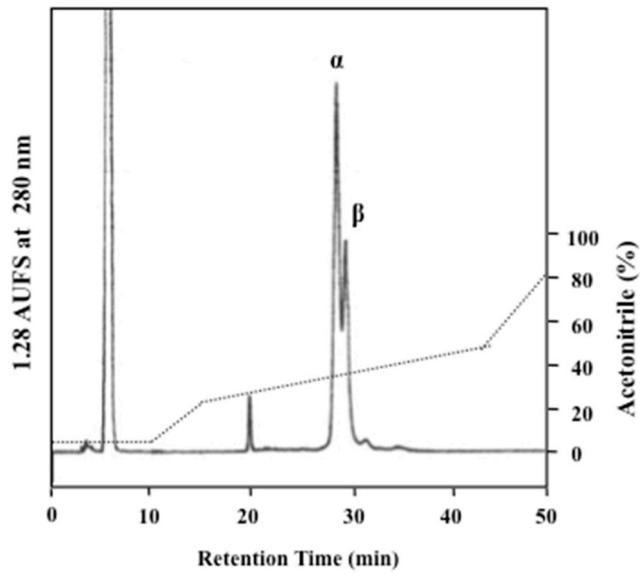


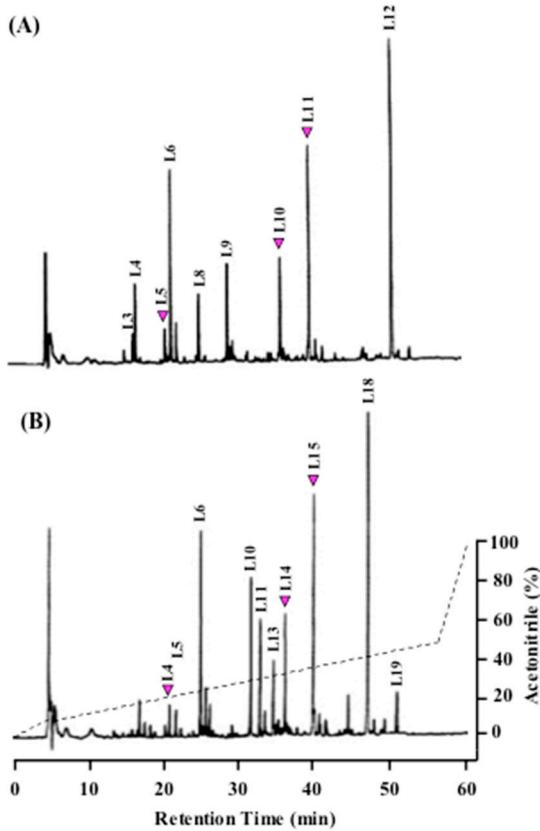
Supplementary Figure S1. Peptide maps of CAM-PPL3A($\alpha+\alpha$), 3B($\alpha+\beta$), and 3C($\beta+\beta$) digested by *Achromobacter* protease I (A) and *Staphylococcus aureus* V8 protease (B). Peptides were separated by reversed-phase HPLC on COSMOSIL® Protein-R column ($\phi 4.6 \times 250$ mm) using a linear gradient of acetonitrile in 0.1% trifluoroacetic acid. Common peaks between α and β subunits were marked by magenta and green-colored arrow heads, respectively.

PPL3 α	ATGATTTCTGGACTATATCTGGTAATTGCAGTGATTCTACCAAATGCAGTGTTATCACAG	60
	<u>M I S G L Y L V I A V I L E P N A V L S Q</u>	
PPL3 β	ATGATTTCTGGACTATATCTGGTGTGGCAGTGATTCTACCAAATGCAGTGTTATCACAG	
	<u>M I S G L Y L V V A V I L E P N A V L S Q</u>	
	Signal sequence	<u>L</u>
PPL3 α	GTTGCCCTCTGAATAATCTTGGAGGACCAGGGAGGCACGCCCTTGTGACGATAAAGCAGTAGCA	120
	<u>V A S E Y L G G P G G D A F D D K A V A</u>	V14
PPL3 β	GTTGCCCTCTGAATAATCTTGGAGGACCAGGGAGGCATGCCCTTGTGATGATAAA <u>CATTAGCA</u>	
	<u>V A S E Y L G G P G G D A F D D K A L A</u>	V16
	<u>I</u>	<u>L5</u> <u>L11</u>
PPL3 α	CAAAATGGTGACATAACAAGAATTGAGATGCAATGTACAGATGTCACCTATATCAA	180
	<u>Q N G D I T R I E M Q C T D V A T Y I K</u>	V19
PPL3 β	CAAAATGGTGACATAACAAGAATCGAGATGCAATGTACAGATGTCACCTATATCAA	180
	<u>Q N G D I T R I E M Q C T D V A T Y I K</u>	V19
PPL3 α	CTTCGTTATGGGAAAGTAGATAGCAGGCCATGGGGATGGGCAATGAGAATTGTATACAG	240
	<u>L R Y G K V D S R Q W G K A N E N C I Q</u>	V7
PPL3 β	CTTCGTTATGGGAAAGTAGATAGCAGGCCATGGGGATGGGCAATGAGAATTGTATACAG	
	<u>L R Y G K V D S R Q W G K A N E N C I Q</u>	V8
	<u>I</u>	<u>V10</u>
PPL3 α	TGGTCAAAAAAGGGAG <u>A</u> AAAGTTGTCACCGAGTTGAGTAGTGGTGAATAACATCACAGC	300
	<u>W S K K G E K V V V H E L S S G E Y I T S</u>	
PPL3 β	TGGTC <u>AAA</u> AGGGAG <u>T</u> AAAGTTGTCACCGAGTTGAGTAGTGGTGAATAACATCACAGC	
	<u>W S K K G V K V V V H E L S S G E Y I T S</u>	
PPL3 α	GCTATTGTACATATGGTAAATATGTACAA <u>TCCATTACTTTCAAGACCAACAAAAGAAC</u>	360
	<u>A I V T Y G K Y V Q S I T F K T N K R T</u>	V21
PPL3 β	GCTATTGTACATATGGTAAATATGTACAA <u>TCCATTACTTTCAAGACCAACAAAAGAAC</u>	
	<u>A I V T Y G K Y V Q S I T F K T N K R T</u>	V21
	<u>I</u>	<u>L4</u>
PPL3 α	CTTCCAAGATCGGGACCAGTGCCACTGAAAAATCCGTACAGTTTAATTCTGGAGGC	420
	<u>L P R C G T S A T E K S V T V L I P G G</u>	
PPL3 β	CTTCCAAGATCGGGACCAGTGCCACTGAAAAATCCGTACAGTTTAATTCTGGAGGC	
	<u>L P R C G T S A T E K S V T V L I P G G</u>	
PPL3 α	CTGAAATACATTTCTGGAGATGGGGTTGAGAATTGATGGATTGCGATTTCATGCTAA	480
	<u>L K Y I S G R M G C R I D G L R F H A K</u>	V20
PPL3 β	CTGAAATACATTTCTGGAGATGGGGTTGAGAATTGATGGATTGCGATTTCATGCTAA	
	<u>L K Y I S G R M G C R I D G L R F H A K</u>	V20
	<u>I</u>	<u>L8</u>
PPL3 α	TGTTGA	486
	<u>C</u> *	
PPL3 β	TGTTGA	
	<u>C</u> *	

Supplementary Figure S2. Nucleotide sequences of cDNAs and the corresponding amino acid sequences of PPL3 subunits. Nucleotide residues and amino acid residues different from PPL3 α and β subunits are indicated by bold characters, respectively. Peptide fragments generated by digestion with *Achromobacter* protease I (L) and *S. aureus* V8 protease (V), respectively, are indicated by lines. Italic letter with underline indicates the signal peptide region. Asterisk indicates the stop codon.



Supplementary Figure S3. Separation of CAM-PPL4 α and β subunits by reversed-phase HPLC. Separation of CAM-PPL4 subunits was conducted by HPLC on a CAPCELL PAK (C8) column (\varnothing 4.6 \times 150 mm) using graded linear gradient of acetonitrile in 0.1 % TFA.



Supplementary Figure S4. Peptide maps of CAM-PPL4 α (A) and β (B) subunits digested by *Achromobacter* protease I. Peptides were separated by reversed-phase HPLC on COSMOSIL® Protein-R column (\varnothing 4.6 \times 250 mm) using a linear gradient of acetonitrile in 0.1% trifluoroacetic acid. Common peaks between α and β subunits were marked by magenta arrow heads.

(A)

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1 ATGGGTGTCTATGTTACATTGTTCTAGTACCATGTCATAATGGCAATACAAGCAGAT 60
M G V Y V Y I V L L V P C L M A I Q A D
Signal sequence

61 GCAAGTTGCCGAGCCCTATCAGAATCATATGGGGTCCAGGTGGTTAACCGTTTGAC 120
A S C G A L S E S Y G G P G G L N R F D
|  
L9

121 GAGAAGGCTTGGTGAAGAACGGTGACATTAAAGAAATAGAATTACTGTGTGGTAGAAGA 180
E K A L V K N G D I K E I E L L C G R R
|  
L10

181 GTAACCGCAATAAGATTAAGATATGGCACAGTGTGGGTACACTTCATGGTGGAAATCC 240
V T A I R L R Y G T V W G T L H G W K S
|  
L11

241 CCACCAAGAAAAAGTTGCCAAGAGATTGGGATGTCGGCAGCAAAGTCATTATACACTG 300
P P G K S C A R D W D V G S K V I Y T L
|  
L6 |  
L8

301 AAACCAAATGAATACGTAAAAGGAGGCACGATCACTTACGATAGATTGTCAATTCTTG 360
K P N E Y V K G A T I T Y D R F V N S L
|  
L4 |  
L10

361 ACATTAACAAATATGAGAGAATTACCAAATGCGGAAAGACCCTGGAAAGACA 420
T L K T N M R E L P K C G K T T G S K T
|  
L5

421 AAATCAGTCGATGGCCGGCGATTAAAGTATATAACCGGAAACTCTGGATGTATTCTTGAC 480
K S V D G R R L K Y I T G N S G C I L D
|  
L3 |  
L12

481 AGAATACAGTTTACTGGCCATTGTGGTAA 510
R I Q F Y W P L W *

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(B)

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1 ATGGTTCTATGTTACATTGTTCTCTATCACCATGTCATTGGCGATGCAAGCAGAT 60
M G F Y V Y I V L L S P C L L A M Q A D
Signal sequence

61 GCAGTTGCACAGCCCTATCAGAATCATATGGGGTCCAGGAGGTTAACCGTTTGAC 120
A V C T A L S E S Y G G P G G L N R F D
|  
L11

121 GAGAACGCACTGGCAAAGAACGGTGATATTAAAGAAATAGAATTACTGTGTGGTAGAAGA 180
E N A L A K N G D I K E I E L L C G R R
|  
L12

181 GTAACCGCATTAGATTACGATATGGCTCAGTTGGGAAACTTCATGGTGGAAATCC 240
V T A I R L R Y G S V W G T L H G W K S
|  
L15

241 CCACCAAGAAAAAGTTGCCAGAGATTGGGATGTCGGTGTCAAAGTCCTTATACACTG 300
P P G K S C A R D W D V G V K V L Y T L
|  
L6 |  
L16

301 CAACCAAATGAATATGTAAGGAGGCACGATCACTTACGACAGATTGTCAATTCTTG 360
Q P N E Y V K G A T I T Y D R F V N S L
|  
L10 |  
L14

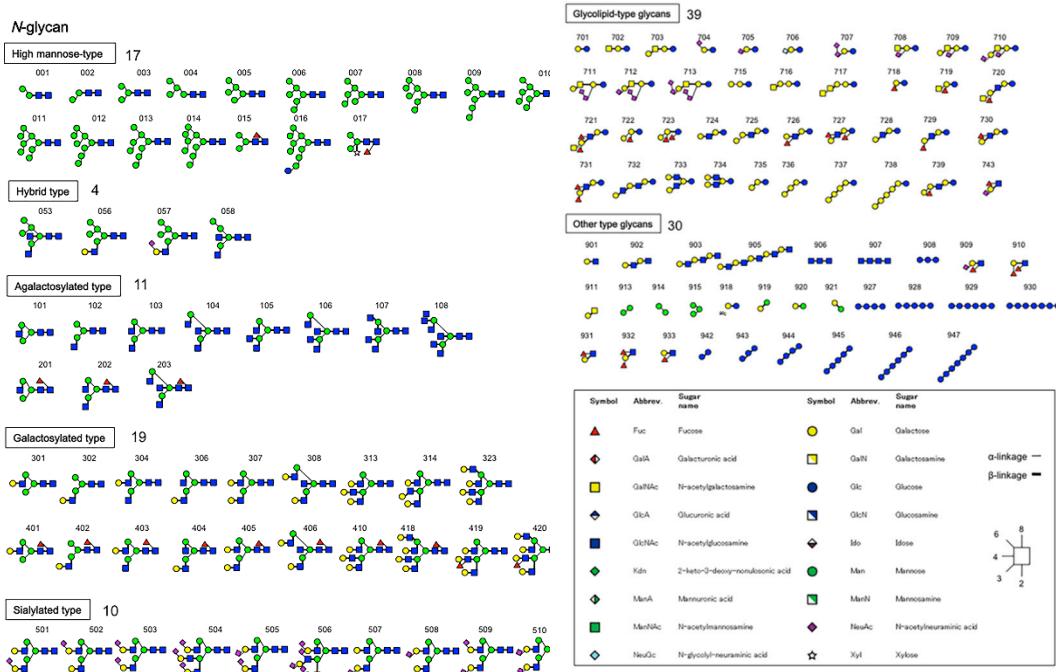
361 ACATTAACAAATATGAGAGAATTGCCAAATGCGGAAAGACCCTGGAAAGACA 420
T L K T N M R E L P K C G K T T G S K T
|  
L4

421 AAATCAATCAATGGCAGGCGTTAAAGTATATTACCGGAAACTCTGGTGTATTCTTGAT 480
K S I N G R R L K Y I T G N S G C I L D
|  
L18

481 AGAATTCAGTTCTACTGGCCATCGTGGTAA 510
R I Q F Y W P S W *

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Supplementary Figure S5. Nucleotide sequences of cDNAs and the corresponding amino acid sequences of PPL4 α (A) and β (B) subunits. Peptide fragments generated by *Achromobacter* protease I (L) digestion are indicated by lines. Italic letter with underline indicates the signal peptide region. Asterisk indicates the stop codon.



Supplementary Figure S6. Schematic representation of oligosaccharide structures. Note that the reducing terminal is pyridylaminated for FAC analysis. Symbols used to represent pyranose rings of monosaccharides are shown in the box at the bottom. Anomeric carbon, i.e. position 1, is placed at the right side, and 2, 3, 4 are placed clockwise. Thin and thick bars represent α -linkage and β -linkage, respectively.

Supplementary Table S1. The amino acid sequences and masses of the peptides generated by cleavage of the CAM-PPL3B with *Achromobacter* protease I (**A**) and *S. aureus* V8 protease (**B**).

(A) *Achromobacter* protease I

Fragment number	Amino acid sequences	Molecular mass (m/z)	
		Calculated	Observed
L4	YVQSITFK	984.55	987.10
L5	EIASEYLGGPGGDAFDDK	[N terminus]	1839.84
L8	YISGRWGCRIDGLRFHAK		2192.18
L9	VDSRQWGWAENCIQWSK		2264.09
L10	AVAQNQGDITRIEMQCTDVATYIK		2597.33
L11	ALAQNQGDITRIEMQCTDVATYIK		2611.34

(B) *S. aureus* V8 protease

Fragment number	Amino acid sequences	Molecular mass (m/z)	
		Calculated	Observed
V7	NCIQWSKKGE	1250.64	1250.01
V8	NCIQWSKKGEKVHVHE	1842.97	1842.29
V9	ITFKTNKRITLPRCGTSATE	2182.18	2181.85
V10	NCIQWSKKGVKVHVHE	1813.00	1812.06
V14	YLGGPGGDAFDDKAVALAQNGDITRIE	2579.24	2579.64
V16	YLGGPGGDAFDDKALAQNGDITRIE	2593.25	2593.96
V17	VATYIKLRYGKVDSRQWGWAENE	2640.37	2640.23
V19	MQCTDVATYIKLRYGKVDSRQWGWAENE	3276.61	3276.47
V20	KSVTVLIPGLKYISGRWGCRIDGLRFHAKC	3546.99	3545.02
V21	LSSGEYITSAVTYGKYVQSITFKTNKRTLPRCGTSATE	4329.26	4325.63

Common peptides between PPL3A ($\alpha+\alpha$) and PPL3B ($\alpha+\beta$), and between PPL3B ($\alpha+\beta$) and PPL3C ($\beta+\beta$) are indicated by magenta and green boxes, respectively.

Supplementary Table S2. The amino acid sequences and masses of the peptides generated by cleavage of the CAM-PPL4 α (A) and β (B) subunits with *Achromobacter* protease I.

(A) PPL4 α

Fragment number	Amino acid sequences	Molecular mass (m/z)	
		Calculated	Observed
L3	SVDGRRILK	929.56	932.82
L4	PNEYVK	748.40	773.46
L5	TNMRELPK	987.54	991.19
L6	SCARDWDVGSK	1280.62	1283.11
L8	VIYTLK	735.48	760.08
L9	SCGALSESYGGPGGLNRFDEK	[N terminus] 2201.05	2203.56
L10	GATTYYDRFVNSLTLK	1797.99	1802.24
L11	EIELLCGRRVTAIRLRYGTVWGLHGWK	3340.88	3344.89
L12	YITGNSGCILDRIQFYWPWL	2502.28	2506.58

(B) PPL4 β

Fragment number	Amino acid sequences	Molecular mass (m/z)	
		Calculated	Observed
L4	TNMRELPK	987.54	990.42
L6	SCARDWDVGVK	1292.66	1295.40
L10	VLYTLPNEYVK	1465.81	1469.29
L11	VCTALSESYGGPGGLNRFDENALAK	[N terminus] 2626.31	2630.86
L14	GATTYYDRFVNSLTLK	1797.99	1802.24
L15	EIELLCGRRVTAIRLRYGTVWGLHGWK	3326.86	3331.88
L18	YITGNSGCILDRIQFYWPWSW	2476.23	2478.06

Common peptides between PPL4 α and β subunits are indicated by magenta boxes.

Supplementary Table S3. Properties of lectin-immobilized columns used for FAC analysis.

Lectin name	Amount of Immobilized lectin (mg/ml gel)	B _t (nmol)	K _d (M)	R ² ^a	Used carbohydrate
PPL2A	0.05	0.02	2.0 x 10 ⁻⁷	0.996	1M2M-5NC-Asn Fmoc
PPL3	0.5	0.63	3.01 x 10 ⁻⁵	0.985	1M2M-5NC-Asn Fmoc
PPL4	1.0	0.98	2.0 x 10 ⁻⁵	0.996	ManapNP

^a the coefficient of determination quantified the degree of linear correlation obtained from a Woolf-Hofstee-type plot in each concentration-dependent analysis. B_t and K_d values were calculated from those determined by concentration-dependent analysis.