Human body is covered by microbiome, a structure composed of billions of bacteria. The oral microbiome is the second most diverse one of the human after that found in the gut. Mouth-gut bacterial transmission causes that oral pathogens colonizing the gut are able to influence the host health and participate in systemic inflammatory diseases. In-depth understanding of the factors involved in dysbiosis is crucial for keeping homeostasis, preventing and treating diseases. Some bacteria, such as oral or gut pathogens, must acquire heme from host environment, which serves as nutritional and virulence factor. Our previous work has resulted in extensive biochemical and functional characterization of one of the major *Porphyromonas gingivalis* heme uptake systems, and enabled us to understand the mechanism of heme acquisition, with the leading role played by the HmuY hemophore-like protein. We characterized this protein, as well similar proteins from other oral pathogens, *Prevotella intermedia* and *Tannerella forsythia*, which are responsible for periodontitis. Importantly, synergistic interactions in heme acquisition between *P. gingivalis* HmuY and its homologs, expressed not only by cohabitating oral pathogens, but also by gut bacteria represented by *Bacteroides fragilis*, may provide *P. gingivalis* with heme, enabling playing its key pathogen role. This project proposes logical continuation of our molecular structure-function studies on this novel family of hemophore-like proteins using a variety of sophisticated methods and techniques. Data gained in this study should clarify the importance of HmuY proteins in the context of Bacteroidetes survival in regard to their ability to cause dysbiosis in microbiome of the oral cavity and intestine, resulting in systemic inflammatory diseases, such as periodontitis or inflammatory bowel disease.