FEBS 20474 FEBS Letters 430 (1998) 425

Answer

Magnus Gustafsson^a, Guy Vandenbussche^b, Tore Curstedt^c, Jean-Marie Ruysschaert^c, Jan Johansson^a

^aDepartment of Medical Biochemistry and Biophysics, Karolinska Institutet, S-171 77 Stockholm, Sweden ^bLaboratoire de Chimie-Physique des Macromolécules aux Interfaces, Université Libre de Bruxelles, Boulevard du Triomphe CP 206/2, 1050 Bruxelles, Belgium

^cDepartment of Clinical Chemistry, Karolinska Hospital, S-171 76 Stockholm, Sweden

Received 8 June 1998

Our 1996 study [1] was undertaken to characterize the secondary structure and the orientation of the KL₄ peptide in a lipid environment, and to relate these data to the known structural properties of pulmonary surfactant proteins B and C (SP-B and SP-C).

Using polarized Fourier transform infrared (FTIR) spectroscopy and CD spectroscopy we unequivocally demonstrated a helical structure and a transmembrane orientation of KL4 in a DPPC/PG bilayer. The monolayer model of KL₄ proposed by Cochrane and Revak [2] is partly based on fluorescence data [2] and Raman spectroscopy data [3] of the peptide in lipid bilayers. Due to the differences between lipid bilayers and monolayers, it is difficult to predict how a transmembrane stretch of 21 residues with charged residues distributed around the helical circumference can be accommodated in a lipid monolayer. No attempt was made in our study to relate the orientation of KL4 in a lipid bilayer to the orientation in a lipid monolayer [1]. Further studies are needed in order to establish the orientation of KL4 in a lipid monolayer. For example, it has been demonstrated that native SP-C adopts a transmembrane orientation in a lipid bilayer [4,5] but the SP-C helix tilt angle to the interface normal changes from \sim 24° in lipid bilayers to \sim 70° in DPPC monolayer films [6]. We noticed that the orientation of KL₄ in a lipid bilayer closely resembled that of native SP-C [4-7] but contrasted to the proposed interaction of SP-B with lipid bilayers [8-10], and therefore suggested that the mechanism of action of KL₄ may be similar to that of SP-C rather than to that of SP-B. We strongly believe that interactions between SP-B, SP-C, and synthetic analogues on the one hand and lipid bilayers on the other are relevant, since these proteins are hydrophobic and need to be transported in a lipid bilayer environment to the interfacial monolayer. It should be remembered that the main location and site of action (bilayer, monolayer, or both) of SP-B and SP-C in lung surfactant remain to be established.

We also pointed out that the KL₄ helix exhibits a mixed nonpolar/polar surface which is different from the amphipathic SP-B helices [8,11] and nonpolar SP-C helix [12]. The spreading of KL₄/DPPC/PG/PA vesicles at an air/water interface is rapid, but slower than the spreading of native SP-C/

DPPC/PG/PA vesicles or vesicles composed of an SP-C/bacteriorhodopsin hybrid mixed with the same lipids [1]. We suggested that this may be caused by the fact that SP-C exhibits a 'mobility gradient' in a phospholipid bilayer, i.e. only the N-terminal end of the helix contains basic residues that can interact with the phospholipid head groups [7], while KL_4 is expected to interact similarly with the phospholipid head groups at both ends of the helix [1].

Studies of the relationships between structure, orientation and activity of SP-B and SP-C, and their analogues, are necessary in order to understand their roles in the adsorption of phospholipids to the alveolar air-liquid interface. Such knowledge is also required for rational design of synthetic analogues of the surfactant proteins.

References

- [1] Gustafsson, M., Vandenbussche, G., Curstedt, T., Ruysschaert, J.-M. and Johansson, J. (1996) FEBS Lett. 384, 185–188.
- [2] Cochrane, C.G. and Revak, S.D. (1991) Science 254, 566–568.
- [3] Vincent, J.S., Revak, S.D., Cochrane, C.G. and Levin, I.W. (1991) Biochemistry 30, 8395–8401.
- [4] Pastrana, B., Mautone, A.J. and Mendelsohn, R. (1991) Biochemistry 30, 10058–10064.
- [5] Vandenbussche, G., Clercx, A., Curstedt, T., Johansson, J., Jörnvall, H. and Ruysschaert, J.-M. (1992) Eur. J. Biochem. 203, 201–209.
- [6] Gericke, A., Flach, C.R. and Mendelsohn, R. (1997) Biophys. J. 73, 492–499.
- [7] Johansson, J., Szyperski, T. and Wüthrich, K. (1995) FEBS Lett. 362, 261–265.
- [8] Andersson, M., Curstedt, T., Jörnvall, H. and Johansson, J. (1995) FEBS Lett. 362, 328–332.
- [9] Vandenbussche, G., Clercx, A., Clercx, M., Curstedt, T., Johansson, J., Jörnvall, H. and Ruysschaert, J.-M. (1992) Biochemistry 31, 9169–9176.
- [10] Morrow, M.R., Pérez-Gil, J., Simatos, G., Boland, C., Stewart, J., Absolom, D., Sarin, V. and Keough, K.M.W. (1993) Biochemistry 32, 4397–4402.
- [11] Liepinsh, E., Andersson, M., Ruysschaert, J.-M. and Otting, G. (1997) Nature Struct. Biol. 4, 793–795.
- [12] Johansson, J., Szyperski, T., Curstedt, T. and Wüthrich, K. (1994) Biochemistry 33, 6015–6023.

0014-5793/98/\$19.00 © 1998 Federation of European Biochemical Societies. All rights reserved. PII: S0014-5793(98)00711-X