Molecular Interactions Derived from Water Activity and Specific Salting-in and Salting-out Effects in Solutions of Two- and Three-Basic Amino Acids and their Salts at 298.15 and 310.15 K

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For the elaboration of interpretations, models, and theories of functioning and activating of protein channels in nerve and muscle cells, the data on Na^+, K^+, Mg^{2+}, Ca^{2+} salts of excitatory amino acids are needed [1,2]. Sodium salts of (S)-aminopenthanedioic acid and (S)-aminobutanedioic acids (glutamate and aspartate) are especially important in the system of nerve impulse transmission. To investigate such complexes of proteins containing hydrophilic anions as aspartate or glutamate is of paramount interest, because colloidal self-assembly is a mean to create a new generation of materials with complex shape and surface chemistry [3,4]. Liquid patches can create robust bonds in super-colloidal architectures.

In this work the study of ion-specific interactions of cations and anions with proteinogene amino acids is undertaken: non-polar amino acid with small aliphatic radical – glycine (ambiphilic), and with the polar hydrophilic amino acids – glutamic acid, aspartic acid, histidine and their salts with charged carboxylic and amino groups playing important role in affinity on protein. With the help of a colligative property – vapour pressure measuring – the cation and anion affinity to the amino acids and their salts has been studied at T=298.15 K and 310.15 K. The cations are alkali (Na^+, K^+) and alkali-earth (Mg^{2+}, Ca^{2+}) metal ions as well as aminomethanamidine (guanidinium, $Gndm^+$) as an ion with irregular charge distribution and complex geometry that stimulates "salting-in" of proteins and shows specific cation binding to acidic amino acid residues, used for denaturation and recurrent protein folding [5]. The anions are OAc^-, Cl^-, NO_3^-, SCN^- varying from salting-out to salting-in.

Activities of water, activity coefficients of water and the corresponding osmotic coefficients of the mixtures have been calculated, both being directly related to the chemical potentials of the different species and therefore to their Gibbs energy.

Ion-specific effects are analyzed based on the concentration dependence of the experimental osmotic coefficients of the solutions of glycine, glutamic acid, aspartic acid, histidine and their salts.

Models of electrostatic and structural contribution are used to fit the experimental data to obtain the corresponding dual and triple interaction parameters. Hard-sphere and electrostatic parts of the osmotic coefficients of aqueous solutions of symmetrical (2-2, 1-1) and non-symmetrical (2-1) amino acid salts are calculated at 298.15 K and 310.15 K in the framework of the equations of g^E (excess Gibbs free energy) model. Mean Spherical Approximation yields reasonable fitting parameters and a picture that is consistent with the experimental data for glutamate and aspartate aqueous solutions.

The modeling of chemical potential in ternary systems is done by an EoS (equation of state). Electrolyte Perturbed-Chain Statistical Associating Fluid Theory has been used to model ternary amino acid + salt + water systems and amino acid salt + salt + water systems. It include the TPT1 of Wertheim, takes into account along with dispersion interactions also association and dipolar interactions in explicit form.

Assuming the hard chain, dispersive and association energy [6,7] as ionic parameters permits the correct description of the maximums and minimums of the osmotic coefficients at both temperatures. Beside of electrostatic interactions, also specific interactions like van der Waals,

dispersion, and ion-dipole effects has been shown to occur in these systems. Thermodynamic properties of these solutions such as fugacity coefficients and activity coefficients of the mixture components are also calculated with ePC-SAFT.

Also, two-parameter fitting (third order terms in the power series) was applied to calculate solute activity coefficients in the ternary solutions.

The decrease in the chemical potential of amino acid salts corresponds to the Hofmeister series. A strong interaction between amino acid and salt due to specific dispersion interactions in amino acid salt systems containing guanidinium-based salt has been revealed to be in agreement with MD and half-empirical quantum-chemical calculations.

REFERENCES

[1] Marcus, Y., Ions in Water and Biophysical Implications: From Chaos to Cosmos, Dordrecht: Springer (2012) 215 p.

[2] Kunz, W. (Ed.): Specific Ion Effects, London: World Scientific (2010)

[3] Duclohier, H. (Ed.): Biophysics of Ion Channels and Deceases, Kerala: Research Signpost (2010)

[4] Harding, S.E., Biophys. Chem., 93 (2001) page 87- 246

[5] Makhatadze, G. I., Fernandez, J., Freire, E., Lilley, T.H., Privalov P.L., J. Chem. Eng. Data, 38 (1993) page 83-87

[6] Gross, J., Sadowski, G., Fluid Phase Equilibr., 168, (2000) page 183-199

[7] Barker, J.A., Henderson, D., J.Chem.Phys., 47, (1967) page 2856