

Short communication

Influence of mouse prolactin-inducible protein in saliva on the aggregation of oral bacteria

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Introduction: Mouse prolactin-inducible protein (mPIP) is secreted in mouse saliva and has been found to bind oral bacteria, showing the highest affinity for streptococci. Comparisons between the oral flora of mPIP knockout mice and their wild-type controls showed differences in the genera colonizing the two groups of mice. These findings suggested a role for mPIP in the colonization of the mouse oral cavity, possibly modulating the oral flora. In this *in vitro* study, we focused on the contribution of this protein to aggregation of oral bacteria, a process thought to promote the clearance of bacteria from the oral cavity, and one that could influence the composition of the oral bacterial community.

Methods: The aggregation of selected human and mouse oral streptococci was measured spectrophotometrically. The aggregation of oral bacteria by saliva from mPIP knockout mice, which lack mPIP, was compared with that of saliva from wild-type mice.

Results: Both wild-type saliva and mPIP knockout mouse saliva induced aggregation of human strain *Streptococcus gordonii* SK120 and mouse streptococci strains M105/6 and M106/2. Bacterial aggregation induced by the saliva of wild-type mice was significantly higher than the aggregation induced by saliva from mPIP knockout mice for all the bacterial strains.

Conclusion: In this study it was confirmed that mPIP plays a role in the aggregation of oral bacteria. The salivary components promoting aggregation of oral bacteria are considered to be part of the oral defense mechanisms so these findings provide insight into a possible function of mPIP in host defense by promoting aggregation of oral bacteria.

Key words: aggregation; bacteria; GCDPF-15; knockout mice; prolactin-inducible protein; saliva; streptococci

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The mouse prolactin-inducible protein/mouse submaxillary gland protein (mPIP/mSMGP) is the murine homologue of human prolactin-inducible protein/gross cystic disease fluid protein-15 (PIP/GCDFP-15), an established marker for both malignant and benign pathological conditions of the human breast. As with human PIP, mPIP messenger RNA is also abundant in the submaxillary gland (24, 30), its expression being limited to the lacrimal and major salivary glands of the

mouse (17, 24–26). Murine PIP was found in mouse lacrimal, submaxillary, and parotid glands and was localized as a diffuse cytoplasmic immunohistochemical staining of serous acinar cells of both lacrimal and submaxillary glands of the mouse (25). In addition, secreted mPIP has been identified in mouse saliva and tears (5, 16, 25).

While a function for human PIP has not yet been defined, several findings suggest a potential role for this protein in immunomodulation and host defense mecha-

nisms (6, 8, 13). It was also proposed that as a CD4-binding factor (1, 2, 10), PIP may provide protection from infection with human immunodeficiency virus (HIV) by interfering with the HIV envelope/CD4 binding (3). Human PIP has also been shown to possess aspartyl protease activity, specifically degrading fibronectin (7). In addition, human PIP was found to bind to several human oral and non-oral bacterial species, including oral streptococci (28, 29).

As with its human counterpart, the exact functions of mPIP are not known. Through *in vitro* studies, we demonstrated that mPIP binds to several strains of both human and mouse oral bacteria, showing the highest affinity for the genus *Streptococcus* (16). Although the consequences of this binding are not known, we suggest that mPIP might modulate the resident oral flora of mice (16). We further demonstrated both quantitative and qualitative differences between the oral flora of mPIP knockout mice that lack mPIP and that of wild-type mice (25).

Salivary components may impact on bacterial colonization of the oral cavity by interacting with oral bacteria in different ways, including binding to microorganisms, resulting in their aggregation and facilitating their clearance from the oral cavity; serving as receptors for microbial adhesion to host surfaces; possessing antibacterial activity; or serving as microbial nutritional substrates (27). Bacterial aggregation is a process thought to promote the clearance of microorganisms from the oral cavity (22) and salivary components that promote this phenomenon are considered components of oral defense systems (9).

The aim of the present study was to further investigate the interaction between mPIP and oral bacteria; specifically, to determine whether mPIP plays a role in the aggregation of oral bacteria and thereby playing a role in non-immune host defense.

Materials and methods

Knockout mice lacking mPIP (mPIP^{-/-}) were generated by gene targeting through homologous recombination (5, 25). The mPIP null mutation was generated by excluding exon 2 from the construct and replacing it with a PGK-neo cassette. Negative selection was carried out through use of a diphtheria toxin A cassette (PGK-DTA) inserted on the 3' end of the construct. The 13.1-kb linearized PIP targeting vector was outsourced to the Gene Targeting & Transgenic Facility, University of Connecticut Health Center, Farmington, CT, for the generation of the knockout mice. Briefly, the targeting vector was electroporated into 129/Svj embryonic stem cells. Embryonic stem cells generated from three confirmed mPIP-targeted clones were injected into 3-day-old C57BL/6 blastocysts, which were implanted into pseudo-pregnant female recipients. Mice positive for the mPIP null gene in the germline were shipped to the

University of Manitoba Central Animal Care Facility where they were backcrossed into a CD1 genetic background.

Saliva was collected from both wild-type and mPIP knockout adult mice as previously described (16, 25). Western blot analysis was used to confirm the absence of mPIP in saliva collected from mPIP knockout mice (5, 25).

Human *Streptococcus gordonii* SK120 strain isolated from the human oral cavity (12) was generously donated by Dr Mogens Kilian (University of Aarhus, Denmark). Streptococcal strains M105/6 and M106/2 were isolated from the mouse oral cavity and characterized by us (25). Bacteria were cultured for 16–24 h in a candle jar on blood agar plates (Blood agar base no. 2; Oxoid, Hampshire, UK), supplemented with 1% laked horse blood (Oxoid). Colonies were used to inoculate 40 ml Todd-Hewitt broth; they were grown for 16 h in a candle jar and harvested by centrifugation at 10,000 g for 10 min.

Bacterial pellets were washed twice and resuspended in phosphate-buffered saline (PBS) to an optical density at 700 nm (OD₇₀₀) of 1 (± 0.02). Bacterial aggregation was measured using a modification of the method of Ericson et al. (9). The aggregation reactions were made by mixing bacterial suspensions with 100–200 µl pooled mouse saliva collected from either mPIP^{-/-} or wild-type (WT) mice to a final volume of 1 ml. The PBS was used as a control for autoaggregation. The reaction mixtures were placed into cuvettes and incubated at room temperature without further mixing. The OD₇₀₀ of the mixtures was measured with a spectrophotometer at set time intervals (10–20 min) for a maximum of 2 h. A decrease in the OD₇₀₀ of the mixture, accompanied by the visualization of macroscopic aggregates floating or settled at the bottom of the cuvettes at the end of the 2-h period, was considered positive for saliva-induced aggregation.

Bacterial aggregation was recorded as a decrease of the OD₇₀₀ of the mixture of bacterial suspension and mouse saliva, expressed as percentage of the optical density of the original mixture. The values determined at each time-point were plotted against time on an *xy* graph, the starting point representing time 0 and 100% optical density. For each experiment, aggregation assays were set up in duplicate and the data obtained from each set of duplicates were averaged. The level of aggregation induced by saliva derived from WT mice was compared with that of mPIP^{-/-} mouse saliva.

Results

Both WT and mPIP^{-/-} mouse saliva were able to aggregate the bacterial strains tested. No autoaggregation was detected in the controls where PBS was used instead of saliva. After 2 h of incubation of bacteria with mouse saliva the level of aggregation induced by the WT mouse saliva was higher than that induced by mPIP^{-/-} mouse saliva, a finding that was consistent for both human strain SK120 and mouse strains M105/6 and M106/2 (Fig. 1).

Among the three strains, the mean difference in OD₇₀₀ between the WT and the PBS control was 25.5 ± 2.1, whereas the mean difference in OD₇₀₀ between the mPIP^{-/-} and the PBS control was 13.3 ± 0.7 (two-tailed *P* < 0.01, Student's unpaired *t*-test).

Discussion

Considered to be a process that promotes the clearance of bacteria from the oral cavity (22), bacterial aggregation has been widely studied and different assays have been developed to determine the aggregation of oral bacteria by human saliva (15). In addition to aggregation of bacteria by human whole saliva, the effect of different components of human saliva on the aggregation of oral bacteria has also been explored (4, 18, 19, 31). However, less is known about the effects of the saliva of other species that are often used in laboratory animal models, such as mice, on bacterial aggregation.

Strains of *Streptococcus* were used in this study because *Streptococcus* species are among the commonest bacteria in the mouth and comprise a significant component of human dental plaque (23). Human *S. gordonii* (SK120) was selected as a positive control when testing mouse saliva for aggregation because it has been shown to bind human PIP (our unpublished data). Also, bacterial aggregation can be strongly strain-dependent (14) and human saliva has been shown to aggregate this strain (20). Mouse streptococci strains M105/6 and M106/2 were randomly selected from a large number of mouse isolates (25). In this study the two mouse *Streptococcus* strains were only classified to the level of genus and, unfortunately, it was not possible to undertake an extensive examination of their biological and physiological characteristics. Identification of oral streptococci from mice to species level is often difficult because of the lack of taxonomic data for mouse isolates. However, in other

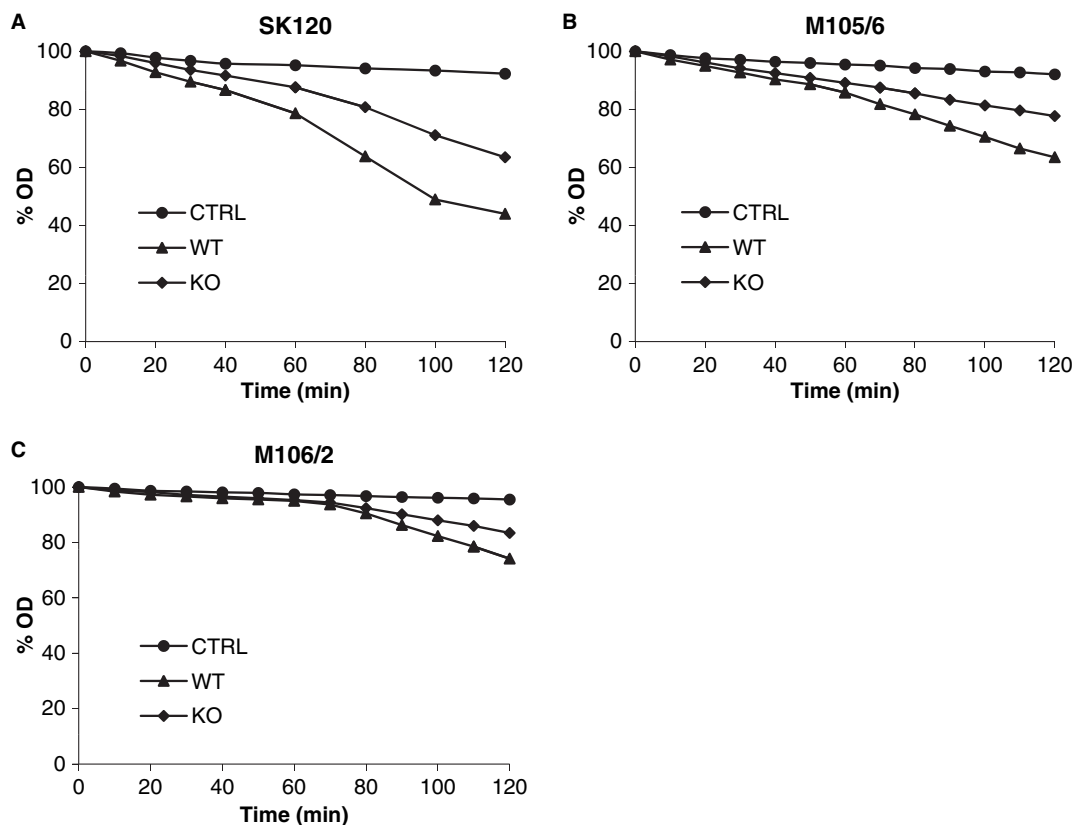


Fig. 1. Bacterial aggregation assays. Saliva from both wild-type (WT) and mPIP^{-/-} (knockout; KO) mice induced aggregation of the human *Streptococcus gordonii* strain SK120 (A) and of mouse oral streptococci strains M105/6 (B) and M106/2 (C). For all three strains, WT saliva induced a higher degree of aggregation than mPIP^{-/-} saliva. No autoaggregation was observed in the phosphate-buffered saline controls (CTRL).

studies (16) we have described mouse strains in terms of their close similarity to well-defined human species.

Previous work from our laboratory (16) has demonstrated that mPIP binds to human and mouse oral bacteria with the highest affinity for streptococci. However, the consequences of this interaction were not known. Suggested hypotheses were that mPIP caused or facilitated bacterial aggregation, mediated adhesion to oral tissues, or caused bacterial lysis, playing a role in innate host defense. This is particularly important because the resident oral flora benefits the host by providing protection against colonization by pathogenic organisms (21).

The significant reduction in aggregation of bacteria by saliva from mPIP^{-/-} compared with WT mice may be attributed to the absence of PIP from the saliva of mPIP^{-/-} mice. However, the role of mPIP in the aggregation of bacteria by mouse saliva has not been defined and saliva contains other carbohydrates and proteins that bind to oral streptococci and may also promote aggregation (18–20, 27, 31). Murine PIP could play a direct role or an

ancillary role to these molecules. Our attempts to produce active recombinant mPIP and to isolate the protein from mouse saliva using antibody-affinity columns to confirm the direct involvement of mPIP in the aggregation of oral bacteria were unsuccessful (25). Similarly, difficulties in purifying human PIP from body fluids were encountered by others, demonstrating that it is a difficult task; this can be attributed to the tendency of PIP to aggregate and form multimers or complexes with other protein species (1, 11). Also, we cannot be sure that the deletion of mPIP in the mouse does not influence the activities or expression of other molecules in mouse saliva that aggregate oral bacteria *in vitro* or *in vivo*. As an example, fibronectin present in human saliva can cause the aggregation of human oral streptococci (30). PIP may degrade fibronectin (7) and consequently influence any fibronectin-based aggregation. However, we can say that independent of a known aggregation mechanism, removal of mPIP from mouse saliva causes a reduction in saliva-induced bacterial aggregation *in vivo*, suggesting that mPIP plays a role

in any process or cascade causing aggregation of mouse oral streptococci by mouse saliva.

In this study we examined the differences between the levels of aggregation induced by mPIP knockout mouse saliva, which lacks mPIP, and wild-type mouse saliva. We demonstrated that mPIP contributes to saliva-induced bacterial aggregation and we suggest that mPIP might play a role in host defense by modulating the resident oral flora by facilitating bacterial aggregation.

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