C-5-08

Functional analysis of Liposome binding peptide selected by cDNA display

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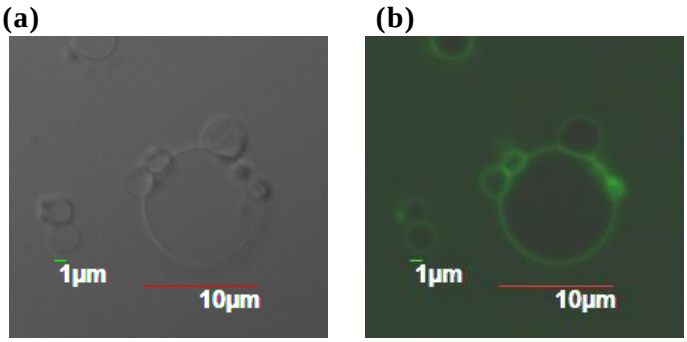
Keywords: mRNA/cDNA display, Liposome membrane-binding peptide, *In vitro* selection

cDNA display is a genotype-phenotype linking method that a peptide is conjugated with its encoded cDNA via a puromycin-linker using a cell-free translation system [1]. cDNA display enables to perform *in vitro* selection from a library of 10^{12} peptide molecules. We previously obtained some kinds of high-affinity peptide aptamers against interleukin-6 receptor by this method [2]. In this study, we tried in vitro selection to obtain peptides that bind with liposome which is artificial lipid bilayer from random peptide (30 residues in length) library. After six rounds of selection, the random sequences have been converged a unique consensus amino acids sequence. Then, we designed and synthesized a peptide modified a fluorescein at its N-terminus by chemical-synthesis and examined whether the peptide can interact with liposome membrane with a confocal laser scanning microscopy. Interestingly, the interaction between the peptide and liposome might depend on the method of preparing liposome. In this presentation, we will show the results and discuss about the interaction between the peptide and liposome in detail.

Fig.1 Interaction between peptides and liposome.



Giant unilamellar liposomes were prepared with dioleoylphosphatidylcholine (DOPC) and incubated peptides (6μM) with for 2h at 25℃.
(a)Differential interference contrast (DIC) image of liposomes.
(b) Fluorescence microscopy image of liposomes (with fluorescent dye labeled peptides). The image was taken from a confocal laser scanning microscopy.

[1] Mochizuki, Y., *et al*., *ACS Comb. Sci*., **13**, 478-485 (2011)
[2] Nemoto, N., *et al*., *Biochem Biophys Res Commun*., **421**, 129-133 (2012)