Abstract: **P2251**

**Association between low-grade inflammation, metabolic factors, vascular biomarkers and gut microbiota in different age groups**

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**Topic(s):**
Basic Science - Vascular Biology and Physiology: Leukocytes, Inflammation, Immunity

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**Background.** Despite the growing interest to the theme, the gut microbiota (GM) composition and functional capacity in relation to cardiovascular diseases (CVD) have been poorly studied. It is not well studied in nonagenarians or centenarians who live much longer than others with postponed CVD. In this study, we assessed GM in association with different metabolic factors in healthy middle-aged adults and the elderly at the turn of a hundred years old.

**Purpose.** Our aim was to study GM in a healthy cohort (HC) with different metabolic risk factors and in an extremely elderly cohort (EC) of long lives from our city.

**Methods.** The study included HC of 104 untreated subjects aged from 25-76y (52±13) carefully selected through the exclusion of CVD and other chronic diseases by means of clinical (with different specialists consultations to exclude any factors of inflammation) and a wide range of laboratory evaluation, ECG, treadmill test, ECHOCG, carotid artery ultrasound and the second group of 20 long lives 97-100y (98±1). EC underwent a complex geriatric assessment, also a wide range of laboratory evaluation, ECG, ECHOCG, carotid artery ultrasound. GM composition was studied by the V3-V4 16S rRNA sequencing. Taxonomic units were identified with QIIME 1.9.1. Statistical analysis was done by using the Phyton v.3.2 programming language. Metabolic reconstruction was performed with PICRUSt algorithm. All GM analyzes performed with age, sex and FDR adjustments.

**Results.** One of the most pronounced differences in GM between groups was a significantly higher representation of antiinflammatory Bifidobacterium genus in long lives (p=0.026 (MaAsLin), LDA=4.304). Among risk factors, high body mass index (BMI) was associated with a high abundance of conditional pathogens of Prevotella genus in HC (?<0.002, GLM) and also in EC (p=0.013, MaAsLin). BMI was correlated with hs-CRP level in EC (p=0.04, rs = 0.634). Median hsCRP in EC was 2.4mg/l(Q3-Q1=5.58), 2.45mg/l(Q3-Q1=2.03) (no significant differences, U-test). Despite this, we found that microbiota of long lives had much higher potential to produce butyrate (anti-inflammatory agent, p=0.016 (MaAsLin), LDA=3.345, PICRUSt algorithm). Average intima-media thickness (IMT) in EC was 1.07±0.16mm, and 0.76±0.2mm in HC, the difference was not significant (p=0.37, t-test). We found the association between the IMT with Serratia (gram negative conditional pathogens) abundance (p=0.37, t-test). We found the association between the IMT with Serratia (gram negative conditional pathogens) abundance (p=0.009) in HC but not in EC.

**Conclusions.** The EC were unexpectedly healthy. Considering the GM analysis, we may propose that EC microbiota protected long lives from the low-grade inflammation and thus protected them from the development of metabolic disorders by producing a high amount of butyrate, one of the most important anti-inflammatory agents in the human body. Conditional pathogens (the inflammation initiators) associated with BMI and IMT as well as butyrate producers may subsequently become a target for cardiovascular prevention.
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