

Oral Microbiome and Type 2 Diabetes Mellitus: The Enigmatic Reciprocal Relationship

Amr TM Saeb*

Genetics and Biotechnology Department, Strategic Center for Diabetes Research, College of medicine, King Saud University, KSA

***Corresponding Author:** Amr TM Saeb, Genetics and Biotechnology Department, Strategic Center for Diabetes Research, College of medicine, King Saud University, KSA.

Received: September 13, 2018; **Published:** September 20, 2018

Type 2 diabetes (T2D) is the leading cause of morbidity and mortality all over the world. It's incidence that has increased by 50% during the past 10 years. This disease has a long history that made it one of the world's oldest diseases. It was described in the historical records of ancient Egypt, Persia, and India. T2D consists of a series of impairments that lead to hyperglycemia and resulting from the combination of resistance to insulin action, insufficient insulin secretion, and undue or inapt glucagon secretion.

On the other hand, the human body encompasses ten folds of the microbial cells more than human cells. Thus, we must look at our microbiome as an ecological community in which the microorganisms literally share (our body) space and interact in commensal, symbiotic and pathogenic manners with each other and with their host. Moreover, the human body contains diverse ecosystems that can differ in temperature, pH, moisture, oxygen, nutrients availability, UV light and/or Substrate that can lead to an ever-changing microbiome. For instance, the human oral cavity contains around 600 taxa with different nature and functions.

The human microbiome has been implicated with several non-infectious diseases, such as pancreatic cancer, inflammatory bowel diseases, depression and anxiety, Obesity and diabetes. The relationship between diabetes, oral health and microbiome represent a reciprocal enigmatic relationship. This reciprocal relationship exhibits an illustration of systemic disease predisposing to oral infection, and when that infection occurs, the oral infection intensifies the progression of systemic disease (Figure 1).

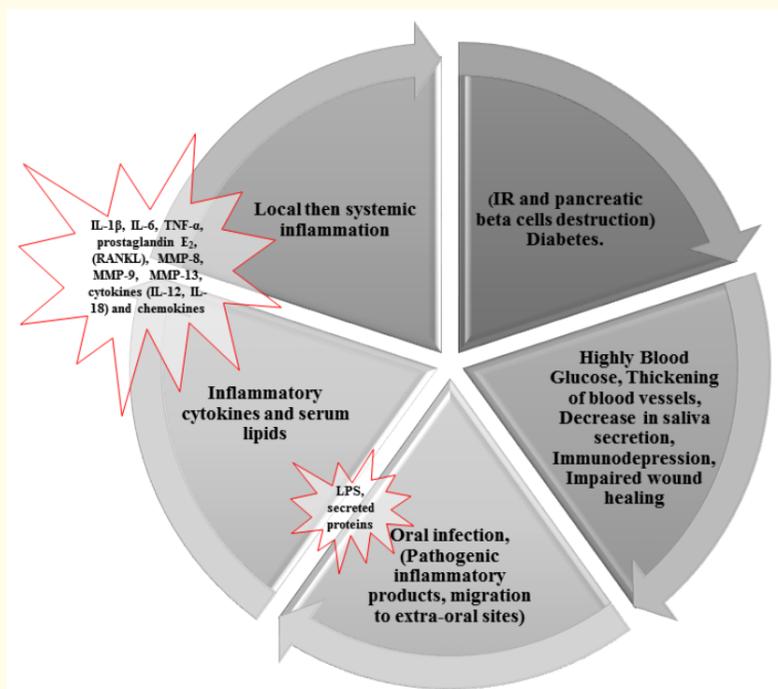


Figure 1: The reciprocal relationship between diabetes and oral infection/health.

There is no doubt that the oral cavity presents a permanent source of infectious agents, and its state often mirrors the progression of systemic pathologies. The Oral bacteria can migrate to extra-oral sites, causing infection and inflammation. It has been suggested that the oral microbiome also plays a role in systemic health through pathogen inhibition, immune regulation, nutrition absorption, and metabolism. The studies that investigated the relationships between the oral microbiota and diabetes are in scarce. However, it was found that retrieval of numerous periodontal pathogens was comparable in both diabetic and non-diabetic participants, but significantly more individuals with diabetes contained *P. gingivalis*. Moreover, it was shown that there are probably elusive modifications in the microbial composition of the subgingival biofilm between diabetic subjects with diabetes and those non-diabetics, but the without clear clinical relevance. The differences may occur from the effect of diabetes in changing the environmental conditions, such as glucose concentration, acidity, and moisture, within the periodontal pocket, that may favor the growth of certain bacterial species on the expense of others.

While, the infectobesity concept suggests that the gut microbiota of obese individuals may be more efficient at extracting energy from a given diet than that of lean individuals, and gut microorganisms can affect host metabolism, influencing inflammation and insulin resistance, the role of swallowed oral bacteria in contributing to these effects has yet to be established. However, the oral microbiome plays an important role in the preservation of a healthy oral environment and in the progression of oral diseases. In addition, the oral microbiome may be important in chronic diseases such as diabetes through direct metabolism of chemical carcinogens and through systemic inflammatory effects.

Most recently, we conducted a study that aimed to compare the microbial diversity and population structure of oral microbiome among normoglycemic, impaired glucose tolerance (IGT) and diabetic subjects. We observed a clear reduction in the biological and phylogenetic diversity in the diabetic and pre-diabetic oral microbiome in comparison with the normoglycemic oral microbiome. However, this reduction was associated with an increase in the pathogenic content of the hyperglycemic microbiomes. The increase of the pathogenic contains in the oral microbiome both pre-diabetic and diabetic group, accompanied by our future pathogenomics, i.e. pathogenicity and virulence factors determinant, may aid to better understanding for the directionality of the enigmatic reciprocal relationship.

Volume 2 Issue 1 Octobert 2018

©All rights reserved by Amr TM Saeb.