

## **Bacterial communities associated with atherosclerotic plaques from Russian individuals with atherosclerosis**

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### **Abstract**

© 2016 Ziganshina et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited. Atherosclerosis is considered a chronic disease of the arterial wall and is the major cause of severe disease and death among individuals all over the world. Some recent studies have established the presence of bacteria in atherosclerotic plaque samples and suggested their possible contribution to the development of cardiovascular disease. The main objective of this preliminary pilot study was to better understand the bacterial diversity and abundance in human atherosclerotic plaques derived from common carotid arteries of individuals with atherosclerosis (Russian nationwide group) and contribute towards the further identification of a main group of atherosclerotic plaque bacteria by 454 pyrosequencing their 16S ribosomal RNA (16S rRNA) genes. The applied approach enabled the detection of bacterial DNA in all atherosclerotic plaques. We found that distinct members of the order Burkholderiales were present at high levels in all atherosclerotic plaques obtained from patients with atherosclerosis with the genus *Curvibacter* being predominant in all plaque samples. Moreover, unclassified Burkholderiales as well as members of the genera *Propionibacterium* and *Ralstonia* were typically the most significant taxa for all atherosclerotic plaques. Other genera such as *Burkholderia*, *Corynebacterium* and *Sediminibacterium* as well as unclassified Comamonadaceae, Oxalobacteraceae, Rhodospirillaceae, Bradyrhizobiaceae and Burkholderiaceae were always found but at low relative abundances of the total 16S rRNA gene population derived from all samples. Also, we found that some bacteria found in plaque samples correlated with some clinical parameters, including total cholesterol, alanine aminotransferase and fibrinogen levels. Finally, our study indicates that some bacterial agents at least partially may be involved in affecting the development of cardiovascular disease through different mechanisms.

<http://dx.doi.org/10.1371/journal.pone.0164836>

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