The importance of chitobiase and N-acetylglucosamine (GlcNAc) uptake in \(N,N'-\text{diacetylchitobiase} [(\text{GlcNAc})_2]\) utilization by *Serratia marcescens* 2170

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INTRODUCTION

Chitin is the second most abundant biopolymer in nature and is composed of \(\beta\)-1,4-linked N-acetylglucosamine (GlcNAc) residues (Shahidi et al., 1999). *Serratia marcescens* 2170 is one of the most effective bacteria for the degradation of chitin. This bacterium is known as an insect pathogen, and chitinase plays an important role in its virulence, together with protease and lecithinase (Grimont & Grimont, 1978). When *S. marcescens* is cultivated in the presence of chitin, four chitinases (A, B, C1 and C2) and a 21 kDa chitin-binding-protein (CBP21) can be detected in the culture supernatant (Suzuki et al., 1998). \(N,N'-\text{Diacetylchitobiase} [(\text{GlcNAc})_2]\) is the minimal substrate for chitinase and CBP21 induction (Watanabe et al., 1997), and is the major product of chitin hydrolysis by chitinases of this bacterium (Suzuki et al., 2002). Therefore, \(\text{(GlcNAc)}_2\) is considered to be the key molecule in the recognition and utilization of chitin. It has been shown that the uptake of \(\text{(GlcNAc)}_2\) is mediated by the phosphoenolpyruvate-dependent sugar phosphotransferase system (PTS), and a \((\text{GlcNAc})_2\)-specific enzyme II permease is involved in the PTS system in *S. marcescens* 2170 (Uchiyama et al., 2003). The PTS sugars are phosphorylated during translocation across the inner membrane. The generated \((\text{GlcNAc})_2\)-6P in the cytoplasm is presumably hydrolysed by phosphochitobiase to \(\text{GlcNAc}\)-6P and GlcNAc. Disruption of the \((\text{GlcNAc})_2\)-specific enzyme II permease encoded by the *chb* operon drastically reduces the production of chitinases and CBP21, and impairs growth on colloidal chitin (Uchiyama et al., 2003).

*S. marcescens* has a gene encoding a chitobiase of 98.5 kDa and 885 amino acids, including the signal sequence (Tews et al., 1996). Chitobiase hydrolyses the \(\beta\)-1,4-glycosidic bond in \((\text{GlcNAc})_2\) and chito-oligosaccharides. Many chitinolytic bacteria possess \(\beta\)-N-acetylglucosaminidas, like the chitobiase of *S. marcescens* (Bassler et al., 1991; Tsujibo et al., 2000; Matsuo et al., 1999; Yang et al., 2006).

Abbreviations: GlcNAc, N-acetylglucosamine; \((\text{GlcNAc})_2\), \(N,N'-\text{diacetylchitobiase}\); \(4\text{-MU-GlcNAc}\), \(4\text{-methylumbelliferyl N-acetyl-\(\beta\)-D-glucosaminide}\); PTS, phosphoenolpyruvate-dependent sugar phosphotransferase system; WS-chitin, water-soluble chitin.
It has been reported that β-N-acetylglucosaminidases located in the periplasm of Vibrio furnissii hydrolyse chito-oligosaccharides to GlcNAc (Bassler et al., 1991). In addition, GlcNAc produced from chito-oligosaccharides is thought to be taken up by GlcNAc permease (Bassler et al., 1991). However, the importance of chitobiase and GlcNAc uptake for the utilization of (GlcNAc)₂ and chito-oligosaccharides in S. marcescens is poorly understood. In this study, to clarify the utilization mechanism of degradation products from chitin by S. marcescens, the contribution of chitobiase and GlcNAc uptake to the utilization of (GlcNAc)₂ was examined.

The gene encoding chitobiase was previously designated chb (Tews et al., 1996). However, this name may cause confusion with the chb operon encoding the genes required for PTS-mediated transport and metabolism of (GlcNAc)₂. Therefore, the gene name chb for chitobiase is not used in this paper; instead, the chitobiase gene is tentatively named ctb.

**METHODS**

**Bacterial strains, plasmids and culture conditions.** S. marcescens 2170 and its mutants were grown at 33 °C with shaking in a yeast extract-supplemented minimal (YEM) medium containing various carbon sources (Montreal & Reese, 1969). The yeast extract concentration in this medium was reduced to 0.025 %. Escherichia coli strains were grown at 30 or 37 °C in Luria–Bertani (LB) medium containing appropriate antibiotics. Growth was monitored by measuring OD₅₆₀ using a mini-photo 518 photometer (Taitec). Antibiotics were used at the following concentrations: ampicillin, 100 µg ml⁻¹; chloramphenicol, 50 µg ml⁻¹; kanamycin, 50 µg ml⁻¹; tetracycline, 25 µg ml⁻¹.

**Construction of mutants with disrupted ctb and nagE genes.** Mutants were constructed by homologous recombination using pir-dependent replication plasmid pFS200 (Uchiyama et al., 2003). A 290 bp internal region of the ctb gene and a 400 bp internal region of the nagE gene were amplified by PCR with primers chb1-F (5'-GACGGCAAGACTGCTCTATTTCCAGC-3') and chb1-R (5'-AACGCGGCCAAACCTGATCCAGGTTTTCG-3') for the ctb mutant, and nagE-F (5'-AAGGCGCTGCTGCCTTTCG-3') and nagE-R (5'-GACGGCGCCATGATACTG-3') for the nagE mutant, using chromosomal DNA of S. marcescens 2170 as a template. PCR products were cloned into pT7Blue T-vector or pUC119 and sequenced. From the plasmids, target regions were excised and cloned into pFS200. The resulting plasmids were first introduced into E. coli S17-1(λpir) by electroporation and then transferred to S. marcescens 2170 by conjugation, as previously described (Uchiyama et al., 2003). Individual transconjugants were selected on LB agar plates containing chloramphenicol and tetracycline. Disruption of the pir gene was confirmed by sequencing the PCR product obtained with primers complementary to the sequence within the chloramphenicol-resistance gene and to the sequence outside of the target region.

**Intracellular, extracellular and total chitobase activities.** The culture supernatant (extracellular fraction) was prepared by centrifugation at 8000 g for 5 min. After removing the supernatant, the cell pellet was suspended in 0.1 M sodium phosphate buffer (pH 6.0). To prepare the intracellular fraction, the cell suspension was then lysed by sonication for 30–120 s. To measure the total activities containing intra- and extracellular activities, the culture was permeabilized by adding chloroform at a ratio of 100 µl ml⁻¹ and vortexing vigorously for 10 s. Chitobiase activity was measured using 4-methylumbelliferyl N-acetyl-β-D-glucosaminide (4-MU-GlcNAc) (Sigma) as the substrate. A 50 µl sample was mixed with 500 µl of 10 µM 4-MU-GlcNAc in 100 mM sodium phosphate buffer (pH 6.0). After incubation for 5 min at 37 °C, the reaction was stopped by adding 500 µl 0.2 M Na₂CO₃. The fluorescence of the liberated 4-MU was measured with excitation at 360 nm and emission at 450 nm using an RF-5300 spectrofluorophotometer (Shimadzu). One unit of chitobiase activity was defined as the amount of enzyme that liberates 1 nmol 4-MU per min.

**SDS-PAGE and activity staining.** SDS-PAGE was carried out as described by Laemmli (1970) using 12.5 % polyacrylamide gels under reducing conditions. After electrophoresis, the gel was washed three times with 2.5 % Triton X-100 for 60–90 min to remove SDS and renature the proteins. The gel was then incubated for 60 min in 0.1 M sodium phosphate buffer (pH 6.0). The polyacrylamide gel was overlaid with an agarose gel containing 0.1 mM 4-MU-GlcNAc in 0.1 M sodium phosphate buffer (pH 6.0) for 10 min. Enzyme activity was detected as fluorescent bands under UV light. Proteins separated by SDS-PAGE were stained with Coomassie brilliant blue R-250.

**Chemicals.** GlcNAc was purchased from Seikagaku Kogyo Co. Water-soluble chitin (WS-chitin) and N,N' -diacetylchitobiose were kindly provided by Yaizu Suisan Chemical Co. The degree of deacetylation of the WS-chitin is 38.8 %, and its approximate molecular mass is 200–300 kDa. WS-chitin is soluble in water due to partial deacetylation and the limited size of the chitin chain. Therefore, it is possible to measure cell growth in medium containing WS-chitin by optical density.

**RESULTS**

**Arrangement of genes and construction of mutants**

(GlcNAc)₂ is the major product of chitin hydrolysis by chitinases of S. marcescens 2170 (Suzuki et al., 2002). Uptake of (GlcNAc)₂ via a (GlcNAc)₂-specific enzyme II permease has been demonstrated previously (Uchiyama et al., 2003). However, the presence of chitobiase in this organism suggests that (GlcNAc)₂ is in part hydrolysed by chitobiase to GlcNAc, and then taken up by GlcNAc permease. S. marcescens has a nag operon (nagEBCAD), highly homologous to the E. coli nag operon, which is involved in GlcNAc uptake and metabolism (Plumbbridge, 1989; Postma et al., 1993). The nagE gene encodes GlcNAc-specific enzyme II permease (Lengeler et al., 1994). The nag operon is positioned near the ctb gene on the genome of S. marcescens. The ctb gene is clustered with genes homologous to E. coli ybfM and ybfN, which are genes with unknown function. nagE and nagBCAD are transcribed in opposite directions. To clarify the contribution of chitobiase and GlcNAc uptake to the utilization of chitin, ctb and nagE mutants were constructed. Mutants were constructed by homologous recombination using pFS200, a pir-dependent replication plasmid containing a chloramphenicol-resistance gene. Briefly, the internal regions of the target genes were cloned into pFS200. The resulting plasmids were transferred from E. coli S17-1(λpir) to S. marcescens 2170 by conjugation, and

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transconjugants were selected based on chloramphenicol resistance. Chloramphenicol-resistant transconjugants should contain the respective plasmids integrated into the target gene on the chromosome by homologous recombination, leading to two incomplete copies of the target gene. Integration of the respective plasmids into the chromosomal DNA of *S. marcescens* 2170 was confirmed by PCR and the desired mutants were obtained.

**Chitobiase production by *S. marcescens* 2170**

When *S. marcescens* QMB1466 is cultivated in a medium containing chitin, (GlcNAc)_2-hydrolysing activity, which is probably due to chitobiase, is detected in the culture supernatant (Monreal & Reese, 1969). In contrast, chitobiase produced in *E. coli* carrying the *S. marcescens* ctb gene is secreted into the periplasm (Tews et al., 1996). Therefore, we first investigated the localization of chitobiase in *S. marcescens*. Wild-type 2170 and the ctb mutant were grown to mid-exponential phase in YEM medium containing 0.2% WS-chitin. The ctb mutant grew more slowly than the wild-type strain. Extra- and intracellular fractions were analysed by SDS-PAGE and activity staining with 4-MU-GlcNAc (Fig. 1). A thin protein band of approximately 96 kDa, which coincided with the predicted molecular mass of chitobiase, was detected in the extracellular fraction of the wild-type strain in SDS-PAGE analysis. This band was considered to be chitobiase because it was not detected in the ctb mutant. In activity-staining analysis, only a single fluorescent band at the position corresponding to the protein band of chitobiase was observed in both fractions of the wild-type strain. This fluorescent band was not observed in the ctb mutant. Accordingly, chitobiase was found to be located both inside and outside the cell. It is worth noting that chitinases and CBP21 were produced normally in the ctb mutant.

We then tried to determine extra- and intracellular chitobiase activity. However, attempts to measure intracellular activity quantitatively failed because chitobiase was inactivated by sonication to disrupt the cells. Therefore, total activity, representing the sum of extra- and intracellular activity, was measured as described in Methods. Significant activities were detected in the wild-type strain, while activities were barely detected in the ctb mutant, indicating that chitobiase is the main enzyme that hydrolys this substrate. In the wild-type strain, total activity (10.1 ± 2.2 U ml⁻¹ per OD₆₆₀ unit) was much higher than extracellular activity (3.5 ± 0.9 U ml⁻¹ per OD₆₆₀ unit). When the extracellular fraction was analysed by SDS-PAGE, weak protein bands presumably derived from cellular proteins were detected, suggesting that some, but not all, extracellular chitobiase activity was released from the cells by cell lysis. Chitobiase from *S. marcescens* possesses the signal sequence in its precursor form, and is secreted into the periplasm when expressed in *E. coli* (Tews et al., 1996). Therefore, intracellular chitobiase is suggested to be mainly located in the periplasm, and is more abundant than extracellular chitobiase. The attempt to extract chitobiase from the periplasm by the osmotic shock procedure was unsuccessful. However, this was not unexpected because it has been reported that the periplasmic proteins of *S. marcescens* are resistant to release by osmotic shock (Cerny & Teuber, 1972).

**Growth of *S. marcescens* strains on various carbon sources**

(GlcNAc)₂ is the major product of chitin hydrolysis by chitinases of *S. marcescens* 2170. Because chitobiase
hydrolyses (GlpNAc)_2 to GlcNAc, it has been thought to be involved in the utilization of (GlpNAc)_2. To clarify the involvement of chitobiase in the utilization of (GlpNAc)_2, S. marcescens 2170 and its mutants were grown in YEM medium containing 0.1 % glycerol, 0.1 % GlcNAc or 0.1 % (GlpNAc)_2 (Fig. 2). The wild-type strain grew well on all carbon sources examined. On the other hand, growth of the ctb mutant on (GlpNAc)_2 was significantly retarded compared with that of the wild-type strain, indicating that chitobiase plays an important role in the utilization of (GlpNAc)_2.

As described above, chitobiase is suggested to be localized both in the periplasm and outside the cells. When chitobiase hydrolyses (GlpNAc)_2 in the periplasm and supernatant, GlcNAc permease is predicted to be required partially for the utilization of (GlpNAc)_2 but not that of glycerol. To test the above prediction, a mutant for nagE, encoding GlcNAc-specific enzyme II permease, was constructed. The nagE mutant grew very slowly on GlcNAc (Fig. 2b), indicating that NagE is the main permease for GlcNAc. Slow growth of the nagE mutant on GlcNAc suggests slight uptake of GlcNAc through other minor pemeases. On (GlpNAc)_2, the nagE mutant initially grew slowly, similar to the ctb mutant, and then it showed a greatly reduced growth rate (Fig. 2a). The nagE mutant produced chitobiase on (GlpNAc)_2 and total activity at 6 h cultivation was 15.9 U ml\(^{-1}\) per OD\(_{660}\) unit. The involvement of NagE in the growth on (GlpNAc)_2 suggests that GlcNAc uptake is important for the utilization of (GlpNAc)_2.

**Induction of chitobiase**

Wild-type and mutant strains were grown to mid-exponential phase in YEM medium containing 0.1 % glucose, glycerol, GlcNAc, (GlpNAc)_2 or glycerol + (GlpNAc)_2. Total chitobiase activities were measured using 4-MU-GlcNAc as substrate (Fig. 3). Chitobiase activity was detected on GlcNAc, (GlpNAc)_2 and glycerol + (GlpNAc)_2 in the wild-type strain. Culture on (GlpNAc)_2 showed fivefold higher activity than that on GlcNAc. Therefore, the expression of chitobiase is induced by GlcNAc and (GlpNAc)_2, and (GlpNAc)_2 is a more effective inducer. On the other hand, the ctb mutant did not show significant chitobiase activity on GlcNAc and (GlpNAc)_2.

In S. marcescens 2170, the LysR-type transcriptional regulator ChiR and (GlpNAc)_2 uptake are essential for the production of all chitinases and CBP21 (Suzuki et al., 2001; Uchiyama et al., 2003). The chbC encodes the (GlpNAc)_2-specific enzyme IIIC component of the PTS. Disruption of chbC drastically reduced the production of chitinases because of a lack of (GlpNAc)_2 uptake, as demonstrated previously (Uchiyama et al., 2003). To examine whether ChiR and (GlpNAc)_2 uptake is required for the induction of chitobiase, chiR and chbC mutants were grown in medium containing GlcNAc or (GlpNAc)_2. As shown in Fig. 3, the chiR mutant (N1) produced chitobiase normally, indicating that chitobiase is not regulated by ChiR. Since the chbC mutant grew very slowly on (GlpNAc)_2 (Fig. 2), chitobiase production was compared in medium containing both 0.1 % glycerol and 0.1 % (GlpNAc)_2, in which the wild-type strain and the chbC mutant grew equally (Uchiyama et al., 2003). Glycerol does not repress chitobiase production of the wild-type strain, as shown in Fig. 3. On the other hand, chitobiase activity of the chbC mutant was very low, indicating that uptake of (GlpNAc)_2 is important for the production of chitobiase. Both mutants produced chitobiase on GlcNAc at the same level as the wild-type strain.

**DISCUSSION**

Many chitinolytic bacteria have β-N-acetylglucosaminidases, which hydrolyse (GlpNAc)_2 and chito-oligosaccharides to GlcNAc (Bassler et al., 1991; Tsujibo et al., 2000;
Matsuo et al., 1999; Yang et al., 2006). This study showed that chitobiase is the main \( \beta \)-N-acetylglucosaminidase for chitin utilization in S. marcescens 2170, because activity against 4-MU-GlcNac was hardly detectable in the ctb mutant, and (GlcNac)\(_2\) is the main product of S. marcescens chitinases. When S. marcescens 2170 was cultivated on chitin, chitobiase activity was detected both inside and outside the cells. S. marcescens chitobiase possesses a signal sequence in its precursor form and is secreted in the periplasm when cloned in E. coli (Tews et al., 1996). Therefore chitobiase inside the cells of S. marcescens 2170 is considered to be localized in the periplasm.

Uchiyama et al. (2003) showed that (GlcNac)\(_2\) molecules are taken up by a (GlcNac)\(_2\)-specific permease into the cytoplasm. In addition to uptake as (GlcNac)\(_2\), a certain portion of (GlcNac)\(_2\) must be converted to GlcNac by chitobiase, mainly in the periplasm, and incorporated into the cytoplasm by the GlcNac-specific enzyme II permease, because ctb and nagE are both required for normal growth on (GlcNac)\(_2\). Therefore, uptake of both (GlcNac)\(_2\) and GlcNac is important for the utilization of (GlcNac)\(_2\) in S. marcescens.

Both ctb and nagE mutants are assumed to essentially take up only (GlcNac)\(_2\) molecules when they are grown on (GlcNac)\(_2\). However, the two mutants grew differently on (GlcNac)\(_2\), as shown in Fig. 2(a). The nagE mutant initially grew slowly at a similar rate to the ctb mutant on (GlcNac)\(_2\), and then the growth rate was greatly reduced. This observation suggests that most of the (GlcNac)\(_2\) in the periplasm was degraded to GlcNac by chitobiase when the growth rate was reduced. In the case of V. furnissii, mutation of NagE, the sole permease of GlcNac, resulted in an increase in the generation time from 1.4 to 2.5 h on (GlcNac)\(_2\) (Bassler et al., 1991). The effect of nagE mutation appeared to be smaller than with S. marcescens. The difference in the effect of the two mutations may be explained by the difference in (GlcNac)\(_2\) permeases (ABC transporter in V. furnissii; PTS permease in S. marcescens 2170). The affinity for (GlcNac)\(_2\) of the ABC transporter is much higher than that of the PTS permease (Keyhani et al., 2000). The high-affinity transporter may enable more effective transport under the conditions in which (GlcNac)\(_2\) concentration is reduced by the action of \( \beta \)-N-acetylglucosaminidases.

The ctb mutant, which takes up only (GlcNac)\(_2\) molecules on (GlcNac)\(_2\), grew more slowly on (GlcNac)\(_2\) than on GlcNac. This means that (GlcNac)\(_2\) is less efficiently fermented by S. marcescens 2170 in the absence of chitobiase. Slower fermentation of (GlcNac)\(_2\) than GlcNac was also demonstrated with E. coli (Keyhani & Roseman, 1997), which belongs to the Enterobacteriaceae, as does S. marcescens. E. coli takes up GlcNac and (GlcNac)\(_2\) by respective PTS permeases (Keyhani & Roseman, 1997), just like S. marcescens, but lacks chitobiase (Yang et al., 2006). Therefore, it is plausible to conclude that S. marcescens possesses chitobiase for efficient utilization of (GlcNac)\(_2\) by converting it to the more readily fermentable sugar GlcNac.

Chitobiase was induced by GlcNac and (GlcNac)\(_2\), and (GlcNac)\(_2\) is a more effective inducer. (GlcNac)\(_2\) uptake and ChiR are essential for the induction of chitinases and CBP21 (Uchiyama et al., 2003; Suzuki et al., 2001). The chiR mutant N1 produced chitobiase normally on (GlcNac)\(_2\). In contrast, the chbc mutant, defective in the (GlcNac)\(_2\)-specific enzyme IIC component of the PTS, did not show any chitobiase activity in a medium containing (GlcNac)\(_2\) and glycerol. These results indicate that uptake of (GlcNac)\(_2\) is important in the induction of chitobiase as well as chitinases and CBP21. The requirement of (GlcNac)\(_2\) uptake for chitobiase production suggests that a certain substrate generated during or after the uptake, such as (GlcNac)\(_2\)-6P, is involved in regulation of the ctb gene. The importance of (GlcNac)\(_2\) uptake for chitobiase production also means that the chbc mutant essentially cannot utilize either GlcNac or (GlcNac)\(_2\) when supplied with (GlcNac)\(_2\) as carbon source, due to the absence of chitobiase. This would explain the very slow growth of the chbc mutant on (GlcNac)\(_2\), as shown in Fig. 2. Unlike chitinases and CBP21, chitobiase is not regulated by ChiR. In S. marcescens, the ctb gene is clustered with the ybfM and ybfN genes located upstream of ctb. Yang et al. (2006) predicted that ybfM is the regulon of NagC, which is a regulator of the nag operon (Vogler & Lengeler, 1989), because of the presence of a possible NagC-binding site upstream from the ybfM gene in S. marcescens. It has been shown that NagC regulates not only the nag operon, but also the cbb operon, responsible for utilization of (GlcNac)\(_2\), and the glmUS genes, involved in the GlcNac

![Fig. 3. Total chitobiase activity. Wild-type and mutant strains were grown to mid-exponential phase in YEM medium containing 0.1 % glucose, 0.1 % glycerol, 0.1 % GlcNac, 0.1 % (GlcNac)\(_2\) or 0.1 % glycerol+0.1 % (GlcNac)\(_2\). Total chitobiase activities were measured using 4-MU-GlcNac. Data are means ± SD of two or three independent experiments.](image-url)
biosynthetic pathway, in *E. coli* (Plumbridge & Pellegrini, 2004; Plumbridge, 1995). The involvement of NagC in chitobiase induction is suggested by the fact that chitobiase is induced by GlcNAc. In addition to NagC, other regulators must be involved in chitobiase induction because chitobiase was more strongly induced by (GlcNAc)₂ than by GlcNAc.

Fig. 4 illustrates a model of the catabolic pathway of degradation products from chitin in *S. marcescens*. Solid arrows indicate the pathways supported by experimental data. Dashed arrows denote the hypothetic pathways with no experimental data. OM, outer membrane; IM, inner membrane.

**Fig. 4.** A model of the catabolic pathway of degradation products from chitin in *S. marcescens*. Solid arrows indicate the pathways supported by experimental data. Dashed arrows denote the hypothetic pathways with no experimental data. OM, outer membrane; IM, inner membrane.

REFERENCES


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