Rapid Response Characterization of New and Manipulated Tobacco Products
Exploring Tobacco Microbial Constituents and the Oral Microbiome of Tobacco Users (Project 3)
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Abstract:

Novel research is needed to improve our understanding of the microbial constituents of tobacco products, and their associated adverse health effects. Research conducted over the past 50 years has provided a firm knowledge base regarding the chemical and physical composition of smokeless tobacco products, smoked tobacco products and cigarette smoke. However, there is a paucity of data regarding the microbial constituents of these products and their impacts on public health. A limited number of microorganisms have been characterized in previous studies, due to the use of traditional culture-based methods. Thus, our long-term goal is to harness the power of next-generation sequencing technologies to comprehensively characterize 1) the bacterial flora of a range of conventional, new and manipulated tobacco products and smoke; 2) the influence of specific groups of bacteria on the production of tobacco-specific N-nitrosamines (TSNAs); and 3) the impacts of tobacco bacterial flora on the oral microbiome of tobacco users. The central hypothesis of our proposal is that tobacco products are characterized by bacterial populations that may influence not only the chemical constituents of tobacco products, but also the health of tobacco users. Our rationale for exploring this hypothesis is that, to our knowledge, no studies have comprehensively characterized the microbial diversity of tobacco products and their subsequent public health effects. As a result, there is a critical knowledge gap with regard to 1) the diversity of tobacco microbial constituents; and 2) whether these constituents should be regulated by FDA. Our specific aims address these critical issues: Aim 1: To explore the bacterial microbiome of conventional, new and manipulated smoked and smokeless tobacco products and smoke, and examine the role of specific genera in TSNA production. Aim 2: To provide novel, baseline data on the composition of the oral microbiome and its associated expressed activities in smokers and smokeless tobacco users compared with that of non-users. Aim 3: To characterize the transient changes--bacterial community composition and expressed metabolic activities--in the oral microbiome after single-use of new and manipulated smoked and smokeless tobacco products. The novel science generated in this study is directly relevant to the FSPTCA because it can be used immediately to inform potential new microbial-related tobacco regulations that have never before been considered despite the reality that the microbiology of tobacco has been of interest to the tobacco industry for the past 60 years.