Distinct colonic hydrogenotrophic communities between Native Africans and African Americans may relate to differences in colorectal cancer frequency

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Background

African Americans (AA) are highly prone to spontaneous colorectal cancer (CRC) whereas Native Africans (NA) rarely get the disease. Thus, the Western diet is suggested as a risk factor for CRC. Hydrogenotrophic microbial communities inhabiting the colon are proposed as potential carcinogenic inducers or indirect protectors.

Objectives

1. Characterize and compare the structure of methanogenic archaea (MA) and sulphate-reducing bacteria (SRB) communities in NA and AA colonic samples.
2. Compare microbial metabolic pathways in both groups.
3. Study hydrogenotrophic communities dynamics during a diet exchange study.

Methods

qPCR and nested PCR approaches targeting MA and SRB 16S rRNA and functional gene sequences were used. Large scale clone libraries were set up and analyzed with statistical tests (UNIFRAC) comparing both groups.

Results

SRB sequences were abundant in all subjects whereas MA sequences were more abundant in NA individuals (75%) than AA (25%). Sequences were affiliated with Desulfovibrio piger, D. desulfuricans and D. fairfieldensis (SRB) and Methanosphaereae stadtmannae, Methanobrevibacter smithii and Methanosarcina sp. Significantly distinct SRB and MA dominant lineages were observed for each group.

Conclusions and future work

These results are coherent with greater breath methane excretion observed for NA and suggest that diet can influence the composition of hydrogenotrophic microbiota, and that these contrasting communities may differentially impact the colon health. Stool and mucosal samples
from the diet exchange studies have been processed and are ready for further analysis. DNA samples will be investigated by a metagenomic approach to determine if other microbial metabolic pathways distinguish these groups.