Periodontal disease is one of the most prevalent diseases of the dentition and is responsible for most of the teeth lost by adults. It has been known for some time to be associated with oral microorganisms.

The microbial population of the oral cavity is one of the most complex of the human body, comprising over 300 species. Some of these grow in vitro with difficulty or not at all.

Until recently, the lack of suitable culture techniques coupled with gaps in our knowledge of the taxonomy of the oral microbiota gave the erroneous impression that the composition of the microbiota in periodontally healthy patients was identical to that of patients with periodontal disease. Periodontal disease was believed to be the result of an increased mass of bacteria rather than qualitative differences in the composition of the microbiota.

Already in the early 1960s, as a postdoctoral student at the Harvard School of Dental Medicine, I had noted that electron microscopic observations of microorganisms associated with periodontal disease, notably necrotizing ulcerative gingivitis ("trench mouth").

A total of 53 extracted teeth were categorized according to their periodontal status. They were carefully processed for transmission electron microscopy, so as to maintain the integrity of the adherent microbial plaque and permit its examination at different levels of the clinical crown. The results revealed distinct qualitative differences in the microbiota of different disease states and between supra- and subgingival microbial populations. They also indicated that certain microbiotas are compatible with periodontal health. [The SCI® indicates that this paper has been cited in over 145 publications.]

Max A. Listgarten
Department of Periodontology
School of Dental Medicine
University of Pennsylvania
Philadelphia, PA 19104

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