Supplementary Information

Exploring the molecular structure of lipids in the design of artificial lipidated antifungal proteins

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1. Supplementary information

1-1. Amino acid sequence of LysM-Q (pI/Mw: 6.99 / 8739.65)

MCTTYTIKSGDTCYAISQARGISLSDFESWNAGIDCNNLQIGQVVCVSKPSTSTTPSPT PSSSSNGFYPLQMRGGHHHHHH

1-2. Amino acid sequence of LysM-muGFP-Q (pI/Mw: 6.04 / 35078.23)

MCTTYTIKSGDTCYAISQARGISLSDFESWNAGIDCNNLQIGQVVCVSKPSTSTTPSPT PSSSSNGHHHHHHSKGEELFTGVVPILVELDGDVNGHKFSVRGEGEGDATNGKLTLKFI CTTGKLPVPWPTLVTTLTYGVLCFSRYPDHMKRHDFFKSAMPEGYVQERTISFKDDGTY KTRAEVKFEGDTLVNRIELKGIDFKEDGNILGHKLEYNFNSHNVYITADKQKNGIKAYF KIRHNVEDGSVQLADHYQQNTPIGDGPVLLPDNHYLSTQSVLSKDPNEKRDHMVLLEDV TAAGITHGMDELYRGGGGSLLQG

Brown: LysM2 domain Blue: Linker sequences derived from PrChiA Green: Hexahistidine tag Purple: Q-tag (FYPLQMRGG) Dark Green: muGFP Orange: Q-tag (LLQG)

1-3. Molecular structure of lipid-modified peptides



Figure S1. Chemical structures of lipid-G₃S-RHK and (lipid)₂-KG₃S-RHK with the values of theoretical molecular weight.

2. Supplementary results

2-1. Results of Fmoc solid phase peptide synthesis

ritem (cu)	i C12-GGGSRHK	ii C14-GGGSRHK	iii C16-GGGSRHK
1	[M+H]+	[M+H] ⁺	[M+H] ⁺
61	879.8	907.8	935.8
6	1913 -		4+
6.			
6	531-		2-
6.	a ' da '		
173) 1644 3855	iv (C12) ₂ -KGGGSRHK	v (C14) ₂ -KGGGSRHK	vi (C16) ₂ -KGGGSRHK
20	[M+H] ⁺	[M+H] ⁺	
233	1190.1	1246.1	1303.2
150	400		
133	et		13-
53	38-		65
	a base mit a la restation differentiation de la construction de la construction de la construction de la constr	en fils fils de meneri de si la ensendat in adat de terre an deta la stant en adat de la sec	

Figure S2. MALDI-TOF-MS results of lipid-GGGS-RHK and (lipid)₂-KGGGS-RHK. (i) C12-, (ii) C14-, (iii) C16-GGGS-RHK, (iv) (C12)₂-, (v) (C14)₂-, and (vi) (C16)₂-KGGGS-RHK.

2-2. Conjugation of Q-Tagged chitinase domains by MTG



Figure S3. (i) SDS-PAGE analysis of unmodified chitinase and chitinase modified with C12-K, C14-K, C16-K, (C12)₂-K, (C14)₂-K and (C16)₂-K by MTG. All conjugation reactions were carried out with 10 μ M Q-tagged chitinase domains, 1% DDM, 10 μ M Lipid-K, and 0.1 U/mL MTG in 10 mM Tris-HCl (pH 8.0) at 37 °C for 1 h. (ii) The raw image of SDS-PAGE gel (rectangular box with red dotted line denotes the part used for (i).

2-3. Qualitative results of antifungal activity test



Figure S4. Representative image of a 96-well plate after culturing *T. viride* in the presence of 0-5 μ M of AmB with 1 μ M of each sample at 60h.

2-4. Antifungal activity test for LysM-C14 and LysM-C16



Figure S5. MIC of LysM-C14 (i) and LysM-C16 (ii) in 20 mM NaPi, pH 7.4, 25°C at 60 h.

2-5. FIC index for LysM-C14 and LysM-C16

$$FIC index = \frac{A}{MIC_A} + \frac{B}{MIC_B} = FIC_A + FIC_B \quad (1)$$

The fractional inhibitory concentration (FIC) index was estimated by the above equation (1). "A" refers to the the minimum inhibitory concentration (MIC) value of AmB in combination with LysM-lipid, where "MIC_A" refers to MIC of AmB alone. "B" refers to the MIC value of LysM-lipid in combination with AmB, where "MIC_B" refers to the MIC of LysM-lipid alone. These values added together output the FIC index value, where < 0.5 indicates synergy, 0.5-4 for indifference, and > 4 for antagonism [16].

A. FIC index of LysM-C14

MICA	AmB Only	2.5	(see Fig. S4)
Α	AmB combination	0.63	(see Fig. S4)
MIC _B B	Protein only Protein combination	2 1	(see Fig. S5(i)) (see Fig. S4)
FIC index o	f AMB and LysM – C1	$4 = \left(\frac{0.63}{2.5}\right)$	$\left(+ \left(\frac{1}{2} \right) \right) = 0.752$

B. FIC index of LysM-C16

MICA	AmB Only	2.5	(see Fig. S4)
Α	AmB combination	0.63	(see Fig. S4)
МІСв	Protein only	2	(see Fig. S5(ii))
В	Protein combination	1	(see Fig. S4)

FIC index of AMB and LysM - C16 =
$$\left(\frac{0.63}{2.5}\right) + \left(\frac{1}{2}\right) = 0.752$$

2-6. Results of DLS measurements



Figure S6. DLS measurements of AmB with LysM-Q or LysM-lipid in 20 mM NaPi, pH 7.4 at 25°C.



Figure S7. DLS measurements of AmB with LysM-C14 (i) or LysM-C16 (ii) during incubation at 4°C or 25°C in 20 mM NaPi (pH 7.4).

(ii) Storage Day 7 (i) Storage Day 1 4°C 25°C 4°C 25°C AmB AmB LM-LM-LM-LM-LM-LM-LM-LM-100% 0% 100% 0% (µM) (µM) C14 C16 C14 C14 **C16 C16** C14 C16 5.00 5.00 2.50 2.50 1.25 1.25 0.6<mark>3</mark> 0.63 0.31 0.31 0.16 0.16 0.00 0.00

2-8. Antifungal activity test with the formulation under different storage conditions

Figure S8. Representative image of a 96-well plate after culturing *T. viride* for 60 h in the presence of $0-5 \mu$ M of AmB with 1 μ M of LysM-C14 and LysM-C16 under different storage conditions. (i) The formulation after 1 day of storage (Day 1) and (ii) after 7 days of storage (Day 7).

2-9. CLSM analysis of interaction with T. viride



Figure S9. CLSM analyses of LysM-muGFP-Q or LysM-muGFP-lipid and combination without AMB in the presence of *T. viride* hyphae in 20 mM NaPi, pH 7.4, at 25°C (bars: 10 µm).



2-10. Statistical analysis of the binding ability of LysM variants with T. viride

Figure S10. Statistical analysis of the fluorescence imaging results by CLSM (Fig. 3b). N = 3; mean \pm SE; **p < 0.01, ***p < 0.001, ****p < 0.0001. "n.s." indicates not significant (p > 0.05) (ANOVA followed by Tukey's multiple comparisons test).

2-11. CLSM analysis of LysM binding activity with α-chitin



Figure S11. CLSM analyses of LysM-muGFP-Q or LysM-muGFP-lipid in the presence of 0.5% α -chitin in 20 mM NaPi, pH 7.4, at 25°C (bars: 10 μ m).



2-12. Cytotoxicity test of LysM-lipids with HeLa cells

Figure S12. Cell viability of combination chitinase modified and AmB in HeLa cells (5,000 cell/well). Cell viability was quantified by Cell Counting Kit-8 (Dojindo) (A) without AmB and (B) with AmB.