

Effect of pH and salts on the binding of free amino acids to the corn protein zein studied by thin-layer chromatography

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Summary. The interaction of free amino acids with the corn protein zein was studied by thin-layer chromatography carried out on cellulose layers covered with zein and the effect of pH and salts on the strength of interaction was elucidated. Only the binding of Arg, His, Lys, Orn and Trp to zein was verified, other amino acids were not retained. Retention of Arg, His, Lys and Orn decreased linearly with increasing concentration of salts the mobile phase indicating the hydrophilic character of amino acidzein interaction. Both alkaline and acidic pH influenced the strength of binding. Principal component analysis indicated the different character of the influence of pH and salts on the interaction. The results suggest that these amino acid residues may account for the binding of other peptides and proteins to zein.

Keywords: Amino acids - Corn protein zein - Salt effect

Introduction

Interactions between amino acids, peptides and proteins have a paramount importance in many biochemical, biological and biotechnological processes. They influence protein structure (Spadaccini et al., 2001), modify biological efficacy (Chen et al., 2000), and enzyme activity (Fulop et al., 2001), participate in ligand recognition (Cordier et al., 2000), modulate the efficacy of active sites of proteinase (Strisovsky et al., 2000), etc.

The character of such type of interactions has been vigorously discussed the conclusions highly depending on the chemical structure of the interacting molecules. Thus, the involvement of electrostatic forces (hydrogen bonds) in the interaction of amino acids (Cox, 2000), in the determination of multiple turns in proteins (Guruprasad et al., 2000), in the modification of protein (Arnold and Oldfield, 2000) and peptide structure (Kasim and Swenson, 2000), in the aggregate formation of peptides (Mong et al., 2001), in the protein–protein interaction (Tanahashi

and Tabira, 2000; Matern et al., 2000) and in the association of proteins (Wang et al., 2000) has been demonstrated. Furthermore, the interaction between the aromatic ring of phenyalanine side chain has been observed (Gorbitz, 2000). The simultaneous occurrence of hydrophobic binding forces and hydrogen bonds has also been reported (De Beer et al., 2000; Wu et al., 2000). It has been illustrated that both hydrophobic and electrostatic interactions may influence peptide-protein binding (Liu et al., 2000) and protein–protein associations (Nusrat et al., 2000).

Chromatographic techniques have been frequently employed for the assessment of various molecular interaction of biological relevance (Cserháti and Valkó, 1994). The use of thin-layer chromatography (TLC) for the study of such interactions has marked advantages: the method is generally rapid, it is easy to carry out, makes possible the simultaneous determination of numerous interaction on one plate, and the amount of the more hydrophobic interactive compounds is extremely low (Zarzycki et al., 1999).

Principal component analysis (PCA), a versatile and easy-to-use multivariate mathematical-statistical method has been developed to contribute to the extraction of maximal information from large data matrices containing numerous columns and rows (Mardia et al., 1979). PCA allows the elucidation of the relationship between the columns and rows of any data matrix without being one the dependent variable. PCA is a so-called projection method representing the original data in smaller dimensions. It calculates the correlations (similarities and dissimilarities) between the columns of the data matrix and

classifies the variables according to the coefficients of correlations taking into considerations simultaneously the magnitude and sign of the coefficients of correlation. PCA has been frequently employed in many fields of up to date research. Thus, it has been used in quantitative structure-activity relationship (QSAR) studies (Drew et al., 1998), for the exploration of molecular structure-property relationships (Seybold, 1999), for the evaluation of molecular lipophilicity (Sarbu and Todor, 1998; Mannhold et al., 1998), for theoretical organic chemistry (Héberger and Lopata, 1998), for quantitative structure-retention studies in chromatography (Héberger and Görgényi, 1999), for the elucidation of structure-biodegradation relationships (Damborsky et al., 1998), for the clustering of amino acids (Zaliani and Gancia, 1999), for the assessment of solvent properties (Katritzky et al., 1999), and polarity indicators in gas-chromatography (Héberger, 1999), etc.

The objectives of the study were the determination of the interaction of free amino acids with the corn protein zein, the elucidation of the influence of pH and various salts on the interaction and the evaluation of the data by PCA.

Materials and methods

L-Amino acids of analytical purity have been purchased from REANAL FINE CHEMICALS (Budapest, Hungary) and were used as received. Microcrystalline cellulose for thin-layer chromatography and solvents of HPLC quality have been obtained from Merck (Darmstadt, Germany). Zein-coated cellulose stationary phase has been prepared by dissolving 0.5 g zein in the mixture of 160 ml of n-propanol and 40 ml of water at 70°C under continuous gentle stirring. After the dissolution of the protein 20 g of microcrystalline cellulose was added and the mixture was stirred for two hours at the same temperature. Solvents have been removed at $70^{\circ} C$ in vacuum. Plates of $20 \times 20 \, \text{cm}$ containing 5 g of stationary phase have been prepared. Untreated cellulose plates served as controls. Amino acids have been dissolved in distilled water: 2-propanol at the concentration of 1 mg/ml, and 2 μ l of the solutions were spotted onto the plates. Amino acids have been developed in distilled water as mobile phase and in aqueous solutions of acetic acid, sodium acetate, sodium chloride and magnesium chloride the concentration of additives varying between 150 and 0.5 mM. Plates have been developed in sandwich chambers $(22 \times 22 \times 3 \text{ cm})$ at ambient temperature; the development distance was approximately 16 cm. After development the plates have been dried at 105°C and the amino acids have been detected by the ninhydrin reagent. Each experiment has been run in quadruplicate. The R_M values characterizing the retention of solutes in reversed-phase thin-layer chromatography (RP-TLC) have been calculated by

$$R_{\rm M} = \log(1/R_{\rm f} - 1) \tag{1}$$

for each amino acid in each mobile phase. When the coefficient of variation of the parallel determinations was higher than 6% the R_M value was omitted from the subsequent calculations. In order to elucidate the effect of eluent additives on the binding of amino acids to zein and cellulose the following equation has been fitted to the experimental data:

$$R_{M} = R_{M0} + b \cdot C \tag{2}$$

where R_M is the R_M value of an amino acid determined in a given mobile phase; R_{M0} is the R_M value determined in distilled water; b is the change

of the R_M value caused by unit change of the concentration of the eluent additive (related to the sensitivity of the strength of the binding of amino acids to zein towards eluent additives), and C is the concentration of additive. Calculations have been performed only for Arg, His, Lys, Orn and Trp because other amino acid did not bind to zein. Calculations have been carried out separately for cellulose and impregnated cellulose stationary phases and for the four eluent additives.

The similarities and differences among the amino acids and eluent additives has been assessed by PCA. The four eluent additives were the variables and the b values of Eq. (2) for Arg, His, Lys, and Orn determined on cellulose and on impregnated cellulose layers were the observations (altogether 8 variables). Trp has been omitted from PCA because its $R_{\rm M}$ value did not depend significantly on the concentration of additives in the mobile phase. The variance explained was set to 99%.

Software for PCA has been prepared by Dr. Barna Bordás, Plant Protection Institute of Hungarian Academy of Sciences (Budapest, Hungary).

Results and discussion

The majority of amino acids was not retained neither on cellulose not on zein-coated cellulose layers that means that they do not bind to these stationary phases. Only amino acids Arg, His, Lys, Orn and Trp showed measurable retention, their mobility was slightly different on cellulose and on zein-coated cellulose layers suggesting the amino acids really interact with the molecules of the protein. The retention of each amino acid except Trp decreased monotonously with increasing concentration of the additive in the mobile phase indicating that the strength of interaction of amino acids with zeinis reduced in ionic environment. This result can be tentatively explained by the supposition that the amino acid-zein interaction is of polar character and amino acids are bound either to the polar peptide bonds or to the polar side chains of the protein. The R_M value of Trp did not depend significantly on the concentration of additives in the mobile phase. This finding can be tentatively explained by the supposition that the hydrophobic part of Trp can bind with hydrophobic forces to the apolar substructures of zein while the polar head group interacts with the same molecular substructures than the other amino acids. As the eluent additives decrease the strength of hydrophilic interactions and increase the strength of hydrophobic ones the unusual retention behaviour of Trp is the result of the interplay of both types of interactive forces. The parameters of the linear relationships between the R_M values of amino acids and the concentration of additives in the mobile phase are compiled in Table 1. The relationship was significant at a significance level of 95% in each instance demonstrating the applicability of Eq. (2). The coefficients of correlation were between 0.8481 and 0.9868 confirming the good reproducibility of the RP-TLC system. Both parameters of Eq. (2) (R_{M0} and b) were different for cellulose and zein-coated cellulose stationary phases proving again the

Table 1. Parameters of the linear relationships between the R_M values of amino acids and the concentration of additives in the mobile phase (C). Cell = cellulose stationary phase; Zein = zein-coated cellulose stationary phase

$(R_{\mathbf{M}} = R_{\mathbf{M}0} + \mathbf{b} \cdot \mathbf{C})$							
Amino acid	Stationary phase	Additive	Parameters				
			R_{M0}	−b × 10	$s_b \times 10^{-2}$	r _{calc} .	
Arg	Zein	Sodium chloride	1.03	2.76	5.23	0.8939	
	Cell		0.51	6.13	8.69	0.9621	
His	Zein		0.33	1.15	2.70	0.8481	
	Cell		0.13	2.62	3.41	0.9677	
Lys	Zein		0.31	1.56	1.91	0.9513	
	Cell		0.56	7.91	12.10	0.9562	
Orn	Zein		0.28	1.48	1.73	0.9550	
	Cell		0.56	7.32	14.41	0.9304	
Arg	Zein	Acetic acid	1.05	3.20	3.98	0.9566	
	Cell		0.69	7.81	19.25	0.8969	
His	Zein		0.33	1.24	2.66	0.8689	
	Cell		0.14	3.38	4.86	0.9609	
Lys	Zein		0.26	1.20	2.31	0.8911	
	Cell		0.69	8.51	16.29	0.9341	
Orn	Zein		0.33	1.26	2.05	0.9183	
	Cell		0.65	7.55	14.29	0.9353	
Arg	Zein	Magnesium chloride	0.84	3.90	7.38	0.9072	
	Cell		0.52	9.87	25.98	0.9099	
His	Zein		0.38	2.35	2.96	0.9555	
	Cell		0.14	5.38	9.25	0.9584	
Lys	Zein		0.26	2.49	2.22	0.9770	
	Cell		0.41	10.47	26.22	0.9174	
Orn	Zein		0.28	2.51	1.68	0.9868	
	Cell		0.41	10.25	24.98	0.9212	
Arg	Zein	Sodium acetate	0.88	2.36	5.23	0.8622	
	Cell		0.61	7.81	16.43	0.9396	
His	Zein		0.32	1.22	2.21	0.9031	
	Cell		0.11	4.07	6.06	0.9682	
Lys	Zein		0.23	1.30	2.98	0.8553	
	Cell		0.76	9.80	33.74	0.8590	
Orn	Zein		0.25	1.08	2.51	0.8685	
	Cell		0.74	9.97	33.54	0.8640	

Table 2. Similarities and differences between the binding characteristics of amino acids to the corn protein zein

Number of principal component	Eigenvalues	Variance explained %	Total variance explained			
1	3.89	97.38	97.38			
2	0.08	2.06	99.44			
Results of principal component load	lings					
Variable	Number of principal component					
	1	2				
b _{NaCl}	0.99	-0.08				
b _{NaCl}						
b _{NaCl} b _{Acetic acid} b _{MgCl} ,	0.99	-0.08				

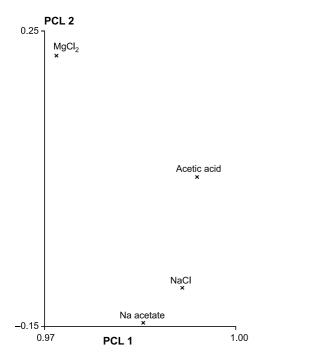


Fig. 1. Similarities and dissimilarities among the effects of eluent additives. Map of principal component loadings

occurrence of the binding of amino acids to zein. The results of PCA are compiled in Table 2. Two principal components explained 99.44% of the total variance that means that two theoretical (background) variables are sufficient to describe the effect of four eluent additives on the strength of amino acid—zein interaction. Unfortunately, PCA does not define these theoretical variables as concrete physical or physicochemical entities, only indicates their mathematical possibility. Each additive has a high loading in the first PC indicating the basic similarity of their influence on the retention of amino acids.

The map of PC loadings is shown in Fig. 1. Eluent additives are widely distributed on the map indicating that each of them exerts a separate effect on the amino-acid–zein binding, suggesting that both the pH and the charge of cation influence differently the binding of amino-acids to zein. This result entirely supports our previous conclusions that the binding of free amino acids to zein is mainly of hydrophilic character involving electrostatical interactions.

The map of PC variables are shown in Fig. 2. The distribution of amino acids on the map demonstrates the marked discrepancy between the retention characteristics of cellulose and zein-coated cellulose. Furthermore, the map illustrates that the effect of eluent additives on the binding of free amino acids is similar on cellulose stationary phase but considerably different on zein coated

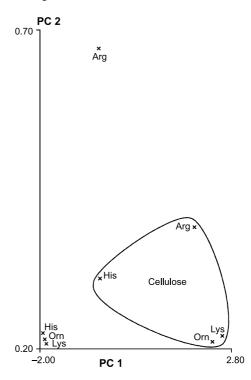


Fig. 2. Similarities and dissimilarities among the binding of amino acids to cellulose and zein-coated cellulose stationary phases. Map of principal component variables

one demonstrating again the deviation between the binding characteristics of cellulose and zein-coated cellulose.

It can be concluded from the data that TLC carried out on cellulose and zein-coated cellulose stationary phases can be successfully employed for the determination of the interaction between free amino acids and the corn protein zein and can be used for the study of the effect of pH and the concentration of ions on the strength of interaction.

References

Arnold WD, Oldfield E (2000) The chemical nature of hydrogen bonding in proteins via NMR: J-couplings, chemical shifts and AIM theory. J Am Chem Soc 122: 12835–12841

Chen VC, Chao L, Chao J (2000) Roles of the P1, P2, and P3 residues in determining inhibitory specificity of kallistain toward human tissue kallikrein. J Biol Chem 275: 38457–38466

Cordier F, Wang C, Grzesiek S, Nicholson LK (2000) Ligand-induced strain in hydrogen bonds of the c-Src SH3 domain detected by NMR. J Mol Biol 304: 497–505

Cox JR (2000) Concepts in biochemistry: teaching noncovalent interactions in biochemistry curriculum through molecular visualization: the search for π interactions. J Chem Educ 77: 1424–1428

Cserháti T, Valkó K (1994) Chromatographic determination of molecular interactions. CRC Press, Boca Raton, FL

Damborsky J, Berglund A, Kuty M, Ansorgová A, Nagata A, Sjöström M (1998) Mechanism based quantitative structure-biodegradation rela-

- tionships for hydrolytic dehalogenation of chloro- and bromoalkanes. Ouant Struct-Act Relat 17: 450–458
- De Beer T, Hoofnagle AN, Enmon JL, Bowers RC, Yamabhai M, Kay BK, Overduin M (2000) Molecular mechanism of NPF recognition by EH domains. Nat Struct Biol 7: 1018–1022
- Drew MGB, Wilden GRH, Spillane WJ, Walsh RM, Ryder CA, Simmie JM (1998) Quantitative structure-activity relationship studies of sulfamates RNHSO₃Na. Distinction between sweet, sweet-bitter and bitter molecules. J Agric Food Chem 46: 3016–3026
- Fulop V, Szeltner Z, Renner V, Polgar L (2001) Structures of prolyl oligopeptidase substrate/inhibitor complex: use of inhibitor binding titration of the catalytic histidine residue. J Biol Chem 276: 1262–1266
- Gorbitz CH (2000) An NH₃⁺...phenyl interaction in L-phenylalanine-L-valine. Acta Crystallogr Sect C C56: 1496–1498
- Guruprasad K, Prasad MS, Kumar GR (2000) Analysis of $\tau\beta$, $\beta\tau$, $\tau\tau$, $\beta\beta$ multiple turns in proteins. J Pept Res 56: 250–263
- Héberger K (1999) Evaluation of polarity indicators and stationary phases by principal component analysis in gas-liquid chromatography. Chemom Intell Lab Syst 47: 41–49
- Héberger K, Görgényi M (1999) Principal component analysis of Kováts indices for carbonyl compounds in capillary gas chromatography. J Chromatogr A 845: 21–31
- Héberger K, Lopata A (1998) Assessment of nucleophilicity and electrophilicity of radicals and of polar and enthalpy effects on radical addition reactions. J Org Chem 63: 8646–8653
- Kasim M, Swenson RP (2000) Conformational energetics of a reverse turn in the *Clostridium beijerinckii* flavodoxin is directly coupled to the modulation of its oxidation-reduction potentials. Biochemistry 39: 15322–15332
- Katritzky AR, Tamm T, Wang Y, Karelson M (1999) A unified treatment of solvent properties. J Chem Inf Comp Sci 39: 692–698
- Liu Z, Sun C, Olejniczak ET, Meadows RP, Betz SF, Oost T, Hemnann J, Wu JC, Fesik SW (2000) Structural basis for binding of Smac/DIABLO to the XIAP BIR3 domain. Nature (London) 408: 1004–1008
- Mannhold R, Cruciani G, Dross K, Rekker R (1998) Multivariate analysis of experimental and computational descriptors of molecular lipophilicity. J Comp-Aid Mol Des 12: 573–581
- Mardia KV, Kent JT, Bibby JM (1979) Multivariate analysis. Academic Press, London, pp 213–254
- Matern H, Yang X, Andrulis E, Sternglanz R, Trepte HH, Gallwitz D (2000) A novel Golgi membrane protein is part of a GTPase-binding protein complex involved in vesicle targeting. EMBO J 19: 4485–4492

- Mong TKK, Niu A, Chow HF, Wu C, Li L, Chen R (2001) β -Alanine-based dendritic β -peptides: dendrimers possessing unusually strong binding ability towards protic solvents and their self-assembly into nanoscale aggregates through hydrogen-bond interactions. Chem Eur J 7: 686–699
- Nusrat A, Chen JA, Foley CS, Liand TW, Tom J, Cromwell M, Quan C, Mrsny RJ (2000) The coiled-coil domain of occludin can act to organize structural and functional elements of the epithelial tight function. J Biol Chem 275: 29816–29822
- Sarbu C, Todor S (1998) Evaluation of lipophilicity by principal component analysis. J Planar Chromatogr Mod TLC 11: 123–126
- Seybold PG (1999) Explorations of molecular structure-property relationships. SAR 10: 101–115
- Spadaccini R, Crescenzi O, Tancredi T, De Cassamassini N, Saviano G, Scognamiglio R, Di Donato A, Temussi PA (2001) Solution structure of a sweet protein: NMR study of MNEI, a single chain monellin. J Mol Biol 305: 505–514
- Strisovsky K, Tessmer U, Langner J, Konvalinka J, Krausslich HG (2000) Systematic mutational analysis of the active-site threonine of HIV-1 proteinase: rethinking the "fireman's grip" hypothesis. Protein Sci 9: 1631–1641
- Tanahashi H, Tabira T (2000) Alzheimer's disease-associated presenilin 2 interacts with DRAL, anLIM-domain protein. Hum Mol Genet 9: 2281–2289
- Wang X, Ching YP, Lam WH, Qi Z, Zhang M, Wang JH (2000) Identification of a common protein association region in the regional Cdk5 activator. J Biol Chem 275: 31763–31769
- Wu G, Chai J, Suber TL, Wu JW, Du C, Wang X, Shi Y (2000) Structural basis of IAP recognition by Smac/DIABLO. Nature (London) 408: 1008–1012
- Zaliani A, Gancia E (1999) MS-WHIM scores for amino acids. A new 3D-description for peptide QSAR and QSPR studies. J Chem Inf Comput Sci 39: 525–533
- Zarzycki PK, Wierzbowska M, Nowakowska J, Chmielewska A, Lamparczyk H (1999) Interactions between native cyclodextrins and n-alcohols studied using thermostated thin-layer chromatography. J Chromatogr A 839: 149–156

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