Characterization of the *Porphyromonas gingivalis* Type IX Secretion Trans-Envelope PorKLMNP Core Complex*

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ABSTRACT

The transport of proteins at the cell surface of *Bacteriodetes* depends on a secretory apparatus known as Type IX secretion system (T9SS). This machine is responsible for the cell surface exposition of various proteins such as adhesins required for gliding motility in *Flavobacteria*, S-layer components in *Tannerella forsythia* and tooth tissue-degrading enzymes in the oral pathogen *Porphyromonas gingivalis*. While a number of subunits of the T9SS have been identified, we lack details on the architecture of this secretion apparatus. Here we provide evidence that five of the genes encoding the core complex of the T9SS are co-transcribed, and that the gene products are distributed in the cell envelope. Protein-protein interaction studies then revealed that these proteins oligomerize and interact through a dense network of contacts.

Porphyromonas gingivalis is the causative agent of gingivitis and periodontal diseases that are responsible for teeth loss (1, 2). It causes severe lesions in periodontal tissues such as the gingiva or the alveolar bone and yields to the disruption of the tooth-supporting structure (3). Periodontitis are considered a major public health concern as it affects ~ 35 % of the population. Tissue alterations and damages are mainly induced by a cocktail of toxin proteins secreted by the bacterium, the gingipains (4). Gingipains act as adhesins or proteases that help the bacterium to adhere to periodontal tissues and to promote gingival tissue invasion by the degradation of matrix proteins, fibrinogen and collagen (5, 6). The secretion of these proteins is a two-step mechanism: gingipains carry a N-terminal signal peptide and are first addressed to the periplasm by the Sec pathway before being transported to the cell surface or to the cell exterior (7). However, the machinery responsible for the translocation of gingipains through the outer membrane remained unknown as genes encoding a potential Type II secretion system (T2SS), the major two-step