Interaction of Porphyromonas gingivalis, which is a predominant periodontal pathogen, with early plaque-forming bacteria plays an important role with respect to colonization in periodontal pockets (4, 12, 13). P. gingivalis interacts with a variety of other oral gram-positive bacteria, including Actinomyces naeslundii (16), Streptococcus gordonii (5), Streptococcus oralis (7), and Streptococcus sanguinis (14); these intergeneric coaggregations may lead to the initial colonization of P. gingivalis in the oral cavity.

A series of studies demonstrated that P. gingivalis 381 strongly coaggregated with S. oralis ATCC 9811; moreover, its fimbriae were primarily responsible for the interaction, in which several domains of the carboxy terminus of fimbrillin participated (1). A recent paper regarding coadhesin of S. oralis by Maeda et al. (6) revealed that glyceraldehyde-3-phosphate dehydrogenase (GAPDH) of group A streptococci binds to S. oralis, which several domains of the carboxy terminus of fimbrillin (11) found that the GAPDH of group A streptococci binds to fibronectin, lysozyme, and the cytoskeletal proteins myosin and actin; they noted that it may function in the colonization of those bacteria. In the present study, kinetic interaction of GAPDH of S. oralis ATCC 9811 with P. gingivalis 381 fimbriae was analyzed based on surface plasmon resonance spectroscopy with a biomolecular interaction analysis system (BIAcore). S. oralis ATCC 9811 was maintained as frozen stocks and was cultured in brain heart infusion broth (BBL Microbiology Systems, Cockeysville, Md.) for 15 h at 35°C in air. Bacterial cells were harvested by centrifugation (High Speed Refrigerated Centrifuge SRX-201; Tomy Seiko Co. Ltd., Tokyo, Japan) at 5,000 × g for 30 min at 4°C; they were subsequently washed three times with 20 mM phosphate buffer supplemented with 0.15 M NaCl (phosphate-buffered saline [PBS] [pH 6.0]) and were suspended in the same buffer.

S. oralis ATCC 9811 GAPDH was purified by mild ultrasonication, 3-[(3-cholamidopropyl)-dimethylammonio]-1-propanesulfonate treatment, ammonium sulfate precipitation, and chromatography with an affinity column coupled with P. gingivalis recombinant fimbrillin (rFimA) as reported previously (6). P. gingivalis 381 rFimA and S. oralis ATCC 9811 recombinant GAPDH (rGAPDH) were prepared in accordance with the methods previously reported (6, 8). Interactions between P. gingivalis rFimA and native and recombinant S. oralis GAPDH were analyzed with a BIAcore 2000 apparatus (Uppsala, Sweden). The carboxymethylated dextran matrix on the CM5 sensor chip (BIAcore) was activated with N-hydroxysuccinimide and N-ethyl-N’-[3-dimethylamino]-propyl]-carbodiimide hydrochloride (1:1) at a flow rate of 5 μl/min at 37°C. Native GAPDH or rGAPDH (20 μg/ml) in 10 mM sodium acetate buffer (pH 4.8) was immobilized on the matrix, because they were immobilized most on the matrix at pH 4.8 among tested pHs. Although the effect of the pH on the protein conformation was not determined in this study, we confirmed that the coaggregation activity between P. gingivalis and S. oralis was almost the same at pH 4.8 as it was at pH 6.0. To equalize the amount (in moles) of the immobilized proteins, the increase in resonance units (RU) produced by immobilization was manually set at 650× (molecular mass of immobilized protein [40 kDa]/molecular mass of fimbrillin [41 kDa]) RU according to the manufacturer’s manual. Excess active sites of the matrix were blocked with 1 M ethanolamine-HCl and washed with 10 mM NaOH. All materials were dissolved in 10 mM PBS (pH 6.0), which also served as a running buffer in the experiments. P. gingivalis rFimA was injected across the active CM5 (GAPDH) and an empty control CM5 surface at a flow rate of 20 μl/min at 37°C. Binding of rFimA was monitored and presented as RU in a sensorgram. One-thousand RU corresponded to a change in the surface concentration of 1 ng/mm² on the sensor chip. At the end of each run the surface was regenerated by successive injections of 10 mM NaOH.
binding profiles of rFimA to the immobilized GAPDH were obtained following subtraction of the response signal from the control surface. Analysis of these kinetic parameters was conducted with BIAevaluation 3.1, a software package (BIAcore), according to the operator’s manual. Protein concentration of the samples was determined with a bicinchoninic acid protein assay kit (Pierce, Rockford, Ill.) utilizing bovine serum albumin as a standard.

The association rate constants (k_{ass}), dissociation rate constants (k_{diss}), and equilibrium association constants (K_{a} = k_{ass}/k_{diss}) of native GAPDH and rGAPDH of S. oralis ATCC 9811 for binding of P. gingivalis rFimA are summarized in Table 1. The representative sensorgrams exhibited in Fig. 1 revealed that the resonance response reflecting P. gingivalis rFimA–S. oralis native GAPDH or rGAPDH interaction occurred in an analyte concentration-dependent manner. S. oralis native GAPDH and rGAPDH were characterized by significantly high k_{ass} values (2.65 \times 10^{4} M^{-1} s^{-1} and 7.41 \times 10^{4} M^{-1} s^{-1}, respectively), which indicated rapid association with rFimA. At the dissociation phase, S. oralis native GAPDH and rGAPDH k_{diss} values were 6.11 \times 10^{-4} M s^{-1} and 1.10 \times 10^{-3} M s^{-1}, respectively, which were representative of high stabilities. Total affinities were presented as K_{a}. K_{a} values of native GAPDH and rGAPDH with rFimA (4.34 \times 10^{-7} M and 6.75 \times 10^{-7} M^{-1}, respectively) demonstrated high affinity.

K_{a} values of many antibody-protein antigen interactions occur within the range 10^{6} to 10^{10} M^{-1} (3). In this study, K_{a} values for P. gingivalis rFimA and S. oralis native GAPDH and rGAPDH were 4.34 \times 10^{7} M^{-1} and 6.75 \times 10^{7} M^{-1}, respectively, which indicated that these interactions were specific. P. gingivalis fimbiae reportedly bind to a variety of components, such as epithelial cells, fibroblasts, components of saliva, and several extracellular matrix proteins (2). Nakamura et al. (9) documented the following K_{a} values between P. gingivalis fimbiae and extracellular matrix proteins: 2.15 \times 10^{6} M^{-1} (laminin), 2.16 \times 10^{6} M^{-1} (fibronectin), 2.26 \times 10^{6} M^{-1} (thrombospondin), 2.76 \times 10^{6} M^{-1} (type I collagen), 3.08 \times 10^{6} M^{-1} (elastin), and 3.79 \times 10^{6} M^{-1} (vitronectin). In addition, Amano (2) reported K_{a} values between P. gingivalis fimbiae and acidic proline-rich protein, basic proline-rich glycoprotein, statherin, fibrinogen, and hemoglobin of 1.63 \times 10^{6} M^{-1}, 1.62 \times 10^{6} M^{-1}, 1.48 \times 10^{6} M^{-1}, 2.16 \times 10^{6} M^{-1}, and 2.43 \times 10^{6} M^{-1}, respectively. The K_{a} value obtained in the present experiment was higher than those of the aforementioned interactions. Consequently, the interaction of P. gingivalis fimbiae with S. oralis GAPDH is considered fairly strong.

Streptococci and actinomyces are believed to be the major initial colonizers of the pellicle on the tooth surface; furthermore, interactions between these bacteria and their substrata aid the establishment of the early biofilm community (4). Nyvad and Kilian (10) reported that S. oralis, S. sanguinis, and S. mitis represent 60 to 90% of cultivable streptococci within the first 4 h of plaque formation. In the present study, S. oralis ATCC 9811 GAPDH demonstrated high affinity with P. gingivalis fimbiae. Extensive reports have shown that the binding interaction of P. gingivalis and streptococci is multimodal; however, considering the conservation of streptococcal GAPDHs (6) and the high affinity of S. oralis GAPDH binding to P. gingivalis fimbiae, early plaque-forming streptococcal GAPDHs may contribute to P. gingivalis colonization in periodontal pockets.

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### Table 1. Kinetic parameters for P. gingivalis rFimA binding to immobilized S. oralis native GAPDH and rGAPDH

<table>
<thead>
<tr>
<th>Ligand</th>
<th>k_{ass} (M^{-1}s^{-1})</th>
<th>k_{diss} (s^{-1})</th>
<th>K_{a} (M^{-1})</th>
</tr>
</thead>
<tbody>
<tr>
<td>S. oralis native GAPDH</td>
<td>2.65 \times 10^{4}</td>
<td>6.11 \times 10^{-4}</td>
<td>4.34 \times 10^{7}</td>
</tr>
<tr>
<td>S. oralis rGAPDH</td>
<td>7.41 \times 10^{4}</td>
<td>1.10 \times 10^{-3}</td>
<td>6.75 \times 10^{7}</td>
</tr>
</tbody>
</table>

a P. gingivalis rFimA was the analyte in each case.

![FIG. 1. Sensorgrams of P. gingivalis rFimA binding to immobilized S. oralis native GAPDH, rGAPDH, and bovine serum albumin in kinetic studies. P. gingivalis rFimA solution was injected over S. oralis native GAPDH, rGAPDH, or bovine serum albumin (BSA) on the sensor chip at various concentrations (0.05 to 0.4 \muM).](http://iai.asm.org/)
REFERENCES