

ABSTRACT

Diabetes mellitus affects > 171 million people worldwide. Unfortunately, despite conventional medical treatment, some diabetic patients do not reach desirable metabolic control. In addition, there are multiple secondary complications of both type 1 (T1D) and type 2 (T2D) diabetes, including kidney damage, nerve damage, cardiovascular disease and other systemic inflammatory conditions like periodontal disease. Numerous studies have shown a correlation between chronic inflammatory periodontal diseases and diabetes, in which both diseases influence the progression and response to treatment of the other. Importantly, many diabetic patients with periodontal disease do not respond well to traditional periodontal treatment, although the mechanism of why is poorly understood.

Although very few differences in the sub-gingival microflora responsible for periodontal disease are found between diabetic and non-diabetic patients with periodontal disease, pathogens do respond to environmental stimuli within the host during infection resulting in the regulation of gene expression to optimize their survival. These genes induced during host infection (*in vivo* growth conditions) may contribute to the overall pathogenicity of these organisms. Although it has been demonstrated that the micro-environment provided by a diabetic host greatly differs from that of a normoglycemic host, investigation into the effect this environment has on *in vivo* induced antigens of oral pathogens has not been explored. Therefore, we hypothesize that *in vivo* induced antigens of pathogenic oral bacteria differ in a diabetic patient population with periodontal disease compared to the normoglycemic patient population with periodontal disease.

It is the goal of this study to utilize *in vivo* induced antigen technology (IVIAT) to determine if the micro-environment induced in a diabetic patient with periodontal disease affects the *in vivo* induced antigens of *Porphyromonas gingivalis* and/or *Aggregatibacter actinomycetemcomitans*, two well characterized oral pathogens known to contribute to disease progression. Defining important virulence properties of these organisms under this secondary disease condition of diabetes, may lead to better treatment of this difficult to treat patient population.