole moment of solvents and amino acid molecules, respectively (Table-3).

σ_{sx} is the distance at which the attractive and repulsive interactions between the solvent and solute molecules are equal and is generally equal to $1/2(\sigma_s + \sigma_x)$, where σ_s and σ_x are the hard sphere diameter of co-solvent and solute molecules, respectively (Table-3) and α is the isothermal expansibility of

the solvent and given by $\left(\frac{\delta \ln V_s}{\delta T}\right)_p = -\left(\frac{\delta \ln d_s}{\delta T}\right)$. Following

Marcus²⁶ and Kim *et al.*²⁷ in order to get this $\Delta P_{t,d-d}^0(i)$ term on mole fraction scale the quantity was again multiplied by the term X_{s1} and

$$X_{s1} = X_s \left(\frac{\mu_s}{\sigma_s^3} \right) \left(\frac{\mu_R}{\sigma_R^3} \right) \quad (8)$$

This is the real mole fraction contribution due to dipole-dipole interaction²⁶. Subtraction of $\Delta P_{t,cav}^0(i)$ and $\Delta P_{t,d-d}^0(i)$

TABLE-3
GIBBS ENERGIES OF TRANSFER $\Delta G_t^0(i)$, $\Delta G_{t,cav}^0(i)$, $\Delta G_{t,dd}^0(i)$, $\Delta G_{t,ch}^0(i)$ AND ENTHALPY OF TRANSFER, $\Delta H_{t,cav}^0(i)$ AND ENTROPIES OF TRANSFER $T\Delta S_t^0(i)$, $T\Delta S_{t,cav}^0(i)$, $T\Delta S_{t,dd}^0(i)$ AND $T\Delta S_{t,ch}^0(i)$ OF GLYCINE, DL-ALANINE, FROM WATER TO AQUEOUS-DMF AT 25 °C (ON MOLE FRACTION SCALE IN kJ mol⁻¹)

Solvents	$\Delta G_t^0(i)$	$\Delta G_{t,cav}^0(i)$	$\Delta G_{t,dd}^0(i)$	$\Delta G_{t,ch}^0(i)$	$T\Delta S_t^0(i)$	$\Delta H_{t,cav}^0(i)$	$T\Delta S_{t,cav}^0(i)$	$T\Delta S_{t,dd}^0(i)$	$T\Delta S_{t,ch}^0(i)$
Glycine									
Water	0	0	0	0	0	0	0	0	0
20 % DMF	7.921	-1.440	0.734	8.627	-14.948	-0.04	1.400	0.692	-17.04
40 % DMF	7.264	-3.980	5.190	6.054	-11.836	-0.115	3.865	5.190	-20.862
60 % DMF	7.469	-4.540	7.840	4.169	-9.332	-0.062	4.478	7.130	-20.940
80 % DMF	7.197	-6.370	15.700	-2.133	-10.655	0.028	6.398	13.900	-30.953
100 % DMF	7.164	-8.110	21.100	-5.826	-10.378	1.050	9.160	15.600	-35.138
Alanine									
Water	0	0	0	0	0	0	0	0	0
20 % DMF	6.119	-1.54	0.580	7.079	-9.203	-0.045	1.495	0.540	-11.238
40 % DMF	5.508	-4.20	4.320	5.388	-3.991	-0.128	4.072	4.300	-12.364
60 % DMF	6.148	-4.78	5.910	5.018	-8.405	0.071	4.851	5.200	-18.456
80 % DMF	5.865	-6.64	10.300	2.205	-8.972	0.026	6.666	8.190	-23.828
100 % DMF	5.668	-8.30	12.500	1.468	-10.356	1.020	9.320	6.040	-25.716

The required diameter and other solvent parameters of DMF and water are taken from ref.²⁶. The required diameter of glycine and alanine are 5.64 and 6.16 Å, as given in ref.^{23,29}. Dipole moment values of α -amino acids are 15.7D for glycine, 15.9D for alanine.

from the total we can get $\Delta P_{t, ch}^0(i)$ of amino acids. The values of, $\Delta P_{t, cav}^0(i)$, $\Delta P_{t, d-d}^0(i)$ and $\Delta P_{t, ch}^0(i)$ are presented in Table-3.

Interactions involved between amino acids and solvent molecules: Fig. 1 shows the variation of $\Delta G_r^0(i)$ with mol % of DMF in aqueous DMF co-solvent system. The $\Delta G_r^0(i)$ values indicate that the amino acids (glycine, DL-alanine) are almost destabilized in N,N-dimethyl formamide-water mixtures. These amino acids are destabilized more regularly up to 100 mol % DMF. $\Delta G_r^0(i)$ is composed of, $\Delta G_{t, cav}^0(i)$, $\Delta G_{t, dd}^0(i)$ and $\Delta G_{t, ch}^0(i)$ or others. So their collective contribution $\Delta G_r^0(i)$ show such little complex nature of variation with mole % of N,N-dimethyl formamide.

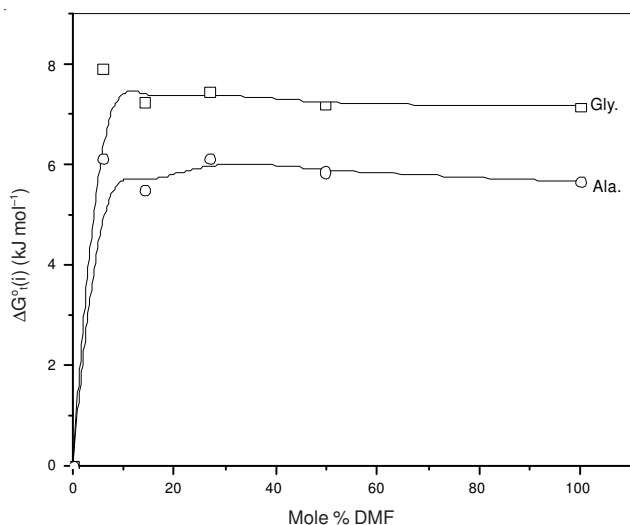


Fig. 1. Variation of $\Delta G_r^0(i)$ of glycine, DL-alanine with mole % DMF aqueous mixture of DMF at 298.15 K

Fig. 2 represents the variation of $\Delta G_{t, ch}^0(i)$ with mole % N,N-dimethyl formamide in aqueous mixture. $\Delta G_{t, ch}^0(i)$ can be obtained after eliminating $\Delta G_{t, cav}^0(i)$ and $\Delta G_{t, d-d}^0(i)$ from the total.

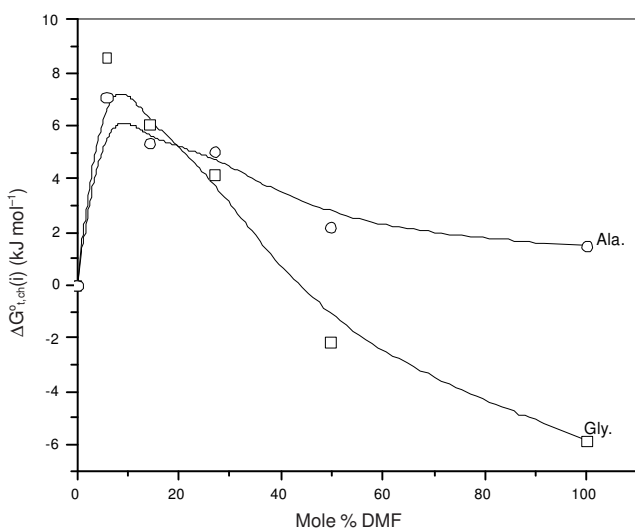


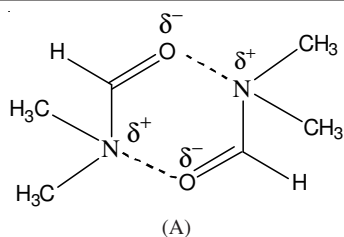
Fig. 2. Variation of $\Delta G_{t, ch}^0(i)$ of glycine, DL-alanine with mole % DMF in aqueous mixture of DMF at 298.15 K

The size of N,N-dimethyl formamide (0.498 \AA)²⁷ is greater than water (0.274 \AA)²⁷. Thus free energy change due to cavity formation is also more negative in N,N-dimethyl formamide relative to water. $\Delta G_{t, cav}^0(i)$ is more negative for DL-alanine having larger hard-sphere diameter (Table-3). On the other hand the dipole moment of N,N-dimethyl formamide (3.82 D)³⁰ is also greater than water (1.85 D)²⁶. Therefore, $\Delta G_{t, d-d}^0(i)$ values are more negative in higher concentration of N,N-dimethyl formamide in this aqueous N,N-dimethyl formamide mixed solvent system. The order of $\Delta G_{t, d-d}^0(i)$ value is Gly. > DL-Ala. As $\Delta G_{t, d-d}^0(i)$ values are guided by dipole moment and hard-sphere diameter of both solutes (here amino acid) as well as solvent, the above order is well supported from Table-3.

$\Delta G_{t, ch}^0(i)$ values of these amino acids represent the free energy change in the water and N,N-dimethyl formamide mixed solvent system due to different short range chemical interactions *i.e.*, acid-base, dispersion, hard-soft, H-bonding, hydrophilic and hydrophobic interactions *etc.* As the proportion of N,N-dimethyl formamide in the mixed solvent system will be gradually increased the solvent character may undergoes a gradual but material change in respect to the above types of chemical interactions. This compositive profile shows upward trends at lower concentration of N,N-dimethyl formamide and reaches a maximum value at *ca.* 8-10 mol % of DMF concentration and then decreases. This indicates the destabilization of α -amino acids. This occurs due to the breakdown of extensive hydrogen bond between protic water and hydrophilic heads (RH^+) of α -amino acids with the introduction of dipolar aprotic DMF in water. Glycine being smaller in size it will be strongly associated with water through hydrogen bonding. Therefore, glycine may be more destabilized (*i.e.*, more inflection) (Table-3) during its transfer from protic water to dipolar aprotic N,N-dimethyl formamide. Here it is important to note that from 0-20 mol % of DMF $\Delta G_{t, ch}^0(i)$ values are higher for glycine than DL-alanine. After 20 mol % of DMF $\Delta G_{t, ch}^0(i)$ values are progressively negative for glycine than DL-alanine. Therefore the order of stability with respect to chemical contribution of solute-solvent interaction upto about 0-20 mol % of N,N-dimethyl formamide is as DL-Ala. > Gly and after that stability is reverse *i.e.*, Gly > DL-Ala.

Water is a protic solvent, while N,N-dimethyl formamide is an aprotic in nature. Thereby anionic part (COO^-) of these amino acids can be more solvated in water than N,N-dimethyl formamide due to acid-base interaction. Furthermore, in respect of H-bonding capacity water is more potential than N,N-dimethyl formamide. So it is expected that amino acids will be less solvated initially with increased concentration of N,N-dimethyl formamide in water-DMF mixtures.

Here it is to be noted that with the increased concentration of DMF the $\Delta G_{t, ch}^0(i)$ values of these amino acids decreases sharply. This decrement is higher for glycine than DL-alanine. Here DMF due to its dipolar aprotic character it can enhance its aproticity through the formation of intermolecular dimeric, $(\text{DMF})_2$ aprotic form (Fig. A) induced by the solutes (*i.e.* amino acids). Therefore DMF may stabilize the α -amino acids through dispersion interaction overcoming destabilization due to poorer H-bonding and hydrophilic hydration with increased mole % of DMF in aqueous-DMF system.



It should be noted that DMF (0.498 \AA)²⁶ is more polarisable than water (0.274 \AA)²⁶. Therefore DMF, here undergo stronger soft-soft and dispersion interactions with amino acids. But here the α -amino acids also induce the hydrophilic hydration and hydrophobic hydration, which to be decreased with the increased DMF concentration.

The NH_3^+ of the zwitterionic α -amino acids (RH^+) takes part in acid-base interaction with DMF. Since DMF has larger basicity than water towards cation as their 'cation-N-centre' type acid-base interactions, the aqueous-DMF mixtures with its increased concentration of DMF acquire co-solvent induced^{18,31} greater basicity. Therefore DMF can take part in acid-base interaction with NH_3^+ moiety of α -amino acids and imparts greater stability for the amino acids in comparison to water. On the other hand with increasing addition of DMF in water, the co-solvent induced acidity of DMF-water mixtures will be decreased to a much greater extent. Therefore COO^- of amino acids (RH^-) experiences instability to greater extent with the increased concentration of DMF in aqueous DMF system. Thus in the context of co-solvent induced acid-base interactions extra stability are not gained by the α -amino acids with increased concentration of DMF. It is to be noted here also that the stability of α -amino acids due to hydrophilic interaction exerted by the water molecules in its higher concentration will be more decreased due to co-solvent induced hydrophilicity with the increased concentration of DMF. In case of hydrophobic hydration it will also be reduced.

Therefore, the lightest α -amino acid *i.e.*, glycine having smaller size (5.64 \AA) will be more stabilized with increased concentration of DMF by acid-base type and relative hydrophilic interaction than others due to greater charge density on it. Here the effect due to size dependent dispersion interaction may play lesser important role than acid-base type and hydrophilic interactions. Therefore with the increased concentration of DMF, $\Delta G_{\text{t, ch}}^0(i)$ values become more negative for glycine than DL-alanine. In case of DL-alanine the dispersion interaction is more significant than acid-base type interaction and hydrophilic interaction. The stability order of glycine and DL-alanine at higher concentration of DMF will support Fig. 2 considering the combined effects of dispersion, acid-base and hydrophilic interactions.

Thus the chemical contribution $\Delta G_{\text{t, ch}}^0(i)$ of transfer free energies, of these homologous α -amino acids are guided by the composite effects of increased dispersion interaction, basicity and decreased acidity, hydrogen bonding effects, hydrophilic interaction and hydrophobic hydration of water and *N,N*-dimethyl formamide mixtures as compared to that of reference solvent (water).

Amino acids induced solvent-solvent interactions in terms of transfer entropy: Fig. 3 represent the variation of

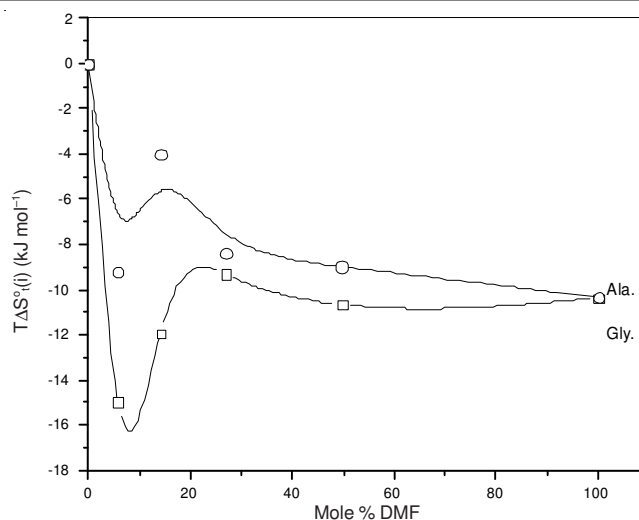
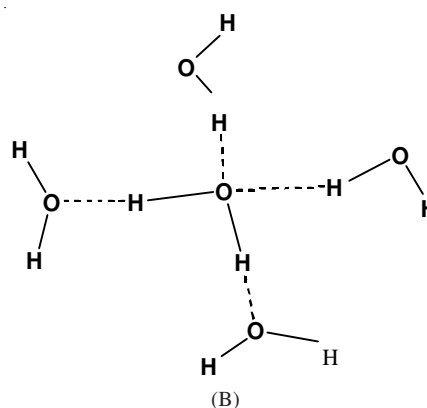


Fig. 3. Variation of $T\Delta S_t^0(i)$ of glycine, DL-alanine with mole % DMF in aqueous mixture of DMF at 298.15 K

$T\Delta S_t^0(i)$ values of these homologous α -amino acids with mole % DMF in DMF-water mixed solvent system. Here the roller coaster behaviour is shown by the amino acids. Now like, $\Delta G_t^0(i)$, $T\Delta S_t^0(i)$ mainly composed of $T\Delta S_{\text{t, cav}}^0(i)$, $T\Delta S_{\text{t, d}}^0(i)$ and $T\Delta S_{\text{t, ch}}^0(i)$ ($T\Delta S_{\text{t, d-id}}^0(i)$ *i.e.*, dipole induced dipole interaction is ignored here). $T\Delta S_{\text{t, cav}}^0(i)$, $T\Delta S_{\text{t, d}}^0(i)$ values are presented in Table-3.

At *ca.* 8 mol % of DMF values shows a broad minima and then it sharply increases upto about 20 mol % of DMF concentration. Above 20-100 mol % of DMF, $T\Delta S_t^0(i)$ values show almost similar trends for both the amino acids. These observations indicate that water molecules adopt 3-D structure due to its extensive intermolecular hydrogen bonding (Fig. B) at lower concentration of DMF and then the hydrogen bonds are broken due to the introduction of dipolar aprotic co-solvent DMF. In higher concentration of this co-solvent molecules dimerisation may occur to form six member ring (Fig. A) to increase dispersion interactions but other types of solvent-solvent interactions may decrease which represent such type of observed results.



$T\Delta S_{\text{t, ch}}^0(i)$ is obtained after subtraction of $T\Delta S_{\text{t, cav}}^0(i)$ and $T\Delta S_{\text{t, d-d}}^0(i)$ from $T\Delta S_t^0(i)$. Fig. 4 represents the variation of $T\Delta S_{\text{t, ch}}^0(i)$ for the α -amino acids glycine and DL-alanine with increased DMF concentration in aqua-DMF mixture at 25 °C. With increase of DMF concentration from $T\Delta S_{\text{t, ch}}^0(i)$ values

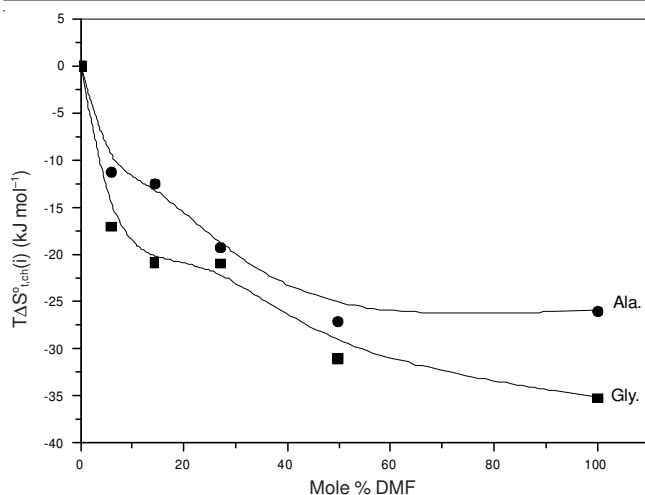


Fig. 4. Variation of $T\Delta S_{t, ch}^0(i)$ of glycine and DL-alanine with mole % DMF of aqueous mixture of DMF at 298.15 K

are decreased more or less regularly. This indicates that the α -amino acids induce dipolar aprotic N,N-dimethylformamide to be dimerized (Fig. A) which is responsible for more dispersion interaction. But here the α -amino acids also induce the hydrophilic hydration and hydrophobic hydration to be decreased with the increased DMF concentration. Comparatively for larger α -amino acid *i.e.*, DL-alanine, the more disorder than glycine is observed due to weak response towards hydrophilic and hydrophobic interactions.

But the solute (amino acids) induced dispersion interaction among large size DMF molecules being the predominant factor over others the overall decrement of $T\Delta S_{t, ch}^0(i)$ values occur throughout the higher concentration of DMF in this aqua-DMF mixed solvent system.

Conclusion

It may be concluded that due to chemical interaction the α -amino acids will be stabilized in DMF having dipolar aprotic character. The zwitterionic α -amino acids induce to adopt 3-D-structuredness of water at water rich concentration in aqua-DMF solvent system.

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