Structural study of voltage dependent channel forming peptides in solution

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Introduction

The ion channel study is a very important factor, when it is tried to elucidate the mechanism of an intercellular signal transduction and of an ionic membrane permeability. But it is difficult to discuss the structure-function relations, because the structure analyses of channel-forming proteins do not completely progress yet. So, a low molecular weight model compounds which can form an ion channel may be able to provide useful information. We have the peptaibols [1] (Fig. 1) as one of such the compounds. Hypelcin A-I, antibiotics and hydrophobic peptide, which is one of the peptaibols is taken up in this experiment,

Hypelcin A-I, obtained from *Hypocrea peltata*, is done instrumental analysis, NMR and CD et al., of already [2, 3]. In attempt to obtain further information about structure, we have performed solution small-angle X-ray scattering (SAXS) experiments in various concentrations of hypelcin A-I.

Ac-U-P-U-A-U-U-Q-U-L-U-G-U-U-P-V-U-U-Q-Q-L-OH

Fig. 1 Primary structure of hypelcin A-I

Experimental

Hypelcin A-I was extracted from the stroma of *H. peltata* and purified by chromatography as reported previously [3]. Four sample solutions (30.0, 22.5, 15.0, and 7.5 mg/mL) used for SAXS measurements were prepared by distilled methanol.

SAXS measurements were carried out by using the optics and detector system SAXES (Small-Angle X-ray Scattering Equipment for Solution) were installed at BL-10C in the Photon Factory, KEK. A wavelength of 1.49 Å was used. X-ray scattering intensity was registered at 512 different angles by using the one-dimensional positive proportional counter.

Results and Discussion

Fig. 2 shows the effect of concentration on the scattering intensity in methanol system.

Hypelcin A-I was dissociated to unfold monomer when analyzed by Guinier and Kratky plots. The analysis by Kratky plots and of scattered intensity in relation to weight-averaged molecular weights revealed that hypelcin A-I was completely monomer in methanol solution. The detailed structure and function hypelcin A-I is now analysing from the scattering curves shown in Fig. 2. In fact, hypelcin A-I takes the helical structure and behaviors as rod like molecules in solution.

These results were in good agreement with the results of CD data and the channel conductance method suggesting the bundle of ideal a-helical structure.

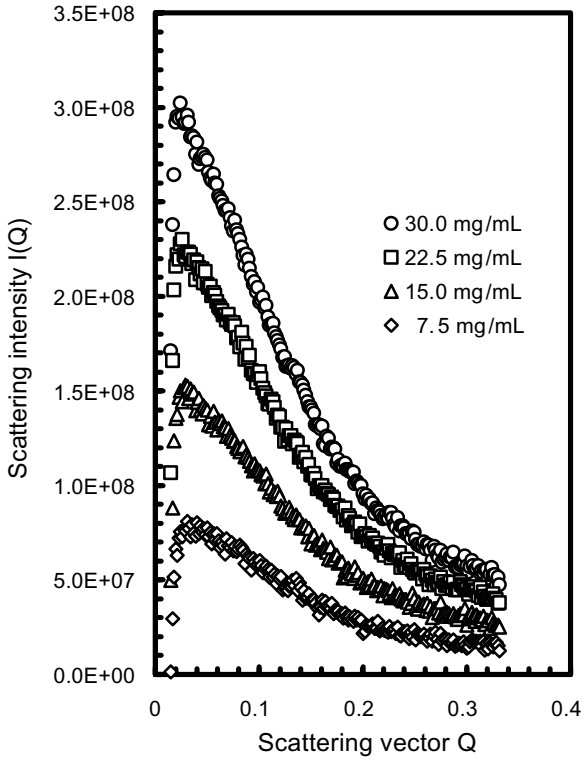

Fig. 2 The effect of concentration on the scattering intensity in methanol system.

References

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