ELSEVIER

Journal of Chromatography A, 741 (1996) 49–57

JOURNAL OF CHROMATOGRAPHY A

Quantitative micellar chromatographic analysis of interaction between peptides and sodium dodecyl sulfate micelles

Lili Lu, Per Lundahl*

Department of Biochemistry, Biomedical Center, Uppsala University, Box 576, S-751 23 Uppsala, Sweden

Received 4 December 1995; revised 12 February 1996; accepted 12 February 1996

Abstract

Interaction between short, water-soluble peptides and sodium dodecyl sulfate (SDS) micelles was analyzed by chromatography of the peptides on a Sephadex G-50 M el bed in an eluent containing the micelles. Peptides that interacted with the micelles showed intermediate elution volumes. In the absence of micelles in the eluent, the peptides (7–16 amino acid residues) were eluted near the total volume, whereas micelles applied as a sample appeared at the void volume. The association constants, K_A, were calculated from the capacity factors k' obtained at different SDS micelle concentrations. The range of the K_A values was $(0.5–11)\times10^4\ M^{-1}$. As a rule, the longest peptides and the positively charged ones interacted most strongly with the micelles, but the amino acid sequences also affected the interaction. Partially hydrophobic peptides that may correspond to interfacial segments of a transmembrane protein, the glucose transporter Glut1, showed relatively weak interactions with SDS micelles. The peptide interaction with sodium 1-decane sulfonate micelles supplemented with SDS was similar to that with SDS micelles, whereas none of several peptides tested interacted significantly with micelles of the non-ionic detergent *n*-dodecyl octaoxyethylene. The peptide–micelle interaction was proposed to occur mostly at the micelle surface as in the protein-decorated micelle structure for SDS–protein complexes.

Keywords: Micellar liquid chromatography; Peptides; Sodium dodecyl sulfate micelles; Glucose transport

1. Introduction

The anionic detergent, sodium dodecyl sulfate (SDS), forms complexes with both water-soluble proteins and membrane proteins. The SDS–protein complexes can be separated by electrophoretic and chromatographic methods for analytical and preparative purposes. Analyses of the hydrodynamic and electrophoretic behavior and the neutron and small-angle X-ray scattering (SAXS) of SDS complexes with water-soluble proteins have led to the proposal of several structural models. In the "necklace model", SDS clusters or micelle-like clusters are arranged along the polymer chain [1,2], whereas in the "protein-decorated micelle structure", based on neutron scattering determinations, the dodecyl chains of the detergent form hydrophobic micelle cores, surrounded by shells consisting of the hydrophilic and amphiphilic stretches of the polypeptide chain and the sulfate head-groups [3,4]. Similarly, SAXS results showed a few micelle-like SDS clusters as the major substructure of the complex [5]. SAXS and cryo-electron microscopic data indicated a protein-decorated micelle structure, which was called a necklace structure [6]. Transmembrane proteins in

*Corresponding author.

PII S0021-9673(96)00143-4

SDS–complexes may retain the tertiary structure of their hydrophobic regions.

Even short peptides interact with SDS micelles, as shown by effects on the electrophoretic mobility of the micelles [7]. The affinity of a hydrophilic polypeptide to SDS micelles presumably depends on the polypeptide length. The aim of the present work was to quantitatively analyze interactions between short hydrophilic peptides and SDS micelles by micellar liquid chromatography (MLC, see Ref. [8]). Suitable model peptides were studied. Some of these corresponded to segments of a transmembrane protein, the human red cell glucose transporter (Glut1). Most peptides had earlier been used in a study of peptide–liposome interactions [9]. Two peptides were synthesized to have different lengths but zero net charge and zero net water-to-oil transfer free energy ($\Delta G_{W/O}$) for the side-chains [10] to test the hypothesis that the association becomes stronger with increasing peptide length, possibly owing to hydrogen-bonds between the sulfate head-groups and the peptide bonds [11]. The association constants (K_A) for the SDS–peptide complexes were determined by MLC, by use of the mathematical model described by Foley [8]. The strengths of peptide interaction with micelles of SDS, sodium 1-decane sulfonate and the non-ionic detergent *n*-dodecyl octaoxyethylene ($C_{12}E_8$) were compared.

2. Experimental

2.1. Materials

Sephadex G-50 M was bought from Pharmacia Biotech (Uppsala, Sweden), sodium dodecyl sulfate (SDS, No. 13760) from Merck (Darmstadt, Germany) and $C_{12}E_8$ from Fluka (Buchs, Switzerland). Sodium 1-decane sulfonate (D 3412), dithioerythritol (DTE), Lys-Tyr-Lys (KYK) and Glu-Asn-Gly (ENG) were obtained from Sigma (St. Louis, MO, USA). Triton X-100 was purchased from Serva (Heidelberg, Germany). Other chemicals were of analytical grade.

The amino acids (W, Y, S, C, G, D, N, R and M, calibration standards from Sigma) were kindly provided by Dr. David Eaker at our Department. The peptides YGSTWPG (P_1), YGSTWPGC (P_1C), YGSTWPGS (P_1S), YGSTWPGCC (P_1CC), YGSTWPGSS (P_1SS), MPSWTGG (P_2), MPSWTGGC (P_2C), MPSWTGGS (P_2S), MPSWTGGCC (P_2CC), MPSWTGGSS (P_2SS), IPCCPVHLKR (P_3), KPSSPARLLK (P_4), MGSTWPG (P_5), YPSWTGG (P_6), MSWTGGSSP (P_7), $a_{51\text{-}64C}$, $b_{125\text{-}134}$, $c_{201\text{-}210}$, $d_{293\text{-}307C}$, $f_{421\text{-}429}$, $g_{478\text{-}492YC}$ and $h_{218\text{-}232YC}$ were synthesized as described in Refs. [9,12]. Peptides YTTNYTTS (P_8) and YTTNYTTSYTTNYTTS (P_8P_8) were synthesized by Dr. Åke Engström, Department of Medical and Physiological Chemistry, Uppsala University, by solid-phase N^{α}-q-fluorenylmethyloxycarbonyl (Fmoc) chemistry, purified by reversed-phase HPLC and analyzed by plasma desorption mass spectrometry [13] using a Bion 20 instrument (Bio-Ion Nordic AB, Uppsala, Sweden). Peptides P_3 and P_4 correspond to hydrophilic segments of chondromodulin-I from fetal bovine cartilage [14]. Peptides $a_{51\text{-}64C}$-$h_{218\text{-}232YC}$ correspond to the segments 51-64 etc (Fig. 6, below) of the human HepG2 hepatoma glucose transporter, which is similar or identical to the human red cell glucose transporter Glut1 [15]. In some cases, C-terminal Cys or Tyr-Cys were added as indicated in the above peptide denotations [12].

2.2. Eluents and micelle concentrations

Eluent A contained 50 m*M* sodium phosphate (pH 7.1) and 1 m*M* Na_2EDTA; eluent B was eluent A supplemented with 3 m*M* NaN_3. Detergent was included in eluent A and B as described below. Upon analysis of peptides containing Cys, 0.2 m*M* DTE was also included.

The values of critical micelle concentration (CMC) and aggregation number (N) used for calculation of micelle concentrations in the eluents were as follows. For SDS in eluent A or B, CMC=1.8 m*M* at 23°C [3,16,17] and N=89 (estimated from data in Fig 7, [18], dashed line, 0.1 *M* NaCl, which has the same ionic strength as the eluents used); for $C_{12}E_8$, CMC=0.11 m*M* at 25°C [19] and N=120 [20]; and for sodium decane sulfonate in eluent B, CMC=28 m*M* at 23°C (measured by weighing of thermostated drops) and $N\approx89$ (estimated). The effect of the presence of SDS in mixed decane sulfonate/dodecyl sulfate micelles was neglected.

2.3. MLC analysis of interactions between micelles and peptides or amino acids

The interactions between peptides or amino acids and SDS micelles were analyzed by MLC at 23±1°C on a 0.5 (diameter)×20-cm Sephadex G-50 M gel bed (HR 5/20 glass column, Pharmacia Biotech) which was equilibrated overnight at 0.1 ml/min with SDS (concentration 1.8, 3, 5, 7, 10, 50 or 100 m*M*) in eluent A (for analysis of peptides without aromatic residues, detection at 220 nm) or eluent B (for analysis of peptides with aromatic residues, detection at 280 nm). The peptides (0.3 mg/ml) were dissolved in the eluent (A or B), containing 10 m*M* SDS. Amino acids (0.5 mg/ml) were dissolved in eluent A containing 10 m*M* SDS. The peptides or amino acids were run at each of the above concentrations of SDS in the eluent, except that 7 m*M* SDS was used only in some cases. Analyses were also done with sample and eluent containing sodium decane sulfonate (32 m*M*) supplemented with SDS (1.6 m*M*, to enhance the solubility), or $C_{12}E_8$ (4.5 m*M*) (see Table 2 below). The total (V_t) and void (V_0) volumes of the gel bed were determined by use of NaN_3 and tobacco mosaic virus, respectively. SDS micelles (supplemented with Triton X-100 at the monomer molar ratio 100:1 for absorbance detection) were eluted slightly after V_0. The small difference was neglected in the calculations below. Peptide–micelle samples (50 μl) were applied and run at a flow-rate of 0.2 ml/min (HPLC pump No. 2248, Pharmacia Biotech). The elution was monitored by a tunable UV photometer (Waters 486, Millipore, Milford, MA). The elution positions of amino acids and peptides of low absorptivity were confirmed by ninhydrin staining [1 mg/ml in ethanol–acetic acid (3:1)] of eluent drops dried on a filter paper.

3. Theory

3.1. The peptide–SDS micelle association constant K_A

MLC was used for the analysis of the peptide–micelle interactions (Fig. 1) and the SDS–peptide association constants, K_A, were calculated essentially as described in Ref. [8]. The presence of an equilibrant M (micelles) in the mobile phase allows an analyte P (peptide) to exist in two forms: as free analyte and in an analyte–equilibrant complex PM. The rapid interchange between these forms results in elution of the analyte in a single zone. The elution volume decreases with increasing micelle concentration in the eluent, as shown below. The peptide retention, expressed as the capacity factor k' [see also Eq. (8)], is given by

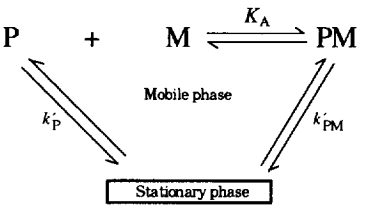

Fig. 1. Retention model for peptide–micelle chemical equilibrium in MLC with P, peptide; M, SDS micelle; PM, peptide–micelle complex; k'_P, the chromatographic capacity factor for the free peptide; k'_{PM}, the chromatographic capacity factor for the peptide–micelle complex, and K_A, the association constant for interaction between peptides and micelles.

$$k' = F_{PM}k'_{PM} + F_Pk'_P \quad (1)$$

where F_{PM}, the stoichiometric fraction of the PM complex, is:

$$F_{PM} = [PM]/\{[PM] + [P]\} \quad (2)$$

and F_P, the fraction of P in free form, is:

$$F_P = [P]/\{[PM] + [P]\} \quad (3)$$

and where k'_{PM} and k'_P are the "limiting" capacity factors of the corresponding entities. In the present work, a small-pore gel was used and the micelles and peptide–micelle "complexes" did not enter the gel beads, i.e., k'_{PM} is zero. Eq. (1) thus becomes

$$k' = F_Pk'_P \quad (4)$$

Furthermore,

$$K_A = [PM]/[P][M] \quad (5)$$

where [M], the concentration of SDS micelles, can be expressed as $[M]=\{[SDS]-CMC\}/N$, where [SDS] is the SDS concentration and N is the micellar aggregation number. We assumed that the interaction

between peptides and micelles did not change the average micellar size. Eq. (4) and Eq. (5) give

$$k' = \{1/(1 + K_A[M])\}k'_P \quad (6)$$

which can be rearranged to read

$$1/k' = (K_A/k'_P)[M] + 1/k'_P \quad (7)$$

in which k' can be expressed as

$$k' = (V_e - V_0)/(V_t - V_0) \quad (8)$$

where V_e is the retention volume of the peptide at the micelle concentration [M] in the eluent; V_t is the total volume and V_0 is the void volume. A plot of $1/k'$ versus [M] yields a straight line with the intercept $1/k_P'$, and the slope K_A/k_P', according to Eq. (7). In the calculations, k_P' was taken to equal 1 (see the legend to Fig. 2).

4. Results and discussion

4.1. Interaction of peptides with SDS micelles

Several peptides (Table 1) were run on Sephadex G-50 M with SDS micelles in the eluent. The reciprocals of the k' values increased linearly with the SDS micellar concentration, at least up to 0.1 m*M* micelles, with a correlation r^2 above 0.99. Some examples are illustrated in Fig. 2 and Fig. 3. The peptide–SDS micelle association constants, K_A, were calculated according to Eq. (7) as described in the Section 3 and in the legend to Fig. 2. The values are given in Table 1. The five P_2 peptides showed much stronger interaction with the SDS micelles than did the P_1 peptides. The sequences of the P_1 and P_2 peptides differed, but the amino acid composition was the same, except for an exchange of Tyr in P_1 for Met in P_2 between the two series of peptides. The sequence effect is further described in Section 4.3. An exchange of the N-terminal Tyr in P_1 to Met to obtain the more hydrophobic peptide P_5 did not increase the affinity for SDS micelles, and substitution of N-terminal Met in P_2 for Tyr to obtain peptide P_6 did not decrease the affinity (Table 1). However, the association constants of the peptides with 7–9 residues in Table 1 increased with decreasing $\Delta G_{w/o}$ values, although the linear correlation was weak ($r^2 = 0.65$) (not shown). For these peptides of about the same length, the hydrophobicity of the side chains thus affected the association between the peptides and the micelles.

Table 1
K_A for peptide–SDS micelle interaction and $\Delta G^a_{w/o}$ of the peptides at pH 7.1[b]

Peptide		K_A ($10^4\ M^{-1}$)	$\Delta G_{w/o}$ (kcal/mol)
Denote	Sequence		
P_1	YGSTWPG	0.9	4.1
P_1S	YGSTWPGS	1.4	3.5
P_1C	YGSTWPGC	1.5	2.1
P_1SS	YGSTWPGSS	2.4	2.9
P_1CC	YGSTWPGCC	2.3	0.1
P_2	MPSWTGG	5.9	0.4
P_2S	MPSWTGGS	11.0	0.2
P_2C	MPSWTGGC	8.9	−1.6
P_2SS	MPSWTGGSS	9.8	−0.8
P_2CC	MPSWTGGCC	10.3	−3.6
P_5	MGSTWPG	0.7	0.4
P_6	YPSWTGG	5.9	4.1
P_8	YTTNYTTS	0.5	9.3
P_8P_8	YTTNYTTSYTTNYTTS	8.7	9.3

[a] Water–oil transfer free energies of side chains of peptides, calculated according to the values given in Table 1 of [10]. The $\Delta G_{w/o}$ value for each peptide is the sum of $\Delta G_{w/o}$ values for every amino acid residue of the peptide. This calculation included the amino and carboxylic groups at the termini. The $\Delta G_{w/o}$ values of Y, G, S, T, W, P, C, N, M, N- and C-terminal are 0.3 (0.7 is given in Ref. [10]; it is not correct), −1.0, −0.6, −1.2, −1.9, 0.2, −2.0, 4.8, −3.4, 5.0 and 4.3 respectively [10].

[b] The net charge (calculated as described in [21,22]) of all peptides was $-0.24 - -0.25 \times 1.6 \times 10^{-19}$ A s.

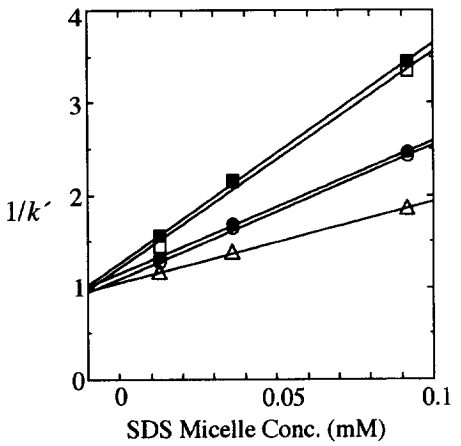

Fig. 2. Dependence of the reciprocal of the capacity factor on the SDS micelle concentration in the mobile phase for five peptides: P_1 (triangles), P_1C (filled circles), P_1S (open circles), P_1CC (filled squares) and P_1SS (open squares). The K_A values were calculated as described in Section 3 and were approximated to equal the slopes K_A/k'_P, for the reason that the intercepts $1/k'_P$ were expected to be 1.0. The experimental values of $(V_e-V_0)/(V_t-V_0)$ were near to 1.0 in the absence of SDS. The use of the intercept values in the figure was found to be less reliable, as the position [M]=0 was not precisely defined, since the peptide samples contained 10 m*M* SDS in all runs, and since the CMC and aggregation number of SDS are difficult to define with sufficient accuracy.

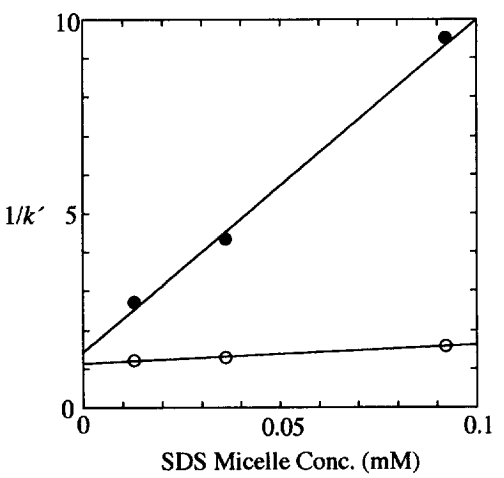

Fig. 3. Dependence of the reciprocal of the capacity factor on the SDS micelle concentration in the mobile phase for P_8 (open circles) and P_8P_8 (filled circles). K_A values were calculated as described in the Section 3, further details being given in the legend to Fig. 2.

4.2. Effect of peptide length

As the P_1 peptide length (seven residues) was increased to eight and nine residues by addition of one or two C-terminal Ser or Cys residues, the interaction strength increased (Fig. 2 and Table 1). Similar results were obtained for the peptides P_2, P_2SS and P_2CC (Table 1). The effect of Cys was the same as that of Ser, contrary to the specific effect of C-terminal Cys in peptide–liposome interaction [9]. In an attempt to distinguish whether the proposed hydrogen-bonds between peptide-bond nitrogen and sulfate-group oxygens [11] participated in the interaction of peptide to SDS micelles or not, the hydrophilic peptides P_8 and P_8P_8 were chosen to have the same charge and $\Delta G_{W/O}$ (calculated as the transfer free energy for transfer of side-chains and terminal groups from water-to-oil [10]). Only the length of the peptide differed. The monomer interacted only weakly with the SDS micelles, whereas the sixteen-residue dimer exhibited strong interaction (Fig. 3 and Table 1). Longer peptides thus showed stronger interaction with SDS micelles than did shorter ones. This may be explained both by hydrogen-bonding and by other cooperative interactions between the peptides and the micelles.

4.3. Effect of peptide sequence

The sequence of peptide P_1 (YGSTWPG) differs from that of peptide P_6 (YPSWTGG) although the amino acid composition is the same. P_6 interacted much more strongly with SDS micelles than did P_1, and similarly, P_2 (MPSWTGG) interacted more strongly than did P_5 (MGSTWPG) (Table 1 and Fig. 4). This shows the importance of the peptide sequence. Peptides P_1 and P_6 in a mixture could be separated by MLC with 10 m*M* SDS in the eluent (Fig. 4A), as could peptides P_2 and P_5 (Fig. 4B). Another nonapeptide, P_7, was chosen to have the same sequence as P_2SS, except that the Pro residue was moved from position 2 to the C-terminus. This sequence modification weakened the interaction between the peptide and the micelles ($k'=0.4$ for P_7 and 0.2 for P_2SS at 5 m*M* SDS). Also this result shows that the peptide sequence can affect the interaction with the SDS micelles.

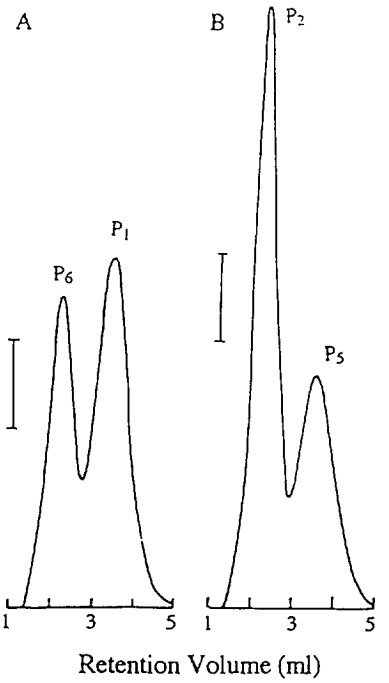

Fig. 4. Separation of (A) P_1 mixed with P_6, and (B) P_2 mixed with P_5, by MLC in eluent A supplemented with 10 m*M* SDS. The bars correspond to an absorbance of 0.02 at 1-cm light path.

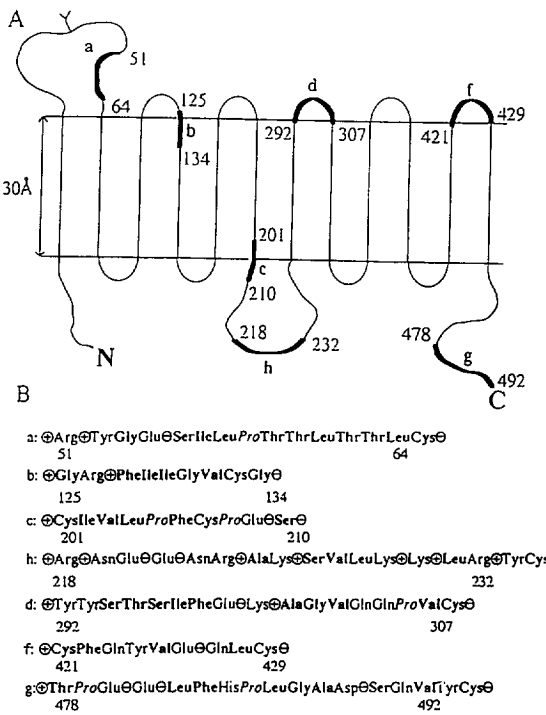

Fig. 5. Position and sequence of selected Glut1 segments. (A) Position of the polypeptide segments (thick lines) a–d and f–h in the topology model of [15]. (B) Sequence of the synthesized polypeptides corresponding to the above segments. Charges at pH 7 are indicated, residues with hydrophobic side chains are given in bold-face and Pro is shown in italics.

4.4. *Interaction of peptides corresponding to segments of Glut1 with SDS micelles*

Peptides a–d and f–h correspond to segments of the glucose transporter from human HepG2 hepatoma cells [15] as indicated in Fig. 5. The hydrophilic peptides, a, h and d (with 12–16 residues) interacted most strongly with SDS (Fig. 6). Even at the CMC these peptides formed peptide–micelle complexes (Fig. 6). The short peptide c, which is negatively charged, interacted less strongly with the micelles (Fig. 6). This peptide contained two Pro residues: according to the hydrogen-bonding hypothesis model of the interactions and hydrogen-bonding in SDS–protein complexes [11], the Pro-Phe-Cys-Pro (see Fig. 5B) segment in peptide c cannot form hydrogen bonds with the head group of SDS, however the two Pro residues may allow adjacent hydrophobic residues Phe and Cys to insert into the hydrophobic micelle core. The peptide g showed weak interaction (see graphs for 1.8 m*M* and 10 m*M* SDS in Fig. 6), presumably because it was repelled

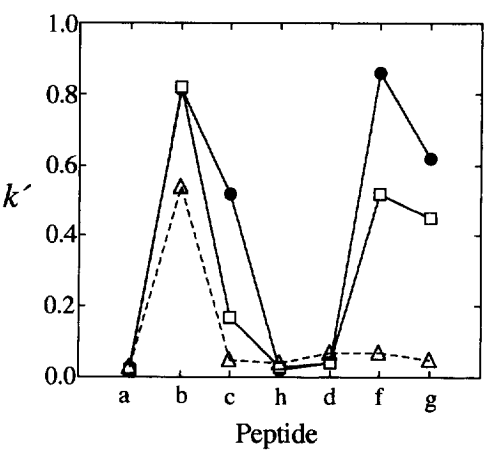

Fig. 6. The capacity factors of peptides corresponding to segments of Glut1 (see Fig. 5) at the SDS concentrations; 1.8 m*M* (the CMC, filled circles), 10 m*M* (squares) and 50 m*M* (triangles), in eluent B.

from the sulfate head-groups of the micelles by four negative charges, only the N-terminal being positively charged. Also the short peptide f showed weak interaction, perhaps owing to a negatively charged side chain. Peptide b showed the weakest interaction among the Glut1 peptides tested, despite a positive net charge, perhaps because the hydrophobic stretch FIIGVCG is situated between a positive and a negative charge in the peptide and is too short to become inserted into the micelle core with hydrogen bonding between the NH– and C=O groups. Peptides b and c correspond to segments that are partially inserted in the membrane of the 12-helical model (Fig. 5, above). Interestingly, several peptides that interacted strongly with liposomes upon immobilized-liposome chromatography [9] associated weakly with the micelles, and vice versa, as illustrated in Fig. 7. Presumably the interactions of peptides with the SDS micelles were mostly of an electrostatic nature (attraction of positively charged groups and, possibly, hydrogen bonding), whereas the peptide interactions with the non-charged liposomes were mostly of hydrophobic character. The two positively charged and hydrophilic peptides, P_3 and P_4, interacted very strongly with SDS micelles

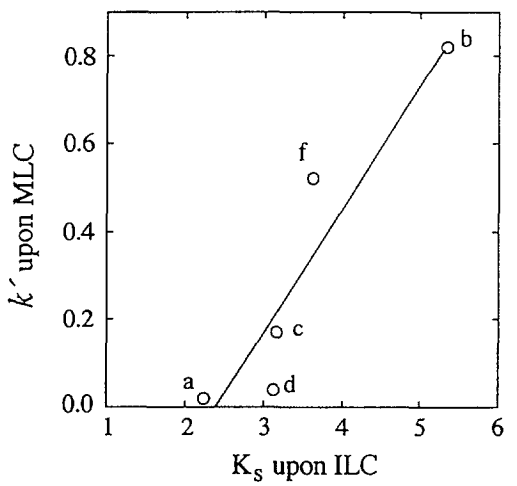

Fig. 7. The capacity factors of the peptides a–d and f that correspond to segments of Glut1 (see Fig. 5 and Fig. 6) on the MLC column with 10 m*M* SDS (*y*-axis), versus the specific capacity factors on an immobilized-phosphatidylcholine–phosphatidylethanolamine (4:1) liposome column (data from Fig. 8B in [9]).

($k' \approx 0.03$ at 1.8 m*M* SDS), indicating that the charge of the peptides affected the peptide–micelle interactions. At pH 11 (0.05 *M* phosphate–NaOH), where the peptides are negatively charged, the peptide–micelle interactions were very weak for P_1SS, P_2SS, P_7, P_8, and P_8P_8 (charge between -2 and $-1 \times 1.6 \times 10^{-19}$ A s).

4.5. Interaction of amino acids and tripeptides with SDS micelles

The interaction between SDS micelles and the amino acids Trp, Tyr, Ser, Cys, Gly, Asp, Asn, Arg and Met was analyzed. Trp showed stronger interaction ($K_A = 0.1 \times 10^4\ M^{-1}$) than did the other amino acids, for which the association was very weak. In [23], amino acids were shown to have different interactions with SDS micelles at pH 2.7, at which pH the amino acids are positively charged. These interactions were probably of an electrostatic nature. At pH 6.5 the binding capacity was decreased. The negatively charged tripeptide ENG showed no interaction with SDS micelles, whereas the positively charged peptide KYK interacted fairly strongly with SDS micelles ($K_A = 7.4 \times 10^4\ M^{-1}$). These results indicate that the electrostatic charge of amino acids and very short peptides strongly affect their interaction with SDS micelles.

4.6. Different detergents

The interaction of peptides with micelles of the anionic detergents SDS and sodium decane sulfonate, and the non-ionic detergent $C_{12}E_8$, were compared. The capacity factors of the peptides were much smaller (the interaction stronger) with SDS micelles than with $C_{12}E_8$ micelles (Table 2). No obvious difference was found in the strength of interaction of peptides with SDS micelles and the mixed sodium decane sulfonate and SDS micelles, to judge from MLC capacity factors (Table 2). This result indicated that the surface structure and the charge of the micelles are important for the interaction with peptide. The sulfate head-group showed only slightly stronger interaction with the peptides than did the sulfonic head-group.

Table 2
The capacity factors k' of peptides upon MLC with different detergents

Peptide	k'[a]			
	SDS[b]	Sodium 1-decane sulfonate[c]	$C_{12}E_8$[d]	No detergent
P_1C	0.6	0.7	1	1
P_2C	0.2	0.3	0.9	0.9
P_8	0.8	0.9	0.9	0.9
P_8P_8	0.2	–	0.8	0.8
a_{51-64C}	0.03[e]	–	0.7	0.7
$b_{125-134}$	0.8[e]	–	0.9	0.9

[a] $k' = (V_e - V_0)/(V_t - V_0)$. Average of 2–5 measurements.
[b] At 5 m*M* SDS (0.036 m*M* micelle concentration).
[c] With 32 m*M* sodium 1-decane sulfonate mixed with 1.6 m*M* SDS (≈0.04 m*M* micelle concentration).
[d] At 4.5 m*M* $C_{12}E_8$ (≈0.04 m*M* micelle concentration).
[e] At 10 m*M* SDS (0.072 m*M* micelle concentration).

5. Conclusions

Even short hydrophilic peptides (7–16 residues) can associate strongly with SDS micelles. The charge, sequence, length and amphiphilic characteristics of the peptides are important for their interaction with SDS micelles. Hydrogen-bonding between the sulfate head-groups and the peptide bond nitrogens [11] may occur. Short hydrophilic peptides do not associate with non-ionic micelles ($C_{12}E_8$). Micelles of sodium decane sulfonate interacted with peptides nearly as strongly as did SDS micelles. Peptides corresponding to hydrophilic segments of Glut1 on the cytoplasmic and extracellular faces [9,15] behaved in SDS solution like water-soluble peptides and showed strong interaction with SDS micelles. Amphiphilic Glut1 peptides that probably corresponded to interfacial polypeptide segments of Glut1 showed weaker and more varying interactions with SDS micelles.

Acknowledgments

We thank Professor Saburo Aimoto, Ms. Shoko Yoshimura, and Dr. Åke Engström for synthesis and analysis of peptides, Dr. David Eaker for linguistic revision of the manuscript, Mrs. Eva Greijer for help and advice, and Professor Toshio Takagi, Lars Haneskog, B.Sc., Eggert Brekkan, B.Sc., and Farideh Beigi, M. Sc. for useful discussion. We are grateful for financial support from the Swedish Research Council for Engineering Sciences, the Swedish Natural Science Research Council, and the O.E. and Edla Johansson Science Foundation.

References

[1] K. Shirahama, K. Tsujii and T. Takagi, J. Biochem. (Tokyo), 75 (1974) 309.
[2] X.H. Guo, N.M. Zhao, S.H. Chen and J. Teixeira, Biopolymers, 29 (1990) 335.
[3] K. Ibel, R.P. May, K. Kirschner, H. Szadkowski, E. Mascher and P. Lundahl, Eur. J. Biochem., 190 (1990) 311.
[4] K. Ibel, R.P. May, M. Sandberg, E. Mascher, E. Greijer and P. Lundahl, Biophys. Chem., 53 (1994) 77.
[5] S. Shinagawa, M. Sato, K. Kameyama and T. Takagi, Langmuir, 10 (1994) 1690.
[6] M. Samsó, J.-R. Daban, S. Hansen and G.R. Jones, Eur. J. Biochem., 232 (1995) 818.
[7] M.R. Karim, S. Shinagawa and T. Takagi, Electrophoresis, 15 (1994) 1141.
[8] J.P. Foley, Anal. Chim. Acta, 231 (1990) 237.
[9] Y. Zhang, S. Aimoto, L. Lu, Q. Yang and P. Lundahl, Anal. Biochem., 229 (1995) 291.
[10] D.M. Engelman, T.A. Steitz and A. Goldman, Annu. Rev. Biophys. Biophys. Chem., 15 (1986) 321.
[11] P. Lundahl, E. Greijer, M. Sandberg, S. Cardell and K.-O. Eriksson, Biochim. Biophys. Acta, 873 (1986) 20.
[12] L. Andersson and P. Lundahl, J. Biol. Chem., 263 (1988) 11414.
[13] B. Sundqvist and R.D. Macfarlane, Mass. Spectrom. Rev., 4 (1985) 421.
[14] Y. Hiraki, H. Tanaka, H. Inoue, J. Kondo, A. Kamizono and F. Suzuki, Biochem. Biophys. Res. Commun., 175 (1991) 971.

[15] M. Mueckler, C. Caruso, S.A. Baldwin, M. Panico, I. Blench, H.R. Morris, W.J. Allard, G.E. Lienhard and H.F. Lodish, Science, 229 (1985) 941.
[16] E. Mascher and P. Lundahl, J. Chromatogr., 476 (1989) 147.
[17] T. Takagi, J. Miyake and T. Nashima, Biochim. Biophys. Acta, 626 (1980) 5.
[18] N.A. Mazer, G.B. Benedek and M.C. Carey, J. Phys. Chem., 80 (1976) 1075.
[19] M.J. Rosen, A.W. Cohen, M. Dahanayake and X.-y. Hua, J. Phys. Chem., 86 (1982) 541.
[20] C. Tanford, Y. Nozaki and M.F. Rohde, J. Phys. Chem., 81 (1977) 1555.
[21] A.-K. Englund and P. Lundahl, Biochim. Biophys. Acta, 1065 (1991) 185.
[22] L. Lu, E. Brekkan, L. Haneskog, Q. Yang and P. Lundahl, Biochim. Biophys. Acta, 1150 (1993) 135.
[23] F. Maley and D.U. Guarino, Biochem. Biophys. Res. Commun., 77 (1977) 1425.