

The chitin utilization mechanisms of a new *Chitinibacter* sp. isolate

SCUT-21

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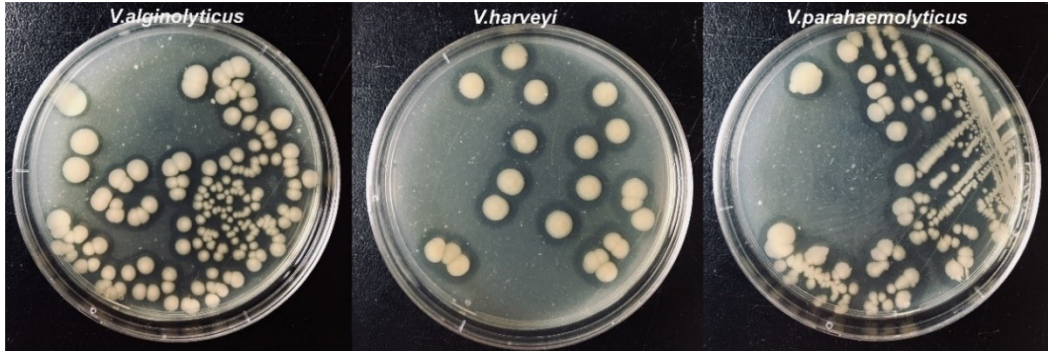
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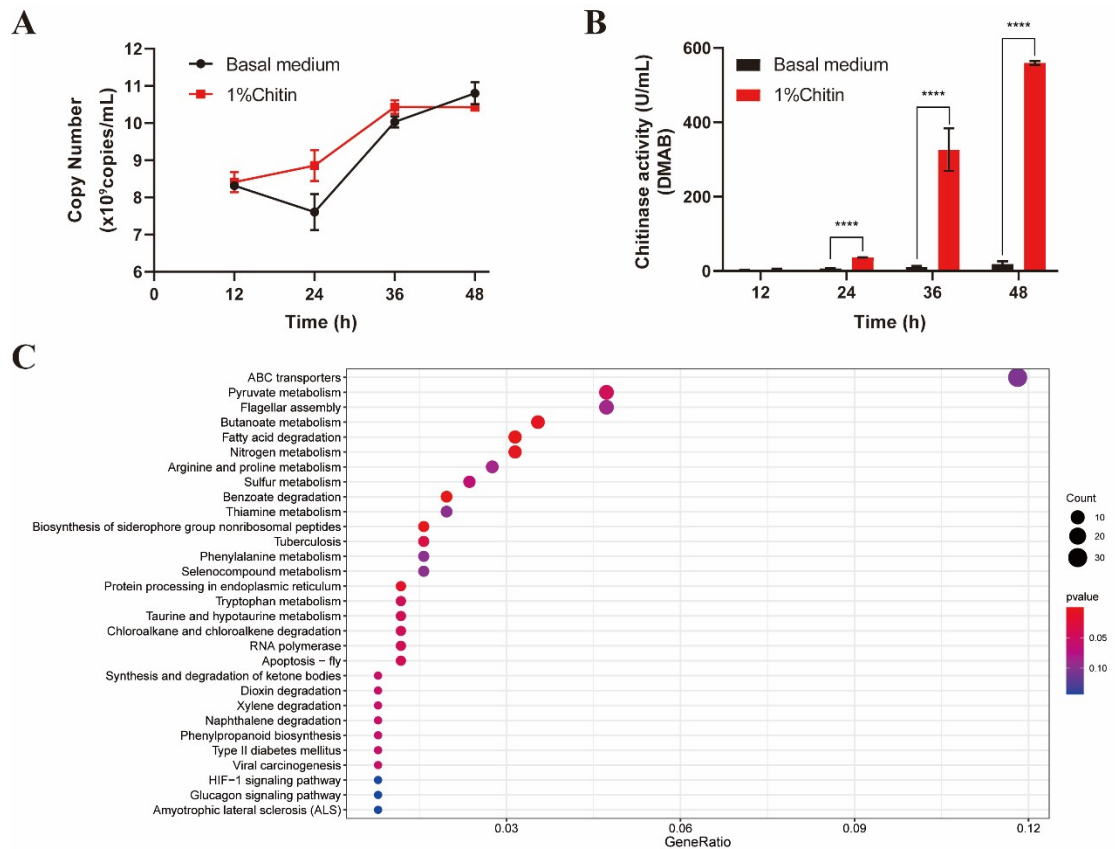
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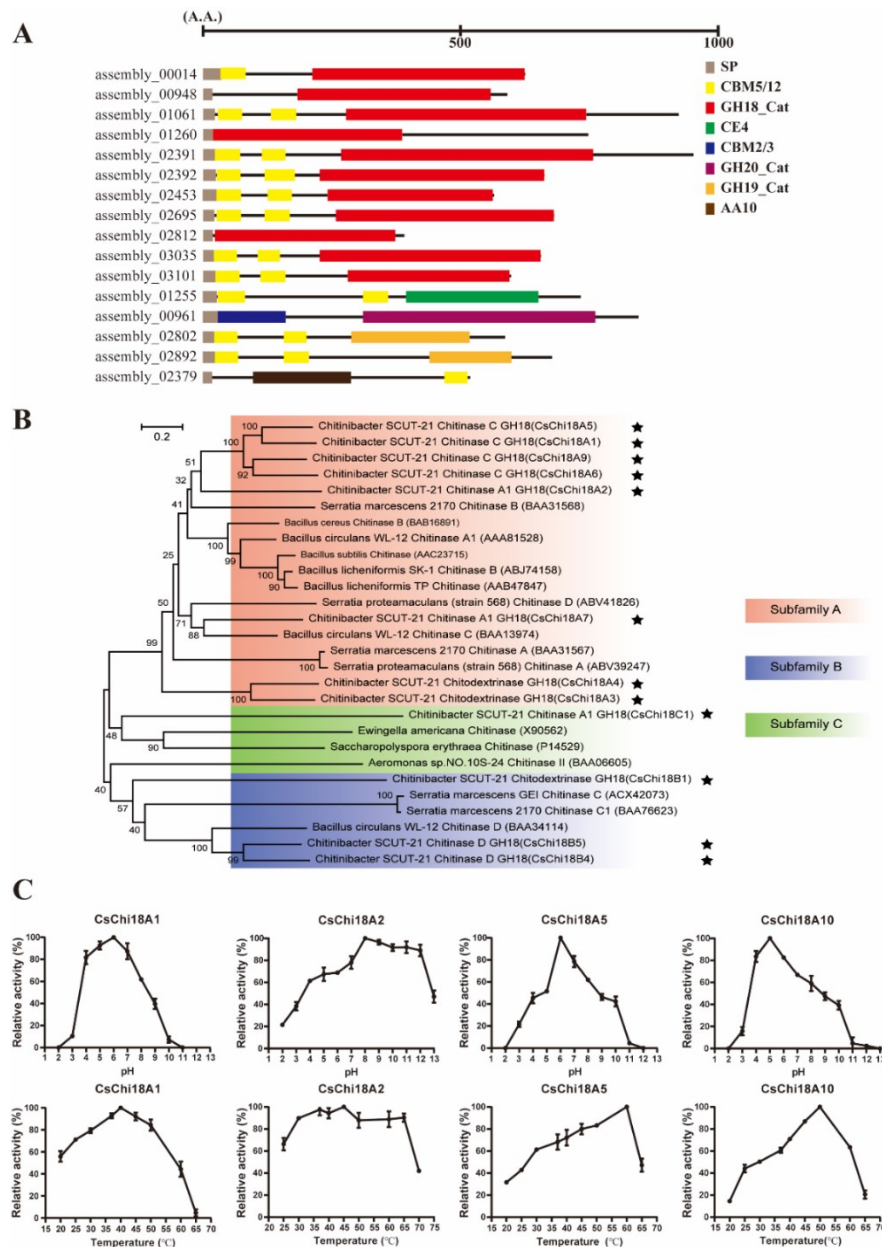
Supplementary Fig. 1. Growth of *Vibrio alginolyticus*, *Vibrio harveyi* and *Vibrio parahaemolyticus* on LB+ colloidal chitin agar plates and the size of hydrolytic circles produced (5 days).



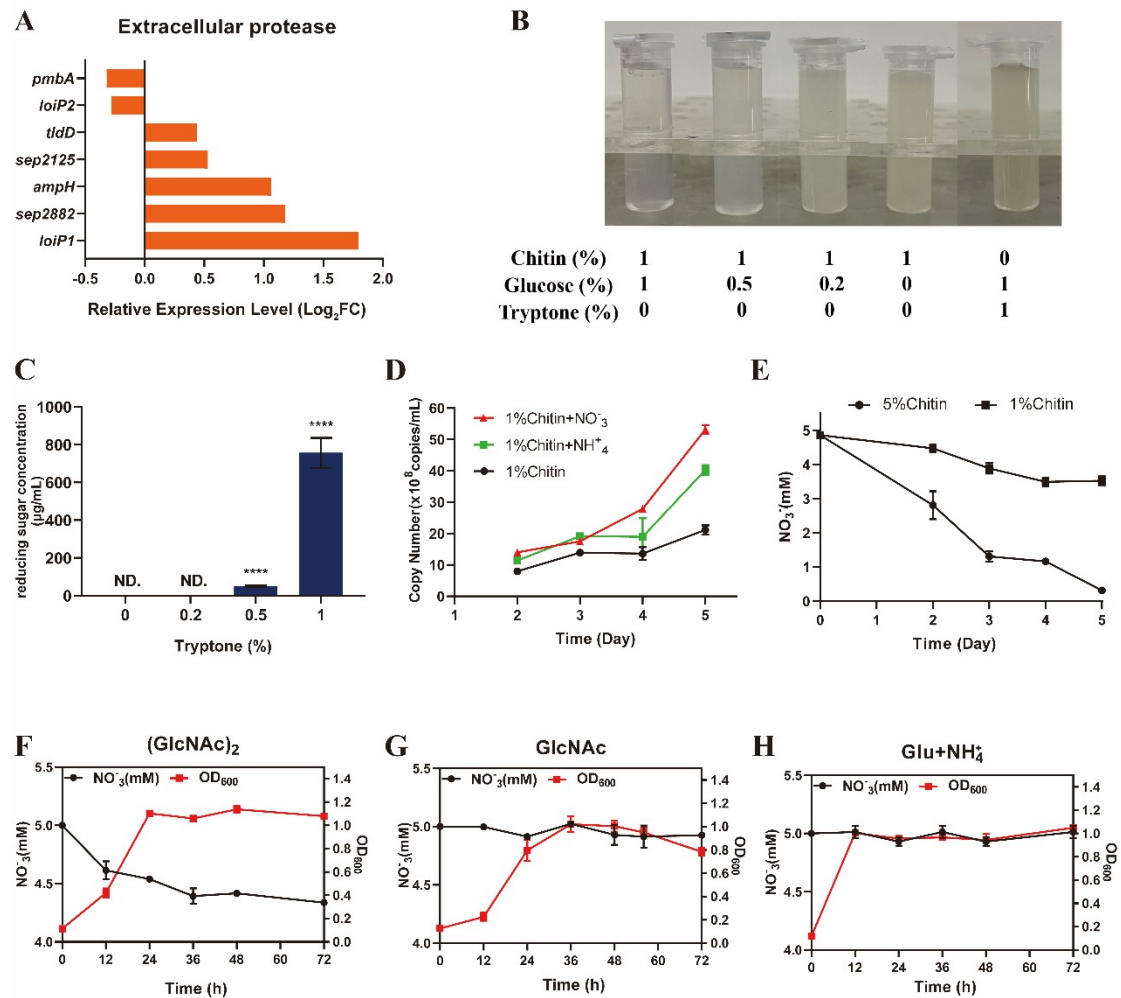
Supplementary Fig. 2. (A) After transferring new mediums, time course of SCUT-21 growth curve in 1% (w/v) chitin powder medium and basal medium; (B) After transferring new mediums time course of chitinase activity produced (tested by DMAB method) by SCUT-21 in 1%(w/v) chitin powder medium and basal medium; (C) Top 20 KEGG enrichment terms among DEGs. Circle size indicates the number of DEGs, while the color indicates p value.



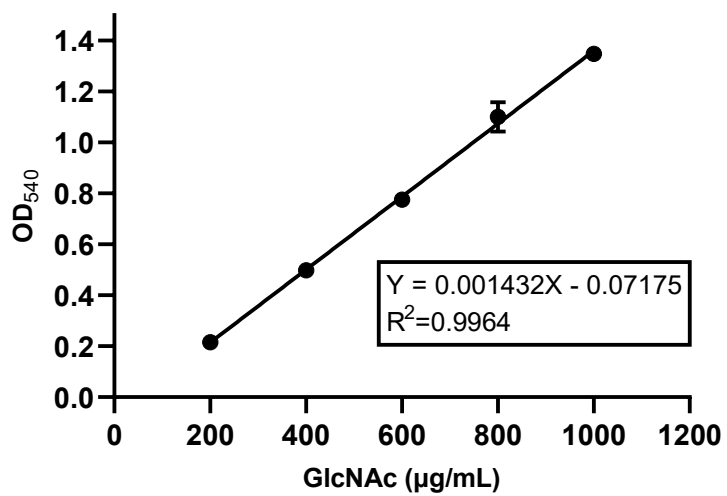
Supplementary Fig. 3. (A) Domain organization of chitinolytic enzymes. Protein domains, as identified with InterProScan data-bases are shown. SP, Singal Peptide; GH18_Cat, Glycoside Hydrolase family 18 Catalytic Domain; GH19_Cat, Glycoside Hydrolase family 19 Catalytic Domain; GH20_Cat, Glycoside Hydrolase family 20 Catalytic Domain; CBM, Carbohydrate-binding module; CE4, carbohydrate esterase 4 (CE4) superfamily; AA10, Auxiliary Activity family 10 (B) Phylogenetic analysis of GH18 chitinases in SCUT-21. The black dot-marked chitinases are from SCUT-21. (C) Enzymatic parameters of the four recombinant chitinases the optimal pH and the optimal temperature.



Supplementary Fig. 4. (A) Regulation of SCUT-21 extracellular protease genes identified by transcriptome analysis. (B) The turbidity of SCUT-21 in 1% chitin medium containing different Concentration of tryptone and glucose (3 days). (C) Effect of different tryptone concentrations on the residual amount of reducing sugar in the culture medium determined by the DMAB method (5 days). (D) Time course of the SCUT-21 growth curve in 1% chitin medium containing different nitrogen sources. (E) Time course of residual nitrate of SCUT-21 in 1% and 5% chitin medium. Time course of residual nitrate (black) and growth curve (red) of SCUT-21 in the (GlcNAc)₂ medium (F), GlcNAc medium (G), and glucose + NH₄⁺ medium (H).



Supplementary Fig. 5. The DNS standard curve of *N*-acetylglucosamine.



Supplementary Table 1. Bacterial strains and plasmids central to this study

Strains	Relevant Genotype	Source
<i>Chitinibacter</i> sp. SCUT-21	wild type	This work
<i>Vibrio harveyi</i>	wild type	This work
<i>Vibrio parahaemolyticus</i>	wild type	This work
<i>Vibrio alginolyticus</i>	wild type	This work
<i>Escherichia coli</i> K-12	wild type	preserved in our laboratory
<i>Escherichia coli</i> Trelief® 5α	F ⁻ φ 80(lacZ) Δ M15 Δ(lacZYA-argF)U169 deoR recA1 endA1 hsdR17 (r K ⁻ , m K ⁺) phoA supE44 λ ⁻ thi-1 gyrA96 relA1	Tsingke Biotechnology Co., Ltd.
<i>Escherichia coli</i> BL21(DE3)	F ⁻ ompT hsdS _B (r _B ⁻ m _B ⁻)gal dcm(DE3)	Tsingke Biotechnology Co., Ltd.
<i>Pichia pastoris</i> GS115	wild type	preserved in our laboratory
Plasmids	Relevant Genotype	Source
pET28(+)		preserved in our laboratory
pET28(+)-CsChi18A1	as pET28(+), assembly_00014	This work
pET28(+)-CsChi18A5	as pET28(+), assembly_02392	This work
pET28(+)-CsChi18A9	as pET28(+), assembly_03035	This work
pET28(+)-CsNAGA	as pET28(+), assembly_00961	This work
pPIC9BM		preserved in our laboratory
pPIC9BM- CsChi18A2	as pPIC9BM, assembly_00948	This work

Supplementary Table 2. Primers used in PCR and RT-qPCR for gene expression

Primers	Primer sequence (5'–3')
27F	AGAGTTTGATCCTGGCTCAG
1492R	TACGACTTAACCCCAATCGC
CsChi18A1F	CGCGGATCCTCTCCTGTTTGGCAGGAA
CsChi18A1R	CCCTCGAGTTGACGTA CTTGACCCA
CsChi18A5F	CGCGGATCCGCTGAGGCGTGGAAGAA
CsChi18A5R	CCCTCGAGTTGACGCGCTTACCCAT
CsChi18A9F	CGCGGATCCGCAACCGCCTGGAACA
CsChi18A9R	CCCTCGAGCTTATTAATATAAGTCATTG
CsNAGA F	CGCGGATCCATGACTAAACCTGCTG
CsNAGA R	CCGCTCGAGTACCGCAACAACGCGG
CsChi18A2F	CGCGGATCCACGGTTGTTTTGAAGAC
CsChi18A2R	CCGACGCGICTTCTTAATCATGCCTTTATA
16sRNA-qpcR-F	GACCAGGTAAGGTTTTTCGC
16sRNA-qpcR-R	AGTTGTTGGGCTTTTCGGAG
CsChi18A2-qpcr-F	AAAGTGGGAACACTACGAAA
CsChi18A2-qpcr-R	CCTGCAACACCAGTAAGAAC
CsChi18A1-qpcr-F	TTGGCAGGAAGGCATTAG
CsChi18A1-qpcr-R	AGTCGGTTTAGCCGTAGG
CsChi18A5-qpcr-F	AGTCGGTTTAGCCGTAGG
CsChi18A5-qpcr-R	AGTCGGTTTAGCCGTAGG
CsChi18A9-qpcr-F	TCTACGGTCGTGCTTTCT
CsChi18A9-qpcr-R	ATCTTGGCTGCCTGTTTC
chiA-qpcr-F	AGTGGGAACACTACGA
chiA-qpcr-R	CTGCAACACCAGTAAGA
narK-qpcr-F	ATCAAAGAGGGCAGCGAA
narK-qpcr-R	ATCAAAGGGCCGAGGAAG

nirB-qpcr-F	GCATCTGTCGTCCTACTTCTC
nirB -qpcr-R	ATGGCGTTTAAATCATCAATC
nirD -qpcr-F	CCACGCAACGACGAAACG
nirD -qpcr-R	GGACTGGCCACCCACAGCT

Supplementary Table 3. Degradation ability of CDBs by hydrolysis halo method (5 days)

Culture medium	Colloidal Chitin	LB+Colloidal Chitin
Strains		
<i>Chitinibacter</i> sp. SCUT-21	4.66 (2.33/0.50)	4.11(1.85/0.45)
<i>Deefgea chitinilytica</i>	4.50 (2.25/0.5)	2.91 (1.89/0.65)
<i>Chitinilyticum litopenaei</i>	4.17 (2.59/0.62)	2.40 (2.45/1.02)
<i>Chitinibacter tainanensis</i>	3.73 (2.05/0.55)	2.88 (2.45/0.85)
<i>Aeromonas hydrophila</i>	3.38 (1.62/0.48)	1.76 (2.78/1.58)
<i>Bacillus cereus</i>	1.22 (1.10/0.90)	1.00 (5.63/5.61)
<i>Roseateles depolymerans</i>	1.14 (2.51/2.2)	0 (0/0.72)
<i>Pelomonas saccharophila</i>	1.02 (0.69/0.68)	1.01 (2.82/2.79)
<i>Chitinimonas taiwanensis</i>	0 (0/0.39)	0 (0/0.24)
<i>Flavobacterium johnsoniae</i>	0 (0/0.32)	0 (0/0.55)
<i>Bacillus tropicus</i>	0 (0/0.48)	0 (0/0.29)
<i>Vibrio alginolyticus</i>	0	1.04 (8.25/7.91)
<i>Vibrio harveyi</i>	0	1.35 (2.50/1.85)
<i>Vibrio parahaemolyticus</i>	0	1.18 (2.35/1.98)

Supplementary Table 4. The physiological and biochemical characteristics of *Chitinibacter* sp.

SCUT-21, *Chitinibacter* sp. GC72 and *Chitinibacter suncheonensis* strain SK16.

Characteristic	<i>Chitinibacter</i> sp. SCUT-21	<i>Chitinibacter</i> sp. GC72	<i>Chitinibacter</i> <i>suncheonensis</i> strain SK16
Gram stain	G ⁻	G ⁻	G ⁻
Growth between temperatures	25°C-40°C	20-37°C	15–37°C
Growth between pH	6.0-9.0	7.0-10.0	7.0-10.0
1%NaCl	+	+	+
Chitin hydrolysis	+	+	+
Cellulose hydrolysis	-	NT	NT
Starch hydrolysis	-	NT	NT
Dextrin hydrolysis	-	+	-
Glucose	+	+	+
D-Maltose	+	-	+
GlcNAc	+	+	+
Arabinose	-	-	-
lactose	-	-	-
Cellobiose	-	-	-
Rhamnose	-	-	-
mannitol	-	-	-
Nitrate reduction	+	NT	+

NOTE: “+” Positive, “-” negative, “NT” not tested.

Supplementary Table 5. Average genomic nucleotide identity analysis of SCUT-21 relative to other strains.

Stains	Genome size (Mbp)	ANI (%)	GenBank accession number	GC count (%)
<i>Chitinibacter</i> sp. GC72	3.46	78.71	GCF_009760905.1	54.00
<i>Chitinibacter fontanus</i> strain STM-7	3.63	78.65	GCF_013423785.1	50.30
<i>Chitinibacter bivalviorum</i> strain 2T18	3.68	77.51	GCF_013403565.1	50.61
<i>Chitinibacter tainanensis</i> DSM 15459	3.43	75.63	GCF_000429785.1	56.10
<i>Chitinibacter</i> sp. ZOR0017	3.48	75.47	GCF_000799095.1	55.90
<i>Deefgea chitinilytica</i>	3.40	74.08	GCF_016881405.1	48.29
<i>Deefgea rivuli</i>	3.71	73.85	GCF_000620145.1	49.03
<i>Chitinilyticum litopenaei</i> DSM 21440	3.97	71.12	GCF_000428145.1	62.64
<i>Chitinilyticum aquatile</i> DSM 21506	3.69	70.82	GCF_000430805.1	60.30
<i>Amantichitinum ursilacus</i>	4.93	70.27	GCF_001294205.1	60.09
<i>Chitinolyticbacter</i> <i>meiyuanensis</i> strain SYBC-H1	4.33	70.20	GCF_008033135.1	63.53

Supplementary Table 6. Significantly differentially expressed chitin-related metabolizes genes in chitin powder medium, compared with Basal medium, cultured SCUT-21.

Gene ID	Description	log₂FC
Chitinolytic enzymes		
assembly_02392	CsChi18A5	5.63
assembly_01255	CsChi18B1	5.00
assembly_03101	CsChi18B5	3.70
assembly_02391	CsChi18A4	3.60
assembly_01254	polysaccharide deacetylase family protein (Cda)	2.52
assembly_02379	CsLPMO	2.43
assembly_02892	CsChi19B	2.26
assembly_00948	CsChi18A2	2.12
assembly_03035	CsChi18A9	2.06
assembly_02802	CsChi19A	1.93
assembly_02695	CsChi18A6	1.60
assembly_02453	CsChi18B4	0.82
assembly_01061	CsChi18A3	0.76
assembly_00014	CsChi18A1	0.42
assembly_02767	CsChi18A7	0.28
assembly_01260	CsChi18C1	0.01
assembly_00961	CsNAGA	0.01
assembly_02812	CsChi18A8	-0.71
assembly_01919	CsChi18B2	-1.38
assembly_02073	CsChi18B3	-2.56
GlcNAc and COS transport System		
GlcNAc transporter		
assembly_00439	PTS system N-acetylglucosamine-specific EIICBA component (nagEIII1)	2.63

assembly_00438	PTS system N-acetylglucosamine-specific EIICBA component (nagEII2)	1.33
assembly_00854	HPr kinase/phosphorylase	0.31
assembly_01945	Phosphoenolpyruvate-protein phosphotransferase (EI)	0.23
(GlcNAc)₂ transporter		
assembly_01006	Putative chitobiose transport system permease protein (chiF)	4.24
assembly_01005	putative chitobiose transport system substrate-binding protein (chiE)	3.19
assembly_01004	Maltose/maltodextrin import ATP-binding protein (malK1)	2.47
assembly_01007	putative chitobiose transport system permease protein (chiG)	1.90
(GlcN)₂ transporter (potential)		
assembly_01268	Putative chitobiose transport system permease protein (chi1)	1.37
assembly_01269	Putative chitobiose transport system permease protein (chi2)	0.38
assembly_01270	Maltose/maltodextrin import ATP-binding protein (malK2)	0.44
(GlcNAc)_n transporter		
assembly_01109	Chitoporin (chiP1)	2.70
assembly_02358	Chitoporin (chiP2)	1.96
GlcNAc intracellular catabolism		
assembly_00556	Glucosamine-6-phosphate deaminase (nagB)	2.15
assembly_02510	N-acetylglucosamine kinase (nagK)	0.57
assembly_02800	Beta-hexosaminidase (nagZ)	0.40
assembly_01009	Glucosamine kinase (gspK)	-0.04

Supplementary Table 7. Significantly differentially expressed carbon-related metabolizes genes in chitin powder medium, compared with Basal medium, cultured SCUT-21.

Gene ID	Description	log₂FC
TCA		
assembly_01841	Isocitrate dehydrogenase kinase/phosphatase (aceK)	1.22
assembly_00652	Dihydrolipoyllysine-residue succinyltransferase component of 2-oxoglutarate dehydrogenase complex (sucB)	1.01
assembly_00649	Succinate--CoA ligase [ADP-forming] subunit alpha (sucD)	0.99
assembly_00653	2-oxoglutarate dehydrogenase E1 component (sucA)	0.95
assembly_00651	Dihydrolipoyl dehydrogenase (lpdA)	0.88
assembly_00650	Succinate--CoA ligase [ADP-forming] subunit beta (sucC)	0.82
assembly_00654	Citrate synthase (prpC)	0.17
assembly_02775	Isocitrate dehydrogenase [NADP] (idh)	-0.06
assembly_00259	Aconitate hydratase B (acnB)	-0.31
Glyoxylate cycle		
assembly_02674	Malate synthase (mls)	3.55
assembly_02675	Isocitrate lyase (icl)	3.31
assembly_01059	Phosphate acetyltransferase (pta1)	2.83
assembly_01836	Phosphate acetyltransferase (pta2)	1.23
assembly_01159	Acetyl-coenzyme A synthetase (acs)	1.10
Bifidum pathway		
assembly_01689	Xylulose-5-phosphate phosphoketolase (xfp)	4.91
assembly_02958	Pyruvate kinase II (pykA1)	3.78
assembly_02513	Transketolase (tkt)	3.56
assembly_02400	Transaldolase (tal)	2.84
assembly_01111	Glyceraldehyde-3-phosphate dehydrogenase A (gapA)	2.56
assembly_01459	Ribose-5-phosphate isomerase A (rpiA)	2.34
assembly_01891	Acetate kinase (ackA)	2.21

assembly_00682	Pyruvate kinase II (pykA2)	2.20
assembly_00167	Enolase (eno)	1.74
assembly_02596	Triosephosphate isomerase (tpi)	1.40
assembly_00073	Ribulose-phosphate 3-epimerase (rpe)	0.88
assembly_02662	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (gpmI)	0.84
assembly_01671	Glyceraldehyde-3-phosphate dehydrogenase 3 (gap)	0.57
assembly_01119	Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex (pdhF)	0.57
assembly_00714	Triosephosphate isomerase (tpi)	0.49
assembly_01118	Pyruvate dehydrogenase E1 component (pdhE)	0.26
Butanoate metabolism		
assembly_00662	Phasin family protein (pha1)	4.39
assembly_00301	Phasin family protein (pha2)	4.31
assembly_00457	Acetyl-CoA acetyltransferase (phaA)	3.31
assembly_00458	Poly(3-hydroxyalkanoate) polymerase subunit (phaC1)	3.26
assembly_02733	(R)-specific enoyl-CoA hydratase (phaJ)	2.88
assembly_00163	Acetoacetyl-CoA reductase (phaB)	2.55
assembly_02512	Poly(3-hydroxyalkanoate) polymerase subunit (phaC2)	1.96
assembly_01635	D-beta-hydroxybutyrate dehydrogenase (bhd1)	1.82
assembly_00110	putative 3-hydroxyacyl-CoA dehydrogenase (hadh)	1.76
assembly_00228	Formate acetyltransferase 1 (pflB)	0.61
assembly_00227	Formate acetyltransferase (pfl)	0.17

Supplementary Table 8. Significantly differentially expressed nitrogen-related metabolizes genes in chitin powder medium, compared with Basal medium, cultured SCUT-21.

Gene ID	Description	log ₂ FC
Nitrate metabolism		
assembly_00645	Nitrate/nitrite transporter (narK)	5.79
assembly_00644	Nitrite reductase [NAD(P)H] (nirB)	3.07
assembly_00643	Nitrite reductase (NADH) small subunit (nirD)	1.70
assembly_00908	Formate-dependent nitrite reductase complex subunit (nrfG)	1.17
assembly_00906	Nitrate/nitrite response regulator protein (narL)	0.99
assembly_00903	Ferredoxin-type protein (napF)	0.56
assembly_00905	Nitrate/nitrite sensor protein (narX)	0.38
assembly_00901	Periplasmic nitrate reductase (napA)	0.34
assembly_00900	Periplasmic nitrate reductase , electron transfer subunit (napB)	0.27
Ccm system		
assembly_00909	Cytochrome c-type biogenesis protein (ccmH)	1.24
assembly_00916	Cytochrome c biogenesis ATP-binding export protein (ccmA)	0.85
assembly_00910	Thiol:disulfide interchange protein (ccmG)	0.82
assembly_00911	Cytochrome c-type biogenesis protein (ccmF)	0.72
assembly_00912	Cytochrome c-type biogenesis protein (ccmE)	0.50
assembly_00914	Heme exporter protein C (ccmC)	0.44
assembly_00915	Heme exporter protein B (ccmB)	0.33
Ammonium metabolism		
assembly_01469	Ferredoxin-dependent glutamate synthase 1 (glu)	3.67
assembly_01468	Glutamate synthase [NADPH] small chain (gltD)	1.86

assembly_01464	Glutamate synthase [NADPH] small chain (gltD)	1.68
assembly_01465	Glutamate synthase [NADPH] large chain (gltB)	0.80
assembly_01000	Ammonia channel (Amt)	0.47
assembly_00782	Glutamine synthetase (glnA)	0.41
Pyrimidine and purine metabolism		
assembly_00015	Dihydroorotate dehydrogenase A (fumarate) (pyrD)	5.22
assembly_02440	Anaerobic ribonucleoside-triphosphate reductase (nrdD)	4.27
assembly_02439	Anaerobic ribonucleoside-triphosphate reductase- activating protein (nrdG)	1.57
assembly_01013	Methanol dehydrogenase activator (act)	1.44
assembly_01434	DNA-directed RNA polymerase subunit beta' (rpoB1)	1.39
assembly_00215	5'-nucleotidase (surE)	1.39
assembly_03137	Deoxyguanosinetriphosphate triphosphohydrolase (dgt)	1.33
assembly_01404	DNA-directed RNA polymerase subunit alpha (rpoA)	1.15
assembly_01435	DNA-directed RNA polymerase subunit beta (rpoB2)	1.10
assembly_03136	Ribonucleoside-diphosphate reductase subunit beta (nrdB)	1.05
assembly_01457	Exopolyphosphatase (ppx)	1.04
assembly_01017	Phosphoglucomutase (algC)	0.83
assembly_01475	Phosphoribosylamine--glycine ligase (purD)	0.77
assembly_02681	Formate-dependent phosphoribosylglycinamide formyltransferase (purT)	0.69
assembly_02684	Putative bifunctional exonuclease/endonuclease protein	0.56
assembly_02703	Adenylate kinase (adk)	0.53
assembly_01158	DNA polymerase III PolC-type (polC)	0.50

Amino Acids biosynthesis		
assembly_00034	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (metE)	4.09
assembly_01356	2-isopropylmalate synthase (leuA)	2.81
assembly_00555	3-isopropylmalate dehydrogenase (leuB)	2.76
assembly_00275	Cyclohexadienyl dehydrogenase (tyrC)	1.79
assembly_00210	LL-diaminopimelate aminotransferase (argD)	1.44
assembly_00033	HTH-type transcriptional regulator (metR)	1.39
assembly_01351	Ketol-acid reductoisomerase (NADP (+)) (ilvC)	1.13
assembly_01350	Acetolactate synthase isozyme 3 small subunit (ilvH)	1.04
assembly_00482	Diaminopimelate epimerase (dapF)	0.95
assembly_01349	Acetolactate synthase isozyme 3 large subunit (ilvI)	0.84
assembly_01869	Phospho-2-dehydro-3-deoxyheptonate aldolase, Phe-sensitive (aroG)	0.76
assembly_00593	Indole-3-glycerol phosphate synthase (trpC)	0.75
assembly_00589	Anthranilate synthase component 1 (trpE)	0.63
assembly_03209	P-protein	0.62
assembly_00211	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (dapD)	0.62
assembly_01648	4-hydroxy-tetrahydrodipicolinate reductase (dapB)	0.54
assembly_02887	Homoserine dehydrogenase (metM)	0.54
assembly_02804	3-phosphoshikimate 1-carboxyvinyltransferase (aroA)	0.52
assembly_00557	3-isopropylmalate dehydratase small subunit 1 (leuD)	0.49
Ribosomal protein		
assembly_01405	30S ribosomal protein S4	1.73
assembly_01437	50S ribosomal protein L10	1.59
assembly_01434	DNA-directed RNA polymerase subunit beta'	1.39
assembly_01404	DNA-directed RNA polymerase subunit alpha	1.15

assembly_01435	DNA-directed RNA polymerase subunit beta	1.10
assembly_01422	30S ribosomal protein S3	1.06
assembly_01406	30S ribosomal protein S11	0.97
assembly_01421	50S ribosomal protein L16	0.92
assembly_01411	30S ribosomal protein S5	0.75
assembly_01436	50S ribosomal protein L7/L12	0.73
assembly_01420	50S ribosomal protein L29	0.61
assembly_01409	50S ribosomal protein L15	0.58
Proteases		
assembly_01739	Metalloprotease (loiP1)	1.80
assembly_02882	putative zinc protease (sep2882)	1.18
assembly_00459	D-alanyl-D-alanine endopeptidase (ampH)	1.06
assembly_02125	Extracellular basic protease (sep2125)	0.53
assembly_00723	Metalloprotease (tldD)	0.44
assembly_01928	Metalloprotease (loiP2)	-0.28
assembly_00012	Metalloprotease (pmbA)	-0.32

Table S9. Significantly differentially expressed other genes in chitin powder medium, compared with Basal medium, cultured SCUT-21.

Gene ID	Description	log₂FC
Regulator factoer		
assembly_00427	Putative anti-sigma factor antagonist	5.46
assembly_01709	Response regulator (pleD)	4.11
assembly_00212	RNA polymerase sigma factor (rpoS)	2.27
assembly_01348	RNA polymerase sigma factor (sigV)	1.30
assembly_00770	ATP-dependent Clp protease ATP-binding subunit (clpX)	0.91
assembly_00771	ATP-dependent Clp protease proteolytic subunit (clpP)	0.72
assembly_01154	HTH-type transcriptional regulator (yofA)	1.70
assembly_02657	HTH-type transcriptional regulator (gntR)	1.54
assembly_00033	HTH-type transcriptional regulator (metR)	1.39
assembly_01618	Response regulator (mprA)	1.35
assembly_02493	DNA-binding transcriptional regulator (ntrC)	1.32
assembly_01819	HTH-type transcriptional regulator (pgrR)	1.13
assembly_01984	Response regulator protein (vraR)	1.01
assembly_00906	Nitrate/nitrite response regulator protein (narL)	0.99
assembly_02002	HTH-type transcriptional regulator (dmlR)	0.88
assembly_02351	putative HTH-type transcriptional regulator (yfiR)	0.81
assembly_00620	HTH-type transcriptional regulator (argP)	0.74
assembly_00783	Response regulator (pleD)	0.73
assembly_01286	Response regulator (pleD)	0.71
assembly_01874	HTH-type transcriptional regulator (dmlR)	0.64
assembly_02088	HTH-type transcriptional regulator (cysL)	0.62
assembly_00107	putative HTH-type transcriptional regulator (ytpP)	0.50

assembly_02949	Chemotaxis response regulator protein-glutamate methylesterase	0.50
assembly_02245	RNA polymerase sigma factor (rpoH)	-1.24
assembly_03157	Sigma factor AlgU regulatory protein (mucB)	-1.80
assembly_03156	Anti-sigma-E factor (rseA)	-2.14
Secretion system		
Type I secretion system		
assembly_00354	Hemolysin secretion protein D (hlyD)	2.66
assembly_00351	Alpha-hemolysin translocation ATP-binding protein (hlyB)	1.06
Type II secretion system		
assembly_02331	Type II secretion system protein I (gspI)	4.52
assembly_03027	Type II secretion system protein D (gspD)	1.78
assembly_01525	Putative type II secretion system protein F (gspF1)	1.20
assembly_03026	Type II secretion system protein G (gspG)	1.19
assembly_03033	Putative type II secretion system protein F (gspF2)	0.94
assembly_03025	Type II secretion system protein G (gspG)	0.84
assembly_03032	putative type II secretion system protein (hxcR)	0.84
assembly_02332	Type II secretion system protein J (gspJ)	0.75
assembly_02327	Putative type II secretion system protein F (gspF)	0.54
Tat secretion system		
assembly_01562	Sec-independent protein translocase protein (tatA)	2.66
assembly_01563	Sec-independent protein translocase protein (tatB)	1.25
assembly_01560	Sec-independent protein translocase protein (tatC)	0.45