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<th>Streptococcus mutans strains harboring collagen-binding adhesin</th>
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INTRODUCTION

*Streptococcus mutans* is regarded as the primary etiologic agent of human dental caries and resides in the oral biofilm dental plaque. To adhere to tooth surfaces in dental plaque and to survive, *S. mutans* produces several extracellular proteins or enzymes, including those classified as wall-anchored proteins. Five genes encoding wall-anchored proteins have been characterized in *S. mutans* up to now: *pac*, *fruA*, *dexA*, *gbpC*, and *wapA* (Ferretti et al., 1989; Okahashi et al., 1989; Burne and Penders, 1992; Igarashi et al., 1995; Sato et al., 1997). This group of proteins is exported, but also is tethered to the peptidoglycan of the cell wall by the extracellular sortase enzyme (Cossart and Jonquieres, 2000). Furthermore, these proteins are characterized by a common structure that has been well-documented (Navarre and Schneewind, 1999).

Recently, we identified a gene tentatively designated *cnm* (DDBJ Acc. #AB102689) involved in the cold-agglutination phenotype of *S. mutans* strain Z1 following in vitro random mutagenesis mediated by the Himar1 minitransposon introduced into the chromosomal DNA of the strain (Sato et al., 2004). This gene encoded a new member of wall-anchored proteins, which was highly homologous to a group of collagen-adhesin proteins from *Staphylococcus aureus* (Patti et al., 1992) as well as other bacteria (Rich et al., 1999; Lannergard et al., 2003; Nallapareddy et al., 2003).

Some strains of *S. mutans* were reported to recognize and bind collagen (Liu et al., 1990; Switalski et al., 1993). Although the extracellular protein antigen I/II of *S. mutans* was reported to be involved in the binding of cells to extracellular matrix proteins including collagen (Love et al., 2000; Beg et al., 2002), Cnm protein may be a strain-specific collagen-binding molecule in this species. In the present communication, we describe the characterization of the collagen-binding activities of the protein and whole cells of the *S. mutans* strains.

MATERIALS & METHODS

Bacterial Strains

The *S. mutans* strain used for random mutagenesis was Z1, which is one of the previously isolated strains from Tokyo Dental College. Its mutant 05A02, in which the *cnm* gene was interrupted by minitransposon insertion, was isolated following application of an *in vitro* random mutagenesis strategy described in detail in our recent report (Sato et al., 2004). Strain Z1 was detected as a colony morphologically specific for *S. mutans* on the Mitis-Salivarius-Bacitracin agar plate and exhibited an *S. mutans*-specific biotype as reported by Shklier and Keene (1974). The nucleotide sequence of the 16S rRNA gene from strain Z1 indicated that this strain belongs to an *S. mutans* species (Bentley et al., 1991).

According to a PCR method recently developed to distinguish serotypes of...
S. mutans (Shibata et al., 2003), strain Z1 was determined to be serotype f. Other S. mutans strains used are ATCC10449, PS14, Ingbrigg, GS-5, MT703, MT8148, V403, UA101, UA159, NG8, LM7, PMZ175, and 109c. Streptococci were maintained and cultured in Todd-Hewitt (TH) broth/agar plates, and kanamycin (Km) was added at 50 μg/mL in the media where indicated. Escherichia coli strain TOP10, obtained from a commercial supplier (Invitrogen, Carlsbad, CA, USA), was used as a host for plasmid pBAD/His and its derivatives, and strain DH5α was routinely used for standard procedures of DNA manipulation (Noran, 1989), except as indicated.

**Nucleotide Sequence Analysis**

We used BLAST programs to search the S. mutans genome Database at the University of Oklahoma's Advanced Center for Genome Technology (http://www.genome.ou.edu/smutans.html) and the International DNA databases (EMBL, GenBank, and DDBJ) for similar amino acid sequences. Sequence analysis and multiple alignment were carried out with the DNASIS-Mac program (Hitachi Software Engineering, Yokohama, Japan).

**Cloning and Expression of the Collagen-binding Domain of the Cnm Protein**

A gene fragment corresponding to the predicted collagen-binding domain of Cnm protein was amplified by PCR with the primers 5′-ATCTGCAGTGAGTCAACATTTCA-3′ and DSHpa3R (5′-CTGTAAGTGGTTGTTCTCGGT-3′) and ligated into the 5′ histidine-tag region (PstI site) of an expression vector, pBAD/HisA (Invitrogen). Following transformation with E.coli strain TOP10, the resulting clones were analyzed as described previously (Noran, 1989). One of these clones, ZAXF, was used for collagen-binding assays along with strain TOP10 harboring the vector pBAD/HisA (strain pBAD) and also harboring plasmid pSBP6 expressing another histidine-tagged protein [strain SBP6 (Sato et al., 2002a)] as negative controls. Cells of these strains grown with or without 2 x 10⁻³% arabinose as an inducer were collected, washed, and subjected to 6 cycles of ultrasonication as described previously (Sato et al., 2002b) to obtain crude cell-free extracts for the collagen-binding assays. Induction of the histidine-tagged proteins was confirmed with SDS-PAGE and CBB staining before the assays.

**Binding of Recombinant Cnm to ECM Proteins**

An ELISA used to analyze the binding ability of recombinant protein to immobilized ECM proteins was carried out according to the procedure described recently (Nallapreddy et al., 2003), with slight modifications. Briefly, ELISA plates (Code 3801-096, Asahi Techno Glass Corporation, Funabashi city, Japan) were coated with 1 μg of ECM proteins or bovine serum albumin (BSA) in 100 mL of PBS (50 mM potassium phosphate, pH 7.2; 150 mM NaCl) and allowed to incubate overnight at 4°C. After the plates were washed with PBST (PBS with 0.01% Tween 20) and blocked with 5% BSA, various amounts of cell-free extracts (10 μg proteins in 20 μL of PBS with 0.1% BSA) were added to the wells and incubated for 1.5 hrs at 37°C. Bound proteins were detected by Anti-His HRP Conjugates (Qiagen) antibody.

**Southern Hybridization Analysis**

The restriction enzyme (HindIII)-digested chromosomal DNA fragments from strain Z1, reference strains including strain UA159, and natural isolates were analyzed by use of the ECL direct nucleic-acid-labeling and detection system (Amersham Co.)
RESULTS

Characteristics of the Cnm Protein Sequence

A nucleotide sequence homologous to the cnm gene was not detected in the UA159 genome database. The DNA databases were then searched for similar proteins with the amino acid sequence deduced from the cnm gene. Similar sequences were found in a group of collagen-binding adhesin proteins, which are also wall-anchored proteins, from staphylococci, enterococci, and equine streptococci. The most similar target sequence regions were those corresponding to the collagen-binding domains (CBD) in collagen-binding adhesin precursor proteins (Cna) from S. aureus strain FDA 574 (54.8% identity) and MRSA strain MW2. The next most similar sequences were the recently reported CBDs of the Enterococcus faecium (Acm, 48.8% identity) and Streptococcus equi (Cne, 48.2% identity). The CBD of the Enterococcus faecalis (Ace, 31.5% identity) was less similar to that of S. mutans Cnm. Multiple alignments of the 5 CBD sequences are presented in Fig. 1.

Another characteristic sequence of the Cnm protein was found in the C-terminal region as a repetitive sequence, which consists of tandem TTTTE(K/A)P, and subsequent 19 TTTTE(A/S/T)P repeats (Fig. 4).

Collagen-binding Assay

Based on the similarities of the N-terminal amino acid sequence deduced from the cnm gene to the CBD in collagen-binding adhesin precursor proteins, a 5′ cnm gene region corresponding to the mature N-terminal region containing the putative CBD region was amplified by PCR and subcloned into a pBAD/HisA expression vector to overexpress the protein. Since ZAXF protein expression was easily confirmed by CBB staining of SDS polyacrylamide gels, we initially attempted to purify the protein using a commercially available ProBond resin column system.
However, the protein aggregated immediately after elution under native conditions with imidazol as recommended by the supplier. In addition, the protein obtained by pH elution did not exhibit any binding activity to collagen. Therefore, we used the crude E.coli extracts as described in MATERIALS & METHODS. The ZAXF protein bound to immobilized collagen type I and laminin but not to fibronectin or BSA (Fig. 2A). Protein from ZAXF cells grown in the absence of arabinose (uninduced ZAXF) and that from strains pBAD and SBP6 cells grown in the presence of 2 x 10^{-3} % arabinose did not exhibit binding to collagen type I and laminin (Fig. 2B).

Biotin-labeled S. mutans Z1 whole cells bound collagen type I and laminin best and interacted with fibronectin to a lesser extent (Fig. 2C). In contrast, mutant 05A02 cells bound only to fibronectin, with binding activity similar to that of Z1 cells. The binding profiles of both the recombinant and whole-cell assays were comparable.

Prevalence of the cnm Gene among S. mutans Strains

To evaluate the occurrence of the cnm gene among different S. mutans strains, we carried out Southern blot analysis of HindIII-digested chromosomal DNA fragments from laboratory strains and isolates, including UA159 and Z1, using the cnm gene fragment as a probe. Five out of the 14 strains examined were cnm-positive (Fig. 3) and exhibited cold-agglutination and collagen/laminin-binding activities, while the other 9 strains did not exhibit these phenotypes. Interestingly, 3 of the 5 positive strains were serotype e or f (LM7, OMZ175, and Z1), but no clonality has been observed among these cnm-positive strains analyzed by AFLP.

DISCUSSION

The Cnm protein exhibited high homology with collagen-binding adhesins from S. aureus, E. faecium, and S. equi (Patti et al., 1992; Lannergard et al., 2003; Nallapareddy et al., 2003). Specifically, the 165-amino-acid sequence from residues 152 to 316 was highly homologous to the CBDs of these collagen-binding adhesins. In addition, several amino acids that are critical for collagen-binding by Cna of S. aureus (Patti et al., 1995; Symersky et al., 1997), including those which form the walls of the groove in Cna accepting collagen molecules (Symersky et al., 1997), were conserved in all 5 CBDs. These results suggested that the observed collagen-binding activity of S. mutans Cnm protein was highly predictable.

Previously identified collagen-binding adhesin molecules (Patti et al., 1992; Rich et al., 1999; Lannergard et al., 2003; Nallapareddy et al., 2003) contained the B repeat regions following the A domain containing the CBD. However, the number of repeats and the length of the repeating units were dependent on species variation. S. mutans Cnm contained 2 seven-residue and 19 six-residue repeating units (Fig. 4) located between the putative CBD and C-terminal wall-associated domain rich in proline and lysine residues. This repeat region of the Cnm protein may correspond to the B domain of the collagen-binding adhesins. Therefore, we conclude that the characteristic domain structure of the Cnm protein, as well as the homology of its putative CBD, was conserved overall.

Specific binding assays with crude E.coli extracts containing a recombinant CBD domain (ZAXF protein) revealed that the S. mutans Cnm protein is a new member of the collagen-binding adhesin family. It is of interest that the ZAXF protein also exhibited an affinity to laminin. This was compatible not only with the demonstrated relative collagen- and laminin-binding properties of intact cells of Z1 and its cnm mutant 05A02, but also with the similar fibronectin-binding abilities retained by both strains. The Southern blot analysis of S. mutans strains, with the cnm gene fragment as a probe, revealed that 9 out of 14 strains, including strain UA159, do not
harbor this gene. More than a decade ago, two reports (Liu et al., 1990; Switalski et al., 1993) demonstrated that approximately 20 and 25% of S. mutans strains tested were able to bind collagen. These ratios were comparable with the present results. Taken together, these results suggested that the collagen-binding of S. mutans cells is likely mediated by the strain-specific Cnm protein.

Oral viridans streptococci are pathogens associated with infective endocarditis, and the binding abilities of these organisms to subendothelial matrix proteins including collagen, sialoproteins, fibronectin, and laminin, as well as blood-derived fibrinogen (fibrin), are regarded as potential virulence factors (Sommer et al., 1992; Scioti et al., 1997; Chia et al., 2000; Beg et al., 2002; Takahashi et al., 2002). Although S. mutans was reported to be responsible for 8-18% of total streptococcal endocarditis (Ryd et al., 1996), and extracellular protein antigen I/II was reported to be involved in binding of S. mutans cells to extracellular matrix protein (Love et al., 2000; Beg et al., 2002), including collagen, it has often been questioned whether S. mutans is a true pathogen in endocarditis. In this respect, strain-specific Cnm protein expression may be an important virulence factor and may provide an answer to this question. Therefore, it will be of interest to compare the percentage of the cnm gene-positive strains isolated from infective endocarditis patients with that from healthy people, and also of interest to see whether the cnm gene-positive or -negative strains differentially induce experimental endocarditis in a rat-model system.

To our knowledge, this is the first report that demonstrates a collagen-binding adhesion from viridans streptococci in human oral indigenous flora.

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