Identification and molecular characterization of tryptophanase encoded by tnaA in Porphyromonas gingivalis

Yasuo Yoshida,1 Takako Sasaki,1 Shuntaro Ito,1,2 Haruki Tamura,1 Kazushi Kunimatsu2 and Hirohisa Kato1

1Department of Dental Pharmacology, Iwate Medical University School of Dentistry, Morioka, Japan
2Department of Periodontology, Iwate Medical University School of Dentistry, Morioka, Japan

Indole produced via the β-elimination reaction of L-tryptophan by pyridoxal 5′-phosphate-dependent tryptophanase (EC 4.1.99.1) has recently been shown to be an extracellular and intercellular signalling molecule in bacteria, and controls bacterial biofilm formation and virulence factors. In the present study, we determined the molecular basis of indole production in the periodontopathogenic bacterium Porphyromonas gingivalis. A database search showed that the amino acid sequence deduced from pg1401 of P. gingivalis W83 is 45% identical with that from tnaA of Escherichia coli K-12, which encodes tryptophanase. Replacement of the pg1401 gene in the chromosomal DNA with the chloramphenicol-resistance gene abolished indole production. The production of indole was restored by the introduction of pg1401, demonstrating that the gene is functionally equivalent to tnaA. However, RT-PCR and RNA ligase-mediated rapid amplification of cDNA ends analyses showed that, unlike E. coli tnaA, pg1401 is expressed alone in P. gingivalis and that the nucleotide sequence of the transcription start site is different, suggesting that the expression of P. gingivalis tnaA is controlled by a unique mechanism. Purified recombinant P. gingivalis tryptophanase exhibited the Michaelis–Menten kinetics values $K_m = 0.20 \pm 0.01$ mM and $k_{cat} = 1.37 \pm 0.06$ s$^{-1}$ in potassium phosphate buffer, but in sodium phosphate buffer, the enzyme showed lower activity. However, the cation in the buffer, K$^+$ or Na$^+$, did not appear to affect the quaternary structure of the enzyme or the binding of pyridoxal 5′-phosphate to the enzyme. The enzyme also degraded S-ethyl-L-cysteine and S-methyl-L-cysteine, but not L-alanine, L-serine or L-cysteine.

INTRODUCTION

Tryptophanase (tryptophan indole-lyase, EC 4.1.99.1) occurs in a wide variety of bacteria. The protein encoded by tnaA is a pyridoxal 5′-phosphate (PLP)-dependent enzyme that catalyses the β-elimination reaction of L-tryptophan to yield indole, ammonium and pyruvate (Snell, 1975). Tryptophanases from Escherichia coli (Phillips, 1987; Watanabe & Snell, 1977) and Proteus vulgaris (Zakomirdina et al., 2002) have also been reported to be associated with the in vitro β-elimination reactions of a wide range of natural and synthetic amino acids. E. coli tryptophanase functions as a tetramer of four 52.8 kDa 471-residue subunits (Deely & Yanofsky, 1981; Kagamiyama et al., 1972), and although the dimeric form of the enzyme can be isolated (Raibaud & Goldberg, 1976) or induced by cold (Erez et al., 1998), it is inactive. In the active form of E. coli tryptophanase, each subunit contains one molecule of PLP that forms a Schiff base with the side chain of Lys-270, but can be removed by dialysis to produce the apoform of the enzyme (Metzler et al., 1991). K$^+$ plays a role in stabilizing the oligomeric structure of tryptophanase, as cold dissociation of the enzyme has been shown to occur slowly in the presence of this cation (Erez et al., 1998), whereas Na$^+$ has been shown to inhibit the activity of the enzyme (Snell, 1975).

Indole is one of the malodorous oral volatile products, which include methyl mercaptan, hydrogen sulphide, skatole and cadaverine (Fosdick & Piez, 1953; Kostelc et al., 1981; Claesson et al., 1990; Goldberg et al., 1994). Interestingly, the molecule was recently reported to decrease biofilm formation by E. coli, but to increase that by Pseudomonas spp. (Lee et al., 2007). The molecule also controls multidrug exporters (Hirakawa et al., 2005) and regulates the pathogenicity island in E. coli (Anyanful et al., 2005). Moreover, a relationship between the ability of Haemophilus influenzae strains to produce indole and cause...
certain infectious diseases, including meningitis, has been reported (Martin et al., 1998). Thus, indole is not only a malodorous product, but also an extracellular and intercellular signalling molecule.

Porphyromonas gingivalis is a Gram-negative, black-pigmented, asaccharolytic obligate anaerobe that has been implicated in the initiation and progression of periodontal disease (Lamont & Jenkinson, 2000). This micro-organism is regarded as a secondary colonizer of oral biofilm (Kolenbrander et al., 2002), and its primary niche is the anaerobic environment of subgingival pockets (Lamont & Jenkinson, 2000). This micro-organism is implicated in the initiation and progression of periodontal disease (Lamont & Jenkinson, 2000). Thus, indole is not only a malodorous product, but also an extracellular and intercellular signalling molecule.

**METHODS**

**Bacterial strains and culture conditions.** P. gingivalis W83 and its derivatives were grown anaerobically at 37 °C in enriched BHI broth, containing 37 mg BHI (Difco) ml⁻¹, 5 mg yeast extract (Difco) ml⁻¹, 1 mg l-cysteine ml⁻¹, 5 μg haemin ml⁻¹ and 1 μg menadione ml⁻¹. When necessary, 20 μg chloramphenicol ml⁻¹ or 10 μg erythromycin ml⁻¹ was added to the medium. E. coli BL21 (Promega), used for protein purification, was grown aerobically in 2 × TY broth (Difco) at 37 °C with 100 μg ampicillin ml⁻¹.

**Construction of mutant strains of P. gingivalis.** A tnaA-deficient mutant strain designated KO100 was constructed by transformation of P. gingivalis W83 with a DNA construct containing the chloramphenicol-resistance gene (cat) flanked by targeting sequences for pgl1401. The upstream targeting sequence, the cat gene and the downstream targeting sequence were individually amplified from P. gingivalis. When necessary, 20 μg chloramphenicol ml⁻¹ or 10 μg erythromycin ml⁻¹ was added to the medium. E. coli BL21 (Promega), used for protein purification, was grown aerobically in 2 × TY broth (Difco) at 37 °C with 100 μg ampicillin ml⁻¹.

**RT-PCR and RNA ligase-mediated rapid amplification of cDNA ends (RLM-RACE).** Total RNA was extracted from a P. gingivalis W83 culture brought to exponential growth using FastPrep Blue tubes (Bio 101) as previously described (Yoshida et al., 2003a). Contaminating DNA in the samples was eliminated by digestion with RNase-free DNase (Takara Bio). The total RNA obtained was used for the following two analyses.

RT-PCR was performed as described by Yoshida et al. (2003a). Briefly, RNA was reverse-transcribed into single-stranded cDNA using PrimeScript Reverse Transcriptase (Takara Bio) according to the manufacturer’s instructions. The gene-specific primers used in RT-PCR are listed in Table 1. Each reverse primer for RT-PCR analysis was also used to synthesize a cDNA from a specific mRNA in the total RNA. The reaction mixtures used as negative controls contained no reverse transcriptase, so that the existence of contaminating genomic DNA in the samples could be evaluated.

RLM-RACE was used to determine the transcription start site of tnaA with total RNA. Rapid amplification of 5’ cDNA ends was carried out using a FirstChoice RLM-RACE kit (Ambion) according to the manufacturer’s instructions. In brief, a 45 base RNA adapter was ligated to the RNA population using T4 RNA ligase. This RNA population was then used as a template for a random-primed reverse transcription reaction. The cDNA product of this reaction was used as a template for PCR using a tnaA-specific outer primer (RACE outer tnaA primer) and a reverse primer to the adaptor (RACE outer adaptor primer). The PCR conditions were as follows: 94 °C for 2 min; 35 cycles of 94 °C for 15 s, 60 °C for 20 s and 72 °C for 30 s; and 72 °C for 5 min. The identity of the product was confirmed using inner gene-specific primers (RACE inner tnaA primer and RACE inner adaptor primer). After the amplicon was purified and then ligated into pMCL210 (Nakano et al., 1995), E. coli was transformed with the ligated mixture. The plasmids isolated from ten different colonies were sequenced with an ABI 3730 Genetic Analyzer (Applied
Preparation of crude enzyme extracts. Crude enzyme extracts of *P. gingivalis* were prepared as described by Yoshida et al. (2002). Briefly, cells grown to an OD<sub>600</sub> of about 0.8 were harvested from 50 ml of culture and then washed with PBS. The cells were sonicated five times for 30 s at 1 min intervals. The supernatant was collected after centrifugation at 15 000 g for 30 min at 4 uC. The concentration of proteins in the crude enzyme extract was determined using a protein assay reagent (Bio-Rad) with BSA as a standard. The samples were stored at 220 uC after adding the same volume of 80 % (v/v) glycerol.

Purification of recombinant TnaA. Recombinant TnaA protein of *P. gingivalis* was purified using the expression vector pGEX-6P-1 (GE Healthcare) as described by Yoshida et al. (2002). The coding sequence of *tnaA* was amplified by PCR with KOD DNA polymerase (Toyobo) from genomic DNA of *P. gingivalis* W83 using the primers 090407-F1 and 090407-R1 and ligated into the pGEX-6P-1 vector via the *BamHI* and *XhoI* restriction sites, juxtaposing the *tnaA* gene downstream of the coding sequence for glutathione S-transferase (GST) and a PreScission protease cleavage site. The resulting plasmid pGEW101-1 was sequenced to verify the correctness of the PCR amplification of the 1523 bp insert and transformed into *E. coli* BL21 cells. Production cultures of 500 ml were inoculated 1 : 1000 with an overnight culture and grown to an OD<sub>600</sub> of 0.7 at 37 uC. After induction of protein expression with 0.5 mM IPTG, the cells were incubated at 37 uC for another 2 h. The cells were then harvested by centrifugation, resuspended in 12 ml PBS, and lysed by ultrasonication. Cell debris was sedimented by centrifugation, and the portion of GST fusion protein that remained in the supernatant was adsorbed onto affinity matrix glutathione-Sepharose 4B and cleaved with PreScission protease according to the manufacturer's protocol (GE Healthcare). The concentration of proteins was determined as described by Pace et al. (1995). The purity of the samples was analysed by SDS-PAGE. N-terminal amino acid sequence determination was carried out to confirm the homogeneity of the recombinant protein. Briefly, the

### Table 1. Oligonucleotide primers used in this study

<table>
<thead>
<tr>
<th>Designation</th>
<th>Sequence (5’–3’)*</th>
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<tr>
<td><strong>Construction of mutants</strong></td>
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</tr>
<tr>
<td>090507 cm-F7</td>
<td>ATGGGAACTGAGGATTTAA</td>
</tr>
<tr>
<td>090507 cm-R8</td>
<td>TTACGCGGCTATGAGGATTTAA</td>
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<td>090507-tn-F1</td>
<td>CGAAAAGTTCAATTCAGGCA</td>
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<tr>
<td>090507-tn-R3</td>
<td>CCACTGCGGATTCAGGCA</td>
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<tr>
<td>090507-tn-R4</td>
<td>CCAGTGATTTTTCTCCCAT</td>
</tr>
<tr>
<td>021208-ermAF-f9</td>
<td>TTACGCGGCTATGAGGATTTAA</td>
</tr>
<tr>
<td>021208-ermAF-r10</td>
<td>CGAACCTGCGGATTCAGGCA</td>
</tr>
<tr>
<td>021208-tn-f3</td>
<td>GCCAGATGGGACGGAATATAC</td>
</tr>
<tr>
<td>021208-tn-r4</td>
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<tr>
<td>021208-tn-f6</td>
<td>AAACGGGAGGAAATATATCTAGT</td>
</tr>
<tr>
<td>090507-tn-R5</td>
<td>GAAATACGCGGATTCAGGCA</td>
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<tr>
<td><strong>RT-PCR</strong></td>
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<tr>
<td>032508-pg03-f1</td>
<td>GGTGTTATGATAGGAGGATTTAA</td>
</tr>
<tr>
<td>040308-pg03-r1</td>
<td>CCACACGACGAAAGCAATG</td>
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<td>033108-pg02-r2</td>
<td>TTAGAATAGAGTGGGATTC</td>
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<tr>
<td>060908-Pgtn-r6</td>
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<td><strong>RLM-RACE</strong></td>
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<tr>
<td>RACE outer adaptor primer</td>
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<tr>
<td>RACE inner adaptor primer</td>
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<td>RACE outer tnaA primer</td>
<td>CCGAGATCGTCAAGGAAAT</td>
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<tr>
<td>RACE inner tnaA primer</td>
<td>ATACATAGTCGCTGGAGG</td>
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<tr>
<td><strong>Purification of TnaA</strong></td>
<td></td>
</tr>
<tr>
<td>090407-F1</td>
<td>AAGGATCCGAAATTCCTTTCAGAATCTTACC</td>
</tr>
<tr>
<td>090407-R1</td>
<td>AAAGATCCGAAATTCCTTTCAGAATCTTACC</td>
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</table>

*The nucleotides underlined in each primer sequence are the positions of restriction endonuclease sites incorporated to facilitate cloning. Bold letters show overlapping regions of the 5’ or 3’ ends of the cat gene or the ermF-ermAM cassette.*

The sequences were analysed using Vector NTI software (Invitrogen).

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Preparation of crude enzyme extracts. Crude enzyme extracts of *P. gingivalis* were prepared as described by Yoshida et al. (2002). Briefly, cells grown to an OD<sub>600</sub> of about 0.8 were harvested from 50 ml of culture and then washed with PBS. The cells were sonicated five times for 30 s at 1 min intervals. The supernatant was collected after centrifugation at 15 000 g for 30 min at 4 °C. The concentration of proteins in the crude enzyme extract was determined using a protein assay reagent (Bio-Rad) with BSA as a standard. The samples were stored at 20 °C after adding the same volume of 80 % (v/v) glycerol.

Purification of recombinant TnaA. Recombinant TnaA protein of *P. gingivalis* was purified using the expression vector pGEX-6P-1 (GE Healthcare) as described by Yoshida et al. (2002). The coding sequence of *tnaA* was amplified by PCR with KOD DNA polymerase (Toyobo) from genomic DNA of *P. gingivalis* W83 using the primers 090407-F1 and 090407-R1 and ligated into the pGEX-6P-1 vector via the *BamHI* and *XhoI* restriction sites, juxtaposing the *tnaA* gene downstream of the coding sequence for glutathione S-transferase (GST) and a PreScission protease cleavage site. The resulting plasmid pGEW101-1 was sequenced to verify the correctness of the PCR amplification of the 1523 bp insert and transformed into *E. coli* BL21 cells. Production cultures of 500 ml were inoculated 1 : 1000 with an overnight culture and grown to an OD<sub>600</sub> of 0.7 at 37 °C. After induction of protein expression with 0.5 mM IPTG, the cells were incubated at 37 °C for another 2 h. The cells were then harvested by centrifugation at 4 °C, resuspended in 12 ml PBS, and lysed by ultrasonication. Cell debris was sedimented by centrifugation, and the portion of GST fusion protein that remained in the supernatant was adsorbed onto affinity matrix glutathione-Sepharose 4B and cleaved with PreScission protease according to the manufacturer’s protocol (GE Healthcare). The concentration of proteins was determined as described by Pace et al. (1995). The purity of the samples was analysed by SDS-PAGE.

N-terminal amino acid sequence determination was carried out to confirm the homogeneity of the recombinant protein. Briefly, the...
protein separated by SDS-PAGE was transferred electrophoretically to
a PVDF membrane. The band visualized by Coomassie brilliant blue
was excised and analysed with a Precise 49X LCL protein sequencer
(Applied Biosystems).

TnaA apoenzyme was prepared by dialysis against 20 mM
potassium phosphate or sodium phosphate buffer (pH 7.5) for
24 h. Reconstitution of the holoenzyme was achieved by incubation
of the apoenzyme with 0.1 mM PLP at 37 °C for 30 min in darkness
as described by Raibaud & Goldberg (1976).

Gel-filtration chromatography. A prepacked gel-filtration column
(Hiroad 16/60 Superdex; GE Healthcare) was used. The mobile phase
used for apoenzyme analysis was identical to that used for dialysis to
prepare each apoenzyme (20 mM potassium phosphate or sodium
phosphate buffer, pH 7.5) to remove the effect of the other cation.
For holoenzyme analysis, each phosphate buffer containing 0.1 mM
PLP was used to avoid the release of PLP from the holoenzyme. The
column was run at 0.5 ml min⁻¹ at 4 °C. The enzyme elution
was monitored at 280 nm. The size of each protein was estimated using a
standard curve made with five commercially available proteins (Gel
Filtration Calibration kit HMW, GE Healthcare).

HPLC analysis. The indole production in an enzymic reaction was
evaluated using reversed-phase HPLC as described by Krstulovic &
Matzura (1979). The reaction mixture contained the following
reagents in a final volume of 100 µl: 167 mM potassium phosphate
buffer (pH 7.5), 0.165 mM PLP, 0.2 mM reduced glutathione,
0.25 mg BSA ml⁻¹, 2 mM L-tryptophan and 50 µg ml⁻¹ crude extract of P. gingivalis
strain W83, KO100 or RS101. After layering with 100 µl toluene, the mixture was incubated for 2 h at 37 °C. An
aliquot (20 µl) of toluene from the sample tube was injected onto a
Capcell Pak C18 UG120 column (4.6 mm × 150 mm; Shiseido) with
50 % (v/v) methanol/water as the mobile phase at a flow rate of 0.5 ml
min⁻¹ at 40 °C. Excitation and emission wavelengths of 285 and
320 nm, respectively, were used.

Enzyme assay. The degradation of L-tryptophan by purified
tryptophanase was examined by measuring the formation of indole as
described by Morino & Snell (1970) with minor modifications.
Briefly, the reaction mixture contained 200 mM potassium or sodium
phosphate buffer (pH 7.5), 0.165 mM PLP, 0.2 mM reduced glutathione,
and varying concentrations of L-tryptophan. After being layered with
100 µl toluene, the mixture was prewarmed for 5 min at 37 °C. The reaction
was initiated by the addition of substrate
1 ml of Ehrlich’s reagent, which was prepared daily by mixing 5 vols 5 % (w/v) p-dimethylaminobenzaldehyde in 95 % (v/v)
ethanol with 12 vols 5 % (v/v) H₂SO₄ in 1-butanol. After 20 min at
room temperature, the mixture was centrifuged, and 100 µl of
the supernatant was examined spectrophotometrically at 568 nm. The amount of indole was calculated from a standard curve. The kinetic parameters were
computed from a Lineweaver–Burk transformation (V / Vmax versus S / Vmax) of the Michaelis–Menten equation, where V (mmol min⁻¹ g⁻¹)
represented the formation of indole and S (mM) was the
concentration of L-tryptophan. The Km value was calculated from the
Vmax value and the molecular mass of P. gingivalis tryptophanase.
Data were obtained from three independent experiments.

The degradation of S-ethyl-L-cysteine, S-methyl-L-cysteine, L-cysteine,
L-alanine and L-serine was measured by assaying pyruvate formation,
as previously described (Yoshida et al., 2002). The assays were carried
out in 100 µl reaction mixtures containing 200 mM potassium
phosphate buffer (pH 7.6), 0.165 mM PLP, 1 µg purified enzyme,
and varying concentrations of each substrate. After 5 min incubation
at 37 °C, the reactions were terminated by the addition of 50 µl of
4.5 % (v/v) trichloroacetic acid. The reaction mixtures were then
centrifuged, and 100 µl aliquots of the supernatants were added to
300 µl 0.67 M sodium acetate (pH 5.2) containing 0.017 % (w/v) 3-
methyl-2-benzothiazolinone hydrazone. After incubation at 50 °C for
30 min, the absorbance at 335 nm was determined. The amounts of
pyruvate were calculated from a standard curve prepared using
crystalline sodium pyruvate. Data were obtained from three independent experiments.

RESULTS

Organization of the tnaA homologue in
P. gingivalis W83

The tnaA genes that encode tryptophanase in Pr. vulgaris
(Kamath & Yanofsky, 1992), Enterobacter aerogenes
(Kawasaki et al., 1993), H. influenzae (Martin et al.,
1998) and E. coli (Deeley & Yanofsky, 1981; Rezwan et al.,
2004) have been sequenced. A database search identified
the ORF pg1401, which was assigned by the J. Craig Venter
Institute (http://www.jcvi.org/), as a homologue of the
tnaA gene in the genome of P. gingivalis W83 (Nelson et al.,
2003). The ORF (1380 bp) is slightly shorter than those of
the tnaA genes from the bacteria described above (1389–
1416 bp). In those organisms, tnaA is located between
tnaC, which encodes a leader peptide, and tnaB, which
codes tryptophanase permease; the latter consists of an
operon with tnaA (Deeley & Yanofsky, 1981) (Fig. 1a).
By contrast, the gene upstream of pg1401 in P. gingivalis,
pg1402, encodes a putative endonuclease/exonuclease/
phosphatase-family protein. The amino acid sequence
encoded by the gene downstream of pg1401 contains an
inosine monophosphate cyclohydrolase domain that is
involved in purine biosynthesis. We have designated this
gene orfX, since the ORF was not identified in the database.
Unexpectedly, no genes homologous to tnaB or tnaC were
identified either in the pg1401 region or in the whole-
genome sequence of P. gingivalis W83, showing that the
genome organization of this region in P. gingivalis is different
from that in other bacteria. However, the amino acid
sequence deduced from pg1401 shows 48.1 %, 50.9 %,
42.0 % and 44.9 % identity with the deduced sequences
from Pr. vulgaris, Ent. aerogenes SM-18, H. influenzae
Eagan, and E. coli K-12, respectively.

Transcription of the tnaA region in P. gingivalis
W83

RT-PCR was used to characterize the transcripts of the
pg1401 region in P. gingivalis W83. The locations of the primer pairs used to detect intragenic and intergenic regions are shown in Fig. 1(a). RT-PCR amplification
generated products of the expected size from an oligonucleotide pair complementary to pg1404/p1403 (Fig. 1b).
In contrast, no PCR products corresponding to the regions
spanning the borders of pg1403/pg1402, pg1402/pg1401 or
pg1401/orfX were amplified, indicating that pg1401 was
transcribed alone. No PCR products were observed from

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total RNA preparations that had not been first reverse transcribed, demonstrating that the RT-PCR products were not derived from contaminated chromosomal DNA. The data also showed expression of orfX, which has not been recognized as an ORF in the database (Fig. 1b).

The transcription start site of pg1401 was determined by RLM-RACE using total RNA extracted from P. gingivalis W83 grown to the early exponential phase. PCR fragments amplified with inner primers were subjected to DNA sequencing of the upstream region up to the transcription start site of pg1401. The junction of the adaptor with P. gingivalis DNA is the 5' end of the transcript. As shown in Fig. 1(c), one clear ending sequence corresponding to a position 52 bp upstream of the first nucleotide of the translation initiation codon was obtained by sequencing of the 5' RLM-RACE PCR product in all ten plasmids analysed.

The tryptophanase of P. gingivalis W83 is encoded by pg1401

To determine whether the product of the pg1401 gene functions as a tryptophanase, a mutant P. gingivalis W83 strain, in which the 1.4 kb gene was replaced by the 0.7 kb cat gene, was constructed (Fig. 2a). The DNA fragment for transformation was prepared using overlap extension PCR. Integration of the PCR products at the expected location in the chromosome of the resulting mutant strain, designated KO100, was confirmed by Southern blot analysis (Fig. 2b). HPLC analysis demonstrated that incubation of crude extract from KO100 with L-tryptophan showed no indole production (Fig. 3). Similarly, a pg1401-restored strain, designated RS101, was constructed from strain KO100, in which the cat gene was replaced by pg1401 linked to the ermF-ermAM cassette (Fig. 2a). As expected, the ability of
crude extracts to produce indole from L-tryptophan was restored by replacement of the cat gene with pg1401. These results confirm that the pg1401 gene encodes tryptophanase, the only enzyme associated with indole production in P. gingivalis. Based on these results, the pg1401 gene of P. gingivalis W83 was redesignated tnaA.

**Enzymic properties of recombinant TnaA from P. gingivalis W83**

To characterize the enzymic properties of tryptophanase from P. gingivalis W83, recombinant TnaA was purified using the pGEX-6P-1 vector system. All purification steps were monitored by SDS-PAGE analysis, as shown in Fig. 4. The protein obtained was judged to be homogeneous in an SDS-PAGE gel stained with Coomassie brilliant blue. The molecular mass of the denatured polypeptide agreed well with the predicted molecular mass (52.5 kDa). The quaternary structure of the recombinant protein might be a heterooligomer consisting of subunits derived from both P. gingivalis and E. coli tryptophanase, since the host E. coli BL21 produces its own tryptophanase. However, this possibility was excluded by protein sequence analysis, which showed that the N-terminal amino acid sequence of the protein obtained was GPLGSEL. The first five amino acids (i.e. GPLGS) are derived from the cloning site of pGEX-6P-1, whereas the remaining two correspond to the second and third amino acids of P. gingivalis tryptophanase. The forward primer used for amplification of P. gingivalis tnaA (Table 1) did not contain the start codon so that the GST–TnaA fusion protein was produced. In contrast, no findings suggesting that the protein contained subunits from E. coli tryptophanase were obtained, indicating that the recombinant tryptophanase of P. gingivalis W83 formed a homooligomer. Indole production by the recombinant enzyme was confirmed by HPLC (Fig. 3d).

The kinetic activity of the recombinant TnaA protein was spectrophotometrically evaluated by determination of its production of indole from L-tryptophan. When potassium

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**Fig. 2.** Construction of derivatives of P. gingivalis W83. (a) Chromosomal gene arrangement of the tnaA region in the parental and mutant strains. The size of each fragment in bp is shown. (b) Verification of the derivatives by Southern blot hybridization. Each chromosomal DNA was digested with Smal. Hybridizations with the tnaA gene probe (left panel), the cat gene probe (centre panel) and the ermF probe (right panel) were carried out at 60 °C for 6 h. Lanes: 1, P. gingivalis W83; 2, P. gingivalis KO100; 3, P. gingivalis RS101. The positions of DNA size standards (in kbp) are shown.

**Fig. 3.** Reversed-phase HPLC profiles of indole production from L-tryptophan. An aliquot (20 μl) of toluene that had been layered on the reaction mixture was injected onto a column with L-tyrosine as an internal standard. The reaction mixtures contained (a) crude extract of P. gingivalis W83, (b) crude extract of P. gingivalis KO100, (c) crude extract of P. gingivalis RS101 or (d) purified recombinant TnaA of P. gingivalis W83. Arrows indicate the elution positions of indole and tyrosine.
phosphate buffer was used in the enzymic reaction, the $K_m$ and $k_{cat}$ values of the protein were $0.20 \pm 0.01$ mM and $1.37 \pm 0.06$ s$^{-1}$, respectively. When the reaction was performed in sodium phosphate buffer, the values were $0.09 \pm 0.01$ mM and $0.24 \pm 0.01$ s$^{-1}$, respectively. Thus, the enzymic activity of TnaA from *P. gingivalis* W83 is much higher in the presence of K$^+$ than Na$^+$. On the basis of these results, the following enzymic characterization experiments were performed using potassium phosphate buffer with the active holoform of TnaA.

The effects of pH and temperature on the enzymic activity of TnaA were determined by using L-tryptophan as a substrate (Fig. 5). The activity of the purified enzyme was highest at pH 7.5. The enzyme was stable up to 40 °C, but only 40% of the activity remained at 60 °C. The enzyme was completely inactivated at temperatures above 70 °C.

To identify substrates other than L-tryptophan for the recombinant TnaA of *P. gingivalis*, several other compounds were assayed. The specificity of the purified enzyme to various substrates is shown in Table 2. In the reactions, enzymic degradation of the substrates invariably resulted in the formation of pyruvate. Thus, the breakdown of substrates other than L-tryptophan was determined by assaying the production of pyruvate. Degradation of L-tryptophan was measured as described above, because indole inhibits the assay using 3-methyl-2-benzothiazoli-nine hydrazone to detect pyruvate formation. The kinetic parameters of *P. gingivalis* TnaA for S-ethyl-L-cysteine were comparable with those for L-tryptophan. In contrast, the $k_{cat}$ and $k_{cat}/K_m$ values of the enzyme for S-methyl-L-cysteine were much lower than those for L-tryptophan. The enzyme had no detectable elimination activity with L-alanine, L-serine or L-cysteine as substrate.

### Quaternary structure of recombinant TnaA from *P. gingivalis* W83

We hypothesized that the difference in enzymic activity of *P. gingivalis* TnaA in the presence of different monovalent cations (K$^+$ and Na$^+$) (Table 2) could be due to a structural change in the enzyme. To evaluate this hypothesis, the quaternary structures of the apo- and holoform of *P. gingivalis* TnaA in the presence of each cation were examined by gel-filtration chromatography (Fig. 6a). In contrast to the results predicted by the hypothesis, no matter which buffer (potassium or sodium
phosphate) was used for dialysis and the mobile phase, both forms of the enzyme eluted at approximately 205.8 kDa, as estimated using a standard curve made with commercially available proteins. This size corresponds to the tetramer of P. gingivalis TnaA. These results showed that the quaternary structure of P. gingivalis TnaA was not affected by K⁺ or Na⁺.

The protein samples used for gel-filtration chromatography were also scanned by spectrophotometric absorption spectra. The holoenzyme in the potassium phosphate and sodium phosphate buffers displayed a characteristic absorption spectrum common to PLP-dependent enzymes, with band maxima at 337 and 423 nm. These maxima were not observed in the spectra of the apoenzyme. The type of phosphate buffer did not affect the absorption spectra of P. gingivalis TnaA, suggesting that the cation (K⁺ or Na⁺) had no significant effect on the binding of PLP. The difference of phosphate buffer did not have marked effects on the spectra of PLP (data not shown).

### DISCUSSION

Tryptophanase degrades tryptophan into pyruvate, ammonia and indole. Of those products, the former two molecules can be used as a carbon or nitrogen source in cells, whereas indole is secreted from the cells. Indole at very high concentrations (5 mM) is toxic to microorganisms, including E. coli, possibly by causing membrane changes that result in the generation of superoxide (Garbe et al., 2000). However, the toxic concentration of indole is approximately 15-fold higher than the physiological concentration observed in stationary-phase supernatants of E. coli. Interestingly, it has been shown that indole has an effect on physiological and pathological functions in bacteria (Aynanful et al., 2005; Hirakawa et al., 2005). Our objective in this study was to determine the molecular basis of indole production in P. gingivalis.

The tnaA and tnaB genes constitute the tna operon in E. coli (Deeley & Yanofsky, 1981), Pr. vulgaris (Kamath & Yanofsky, 1992), Ent. aerogenes (Kawasaki et al., 1993), and H. influenzae (Martin et al., 1998). In vitro transcription experiments located the presumptive tna promoter at more than 300 nt from the tnaA initiation codon in E. coli. This promoter requires a cAMP–CAMP receptor protein (CRP) for activity (Deeley & Yanofsky, 1982). The long transcribed leader region between the promoter and tnaA includes a coding region for a short leader peptide, designated TnaC. This peptide plays an essential role in the full induction of the tna operon, as well as in setting the basal uninduced level of tna expression (Stewart & Yanofsky, 1986). In contrast, no nucleotide sequences homologous to tnaB, tnaC or the CRP-binding region are present around tnaA in P. gingivalis. In addition, the gene does not consist of an operon with any genes. These findings suggest that the gene arrangement around tnaA in P. gingivalis is unique and that the expression of tnaA is controlled by a mechanism distinct from that in E. coli and other bacteria. The tryptophanase of E. coli is overexpressed and becomes one of the most abundant proteins when cells experience alkaline stress (Blankenhorn et al., 1999). The transcriptional data presented here would be helpful for further research along these lines.

When potassium phosphate buffer was used in the reaction mixture, the Kᵢₐₗ value (0.20 ± 0.01 mM) of TnaA from P. gingivalis W83 for L-tryptophan was slightly lower than those from the other bacteria, including E. coli B (0.32 mM) (Newton et al., 1965; Watanabe & Snell, 1977) and Bacillus alvei (0.27 mM) (Hoch et al., 1966), indicating that the affinity of P. gingivalis tryptophanase to L-tryptophan was comparable with those of E. coli and B. alvei. Its kₑₜ and kₑₜ/Kᵢₐₗ values (1.37 ± 0.06 s⁻¹ and 6.87 ± 0.11 mM⁻¹ s⁻¹) was also less than those in E. coli (6.8 s⁻¹ and 30 mM⁻¹ s⁻¹) (Phillips & Gollnick, 1989) and Pr. vulgaris (6.3 s⁻¹ and 23 mM⁻¹ s⁻¹) (Demidkina et al., 2003). Thus, the enzymic activity of tryptophanase from P. gingivalis was lower than that from E. coli and Pr. vulgaris. This investigation also demonstrated that P. gingivalis TnaA still has a weak enzymic activity in the presence of Na⁺, although NaCl showed an inhibitory effect on P. gingivalis TnaA (data not shown). In contrast, E. coli tryptophanase had almost no enzymic activity in the presence of only Na⁺ (Honda & Tokushige, 1986). Comparison of the Kᵢₐₗ values did not suggest that Na⁺ lowers the affinity of the substrate to the enzyme. Since the cation in the buffer, K⁺ or Na⁺, did not appear to affect

### Table 2. Steady-state kinetic parameters for TnaA from P. gingivalis W83

<table>
<thead>
<tr>
<th>Substrate</th>
<th>Kᵢₐₗ (mM)</th>
<th>kₑₜ (s⁻¹)</th>
<th>kₑₜ/Kᵢₐₗ (mM⁻¹ s⁻¹)</th>
</tr>
</thead>
<tbody>
<tr>
<td>L-Tryptophan</td>
<td>0.20 ± 0.01 (0.09 ± 0.01)</td>
<td>1.37 ± 0.06 (0.24 ± 0.01)</td>
<td>6.87 ± 0.1 (2.53 ± 0.09)</td>
</tr>
<tr>
<td>S-Methyl-L-cysteine</td>
<td>2.04 ± 0.18</td>
<td>0.50 ± 0.05</td>
<td>0.25 ± 0.004</td>
</tr>
<tr>
<td>S-Ethyl-L-cysteine</td>
<td>0.26 ± 0.01</td>
<td>1.87 ± 0.03</td>
<td>7.15 ± 0.17</td>
</tr>
</tbody>
</table>
either the quaternary structure of TnaA from *P. gingivalis* W83 or the binding of PLP to the apoenzyme (Fig. 6), K⁺ may function as an activator for the catalysing enzyme. Honda & Tokushige (1986) reported that NH₄⁺ is an active cation for *E. coli* tryptophanase in addition to K⁺. Morino & Snell (1967) reported that dissociation of the tetrameric holoenzyme of *E. coli* TnaA into the dimeric apoenzyme was accelerated by K⁺, and that in the absence of the cation the apoenzyme remained tetrameric even at low temperatures. However, Erez *et al.* (1998) concluded that incubation of the tetrameric form of *E. coli* TnaA in potassium phosphate buffer at 5 °C led to the conversion of approximately 24 % of the protein into a dimeric form. Contrary to these conflicting reports, we did not observe dissociation of *P. gingivalis* TnaA into the dimeric form in the presence or absence of K⁺ at 4 °C. The findings suggest that the quaternary structure of TnaA from *P. gingivalis* W83 is more stable in the absence of K⁺ than that from *E. coli*. X-ray crystal structural analyses demonstrated that the tryptophanases from *E. coli* and *Pr. vulgaris* contain K⁺-binding sites close to the active site, and that K⁺ ions interact with the O² atom of Gly-72 in one subunit and the backbone carbonyl O atoms of Gly-55 and Pro-275 (Isupov *et al.*, 1998; Ku *et al.*, 2006). *P. gingivalis* TnaA contained Glu-72 and Gly-55, even though Pro-275 was replaced by Asn. Structural studies are necessary to understand the stability of *P. gingivalis* TnaA in the presence or absence of K⁺.

In conclusion, the molecular basis of indole production in *P. gingivalis* was elucidated. Transcripts of *P. gingivalis tnaA* and the encoded protein were characterized. However, the expression mechanism of the gene, which appears to be different in *P. gingivalis* and other bacteria, remains to be elucidated. Further studies of the expression of *P. gingivalis tnaA* are under way to clarify the relationship between indole production and the physiological and pathological functions of this micro-organism.

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