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Dipeptide utilization by the periodontal pathogens *Porphyromonas gingivalis*, *Prevotella intermedia*, *Prevotella nigrescens* and *Fusobacterium nucleatum*

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Porphyromonas gingivalis, Prevotella intermedia, Prevotella nigrescens and Fusobacterium nucleatum, which can frequently be isolated from periodontal pockets, preferentially utilize proteins and peptides as growth substrates. In this study, we determined the size of peptide that is preferentially utilized as a source of energy and material for cell growth by *P. gingivalis, P. intermedia, P. nigrescens* and *F. nucleatum* using various sizes of poly amino acids consisting of two to approximately 100 molecules of aspartate or glutamate. Resting cells of *P. gingivalis, P. intermedia* and *P. nigrescens* utilized aspartylaspartate, while cells of *P. gingivalis* and *F. nucleatum* utilized glutamylglutamate. The addition of aspartylaspartate to the culture medium increased the growth of *P. gingivalis, P. intermedia* and *F. nucleatum*. These results clearly indicate that dipeptides such as aspartylaspartate and glutamylglutamate can be utilized as growth substrates for *P. gingivalis, P. intermedia*, *P. nigrescens* and *F. nucleatum*.

Key words: *Porphyromonas gingivalis*;

Prevotella intermedia; Prevotella nigrescens; Fusobacterium nucleatum; dipeptide; protease

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Periodontal pathogens such as *Porphyromonas gingivalis* are known to induce periodontitis through their biological activities, which produce, for example, cytotoxic metabolic end products, proteases and immunoactive cell components (5, 11, 12). These bacteria are frequently found in periodontal pockets and preferentially utilize proteins and peptides as sources of energy and cell material, as these amino acid com-

pounds are supplied abundantly and continuously from gingival crevicular fluid or inflammatory exudate.

P. gingivalis cells grow efficiently on peptides rather than free amino acids (9, 15, 16, 21, 26). Other periodontal pathogens, including *Prevotella intermedia*, *Prevotella nigrescens* (16, 24) and *Fusobacterium nucleatum* (4, 14), also prefer peptides to free amino acids as growth substrates. In particular, *P.*

gingivalis is reported to degrade the dipeptides L-aspartyl-L-aspartate and Lglutamyl-L-glutamate (22, 23), while *F. nucleatum* is reported to degrade the dipeptides L-cysteinylglycine and L-methionyl-L-methionine (25). However, the sizes and types of peptides utilized as growth substrates by these periodontopathic bacteria are still unknown. Although Wyss (27) showed that aspartame (L-phenylalanyl-L- methylaspartate) can support the growth of *P. gingivalis* in his chemically defined medium lacking phenylalanine, there is little information on simple peptides as growth substrates for periodontal pathogens. Such information may be useful in exploring the metabolic and growth properties of peptide-dependent bacteria and in developing simple chemically defined media for these bacteria.

Therefore, we determined the sizes of peptides preferentially utilized as metabolic substrates by *P. gingivalis*, *P. intermedia*, *P. nigrescens* and *F. nucleatum* using various sizes of poly amino acids consisting of two to approximately 100 molecules of the single amino acids aspartate and glutamate. Using this approach, we have demonstrated that dipeptides can support the growth of these periodontal pathogens.

Materials and methods Bacterial strains and growth conditions

P. gingivalis ATCC 33277 and W83, P. intermedia ATCC 25611, P. nigrescens ATCC 25261, and F. nucleatum ATCC 25586 and ATCC 10953 were used in this study. The bacteria were grown in modified BM medium (23) containing 1% tryptone (Difco, Detroit, MI), 1% proteose peptone (Difco), 0.5% yeast extract (Difco), 0.5% NaCl, 5µg/ml of hemin and 0.5 µg/ml of menadione in 38 mM potassium phosphate buffer (pH 7.0) in an anaerobic chamber (N_2 , 80%; H₂, 10%; CO₂, 10%; NHC-type, Hirasawa Works, Tokyo, Japan) at 37°C. Bacterial purity was regularly confirmed by microscopic examination of gramstained smears and by culturing on blood agar plates containing hemin and menadione.

Utilization of aspartate, glutamate, polyaspartate and polyglutamate by bacterial cells

The bacterial cells were harvested by centrifugation during the logarithmic growth phase (15–18h after inoculation). Unless otherwise indicated, the experiments described below were carried out in another anaerobic chamber (N₂, 90%; H₂, 10%; NH-type, Hirasawa Works). During centrifugation and transportation between the anaerobic chambers, the cells were protected from oxygen exposure in double-sealed centrifuge tubes. The bacterial cells were washed twice with 25mM potassium

phosphate buffer (pH 7.0) containing 50 mM NaCl plus 5mM MgCl₂ and suspended in the same buffer (2.0-2.2mg dry weight/ml). The cell suspension (1.5 ml) was incubated at 37°C for 10min and then mixed with 1.5 ml of prewarmed aspartate, glutamate, polyaspartate or polyglutamate solution. The polyaspartates used in this study were aspartylaspartate, tri-aspartate, tetraaspartate, hexa-aspartate and (Asp)₁₀₀ consisting of approximately 100 aspartates. Polyglutamates were glutamylglutamate (Glu)₅₋₁₀ consisting of approximately 5–10 glutamates and $(Glu)_{10-20}$ consisting of approximately 10-20 glutamates. The final concentration of each substrate in the reaction mixture was approximately 10 mM when converted to free amino acids. At 0 and 60 min after addition of substrates, the cell suspension was sampled, mixed with perchloric acid at a final concentration of 6% and stored at 4°C for the analysis of carboxylic acids and ammonia.

Assay of metabolic end products

Carboxylic acids, including formic, acetic, propionic, lactic, malic, succinic, butyric, isobutyric, valeric and isovaleric acids, were analyzed using a carboxylic acid analyzer (model S-3000X, Tokyo Rikakikai, Tokyo, Japan), as described previously (20, 21). Ammonia



Fig. 1. Ammonia production from free amino acids and peptides by resting cells of *P. gingivalis*, *P. intermedia*, *P. nigrescens* and *F. nucleatum*. (**A**) aspartate (Asp) and polyaspartate (Asp_n) utilization by *P. gingivalis*; (**B**) glutamate (Glu) and polyglutamate (Glu_n) utilization by *P. gingivalis*; (**C**) aspartate (Asp) and polyglutamate (Glu_n) utilization by *P. intermedia and P. nigrescens*; (**D**) glutamate (Glu) and polyglutamate (Glu_n) utilization by *F. nucleatum*; Asp_n, polyaspartate consisting of *n* aspartates; Glu_n, polyglutamate consisting of *n* glutamates. Data are given as means with standard deviations obtained from three independent experiments. Little ammonia production (>0.1 mM) was observed in the absence of free amino acids or peptides.

was assayed enzymatically using glutamate dehydrogenase (1).

Bacterial growth response to aspartate, glutamate, aspartylaspartate and glutamylglutamate

BM media whose concentrations of tryptone and proteose peptone were decreased to 0.25% were defined as 1/4 BM media. They were aseptically supplemented with 0, 2, 5 or 10mM aspartate or glutamate, or with 0, 1, 2.5 or 5mM aspartylaspartate or glutamylglutamate. Each well of sterile 96-well plastic plates was filled with 200 µl of the supplemented 1/4BM media, and inoculated with the bacterial cell culture (2µl) grown until the logarithmic growth phase, as described above. After anaerobic incubation in the NHC-type chamber at 35°C for 48h, bacterial growth was determined using a microplate reader at 650nm.

Assay of bacterial dipeptidase activity

The bacterial cells were harvested and washed as described above, and suspended in $25 \,\text{mM}$ potassium phosphate buffer (pH7.0) containing $50 \,\text{mM}$ NaCl and $5 \,\text{mM}$ MgCl₂ at an optical density (at $660 \,\text{nm}$) of 1 in the NH-type anaerobic chamber. After preincubation at 35° C for $10 \,\text{min}$, 2ml of cell suspension and 2ml of 2mM L-aspartyl- β -naphtylamide or L-glutamyl-*p*-nitroanilide were mixed and additionally incubated for at 35° C. These mixtures were sampled at 0, 30 and 60 min after incubation. Cellbound dipeptidase activities were esti-

mated as the amount of β -naphtylamine (18) or *p*-nitroaniline (3) released from the substrate.

Part of the cell suspensions was oscillated anaerobically (2A, 190W, 4°C, 6 min) and centrifuged (10000g, 4°C, 10 min) as described previously (24). The resultant cell extracts were assayed for intracellular dipeptidase activities in the NH-type anaerobic chamber. The reaction mixture (2ml) contained cell extracts and 1mM aspartylaspartate or glutamylglutamate in 0.1 M Tris-HCl buffer (pH7.0). After preincubation at 35°C for 10min, the cell extracts were added to start the reaction. Aliquots of the mixture were sampled $(300 \,\mu l)$ periodically and mixed immediately with 30µl of perchloric acid in order to stop the reaction. The amounts of aspartate or glutamate released from aspartylaspartate or glutamylglutamate were quantified enzymatically (7, 10).

Chemicals and enzyme preparations

Polyaspartates, polyglutamates and aspartyl- β -naphtylamide were purchased from Sigma Chemical Co., St. Louis, MO. Enzyme preparations were purchased from Roche Diagnostics, Basel, Switzerland. Glutamyl-*p*-nitroanilide was obtained from Peptide Institute, Inc., Osaka, Japan.

Results and Discussion

P. gingivalis strains utilized aspartylaspartate and glutamylglutamate efficiently and produced significant amounts of ammonia (Fig. 1). *P. inter*- media and P. nigrescens strains utilized aspartylaspartate, while F. nucleatum glutamylglutamate. strains utilized These results clearly indicate that the periodontal pathogens P. gingivalis, P. intermedia, P. nigrescens and F. nucleatum preferentially utilize dipeptides as metabolic substrates over various other sizes of peptides. After dipeptides, P. gingivalis and P. nigrescens preferentially utilized tetra-aspartate. P. gingivalis also utilized the other peptides slowly. P. intermedia and P. nigrescens did not utilize glutamylglutamate, while F. nucleatum did not utilize aspartylaspartate.

From the dipeptides, P. gingivalis strains produced significant amounts of carboxylic acids in addition to ammonia (Table 1). The acidic end products of P. gingivalis from aspartylaspartate and glutamylglutamte were consistent with the results of our previous experiments (22, 23), in which acetate, propionate, succinate and butyrate were mainly produced. As reported previously (2, 24), P. intermedia and P. nigrescens degraded aspartate to formate, acetate, succinate and ammonia, while F. nucleatum metabolized glutamate to acetate, butyrate and ammonia (Fig.1 and Table 1). The end-product profiles of P. intermedia, P. nigrescens and F. nucleatum from dipeptides were similar to those from the corresponding free amino acids, implying that dipeptides can be hydrolyzed to amino acids and subsequently degraded in the same way as the corresponding free amino acids. In contrast to Prevotella and Fusobacterium species, P. gingivalis did not util-

Table 1. End products from dipeptides and/or free amino acids for P. gingivalis, P. intermedia, P. nigrescens and F. nucleatum

Strain	Substrate	Formate	Acetate	Propionate	Malate	Succinate	Butyrate
P. gingivalis ATCC 33277	$\begin{array}{c} Asp_2 \\ Glu_2 \end{array}$	nd nd	$\begin{array}{c} 1.87 \pm 0.27 \\ 0.05 \pm 0.01 \end{array}$	$\begin{array}{c} 0.06 \pm 0.02 \\ 0.34 \pm 0.07 \end{array}$	nd nd	$\begin{array}{c} 0.33 \pm 0.06 \\ 0.01 \pm 0.00 \end{array}$	$\begin{array}{c} 0.81 \pm 0.12 \\ 1.02 \pm 0.24 \end{array}$
P. gingivalis W83	$\begin{array}{c} Asp_2 \\ Glu_2 \end{array}$	nd nd	$\begin{array}{c} 1.23 \pm 0.35 \\ 0.03 \pm 0.01 \end{array}$	$\begin{array}{c} 0.16 \pm 0.02 \\ 0.31 \pm 0.06 \end{array}$	nd nd	$\begin{array}{c} 0.06 \pm 0.01 \\ 0.03 \pm 0.01 \end{array}$	$\begin{array}{c} 0.65 \pm 0.13 \\ 1.61 \pm 0.21 \end{array}$
P. intermedia ATCC 25611	Asp Asp ₂	$\begin{array}{c} 1.20 \pm 0.11 \\ 0.17 \pm 0.02 \end{array}$	$\begin{array}{c} 2.23 \pm 0.26 \\ 0.36 \pm 0.01 \end{array}$	nd nd	$\begin{array}{c} 0.13 \pm 0.01 \\ 0.01 \pm 0.00 \end{array}$	$\begin{array}{c} 3.26 \pm 0.46 \\ 0.54 \pm 0.03 \end{array}$	nd nd
P. nigrescens ATCC 25261	Asp Asp ₂	$\begin{array}{c} 0.17 \pm 0.01 \\ 1.43 \pm 0.35 \end{array}$	$\begin{array}{c} 0.89 \pm 0.07 \\ 2.78 \pm 0.32 \end{array}$	nd nd	0.02 ± 0.00 0.39 ± 0.02	$\begin{array}{c} 1.63 \pm 0.02 \\ 4.12 \pm 0.21 \end{array}$	nd nd
F. nucleatum ATCC 25586	$\begin{array}{c} Glu\\ Glu_2 \end{array}$	$\begin{array}{c} 0.05 \pm 0.02 \\ 0.04 \pm 0.01 \end{array}$	9.94 ± 0.73 7.34 ± 0.52	nd nd	nd nd	$\begin{array}{c} 0.01 \pm 0.00 \\ 0.01 \pm 0.00 \end{array}$	$\begin{array}{c} 3.99 \pm 0.51 \\ 2.89 \pm 0.81 \end{array}$
F. nucleatum ATCC 10953	$\begin{array}{c} Glu\\ Glu_2 \end{array}$	$\begin{array}{c} 0.04 \pm 0.01 \\ \text{nd} \end{array}$	9.81 ± 1.00 1.92 ± 0.12	nd nd	nd nd	$\begin{array}{c} 0.02 \pm 0.00 \\ nd \end{array}$	$\begin{array}{c} 2.92 \pm 0.35 \\ 0.46 \pm 0.05 \end{array}$

Values are given as the means \pm standard deviations obtained from three independent experiments. Asp, aspartate; Asp₂, aspartylaspartate; Glu, glutamate; Glu₂, glutamylglutamate.

nd, not detected.

Table 2. Intracellular dipeptidase activity of P. gingivalis, P. intermedia, P. nigrescens and F. nucleatum

Strain	Substrate	Activity (U/g of protein)
P. gingivalis ATCC 33277	Asp ₂	41.0±23.9
	Glu ₂	42.2 ± 28.6
P. gingivalis W83	Asp_2	22.8 ± 3.5
	Glu ₂	35.4 ± 12.5
P. intermedia ATCC 25611	Asp ₂	33.5 ± 7.3
P. nigresecns ATCC 25261	Asp_2	68.1 ± 12.1
F. nucleatum ATCC 25586	Glu ₂	36.0 ± 6.5
F. nucleatum ATCC 10953	Glu ₂	24.6 ± 5.2

Values are given as the means \pm standard deviations obtained from three independent experiments.

Asp₂, aspartylaspartate; Glu₂, glutamylglutamate.

ize free amino acids, aspartate or glutamate (Fig. 1).

There are two possible pathways for dipeptide metabolism: (1) transport in the dipeptide form and subsequent intracellular hydrolysis to amino acids, or (2) extacellular hydrolysis to amino acids and subsequent transport of amino acids. In this study, all the tested strains had intracellular dipeptidase activities (Table 2), while none of the strains had cell-bound dipeptidase activity, except *F. nucleatum* ATCC 10953 which had weak aspartate dipeptidase activity (data not shown). In addition, *P. gingivalis* strains did not utilize the free amino acids aspartate and glutamate, and one of the tested strains (*P. nigrescens* ATCC 25261) had a higher metabolic rate for aspartylaspartate than for aspartate (Fig. 1 and Table 1). Together, these results suggest that *P. gingivalis*, *P. intermedia*, *P. nigrescens* and *F. nucleatum* strains incorporate dipeptides via a transport system specific for dipeptides, as do other peptide-utilizing bacteria (13), and subsequently degrade the dipeptides into free amino acids using intracellular dipeptidases.

In addition to a dipeptide transport system, most peptide-utilizing bacteria have been reported to have tripeptide and/or oligopeptide transport systems capable of transporting peptides longer than dipeptides (13). However, P. intermedia and F. nucleatum appeared to have no transport activity for oligopeptides longer than dipeptides. This may depend on the amino acid composition of peptides, but further study is needed to elucidate this. The utilization of tetrapeptides by P. gingivalis and P. nigrescens may suggest that these bacteria have a transport system for tetrapeptides. However, it is also possible that P. gingivalis and P. nigrescens degrade tetrapeptides into dipeptide using extracellular proteases, for example dipeptidyl peptidases (5, 18). The slow metabolism of longer peptides by P. gingivalis also suggests the involvement of extracelular proteases in the hydrolysis of the peptides into dipeptides.

Dipeptides supported the growth of



Fig. 2. Growth response to free amino acids and dipeptides of *P. gingivalis*, *P. intermedia*, *P. nigrescens* and *F. nucleatum*. (A) Growth of *P. gingivalis* ATCC 33277 (circle) and W83 (square) in the presence of aspartylaspartate (open symbol) and glutamylglutamate (closed symbol); (B) growth of *P. intermedia* ATCC 25611 (circle) and *P. nigrescens* ATCC 25261 (square) in the presence of aspartate (open symbol) and aspartylaspartate (closed symbol); (C) growth of *F. nucleatum* ATCC 25586 (circle) and ATCC 10953 (square) in the presence of glutamate (open symbol) and glutamylglutamate (closed symbol). *Significantly different from controls (P < 0.05 by Dunnett test). The substrate concentrations in parentheses are for aspartate or glutamate. Data are given as means with standard deviations obtained from three independent experiments.

all the tested strains of P. gingivalis, P. intermedia, P. nigrescens and F. nucleatum in a concentration-dependent manner up to 5mM (Fig. 2), indicating that dipeptides can be utilized as a source of energy and cell growth material. P. intermedia, P. nigrescens and F. nucleatum also increased their growth in the presence of the corresponding free amino acids (Fig.2), while aspartate and glutamate had no effect on the growth of P. gingivalis. Wyss (28) reported that some strains of P. gingivalis grew in his chemically defined medium consisting of free amino acids as nitrogen sources, although these bacteria required fetal calf serum for maximum growth. This discrepancy may be a result of differences in bacterial strains and bacterial growth conditions.

The growth response of *P. gingivalis* ATCC 33277 was greater than that of strain W83 (Fig.2A), although the resting cells of these two strains had similar ammonia production (Fig.1A). This may be a result of bacterial strain-dependent differences in energy efficiency and/or phenotypic characteristics such as nutrition requirements.

The periodontal pathogens tested in this study can grow on aspartate, glutamate and/or dipeptides of these amino acids. Both aspartate and glutamate are among the major amino acids contained in saliva (19), gingival crevicular fluid (19) and dental plaque fluid (6, 8, 17). It is possible that P. intermedia, P. nigrescens and F. nucleatum adapt to the oral environment where such amino acids are continuously and abundantly supplied. These oral fluids also contain various proteins and glycoproteins such as albumin and mucin, which contain aspartate and glutamate. P. gingivalis, P. intermedia and P. nigrescens may generate aspartate- and/or glutamate-containing dipeptides from these proteins and glycoproteins by proteolytic activity (5, 18), and supply these peptides to both themselves and other dipeptide-utilizing but nonproteolytic bacteria such as F. nucleatum and Peptostreptococcus micros (25).

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