Gut microbiome correlations with cardiotoxicity biomarkers (LV-GLS, LVEF, Troponin I, NTproBNP) in breast cancer patients prior to treatment

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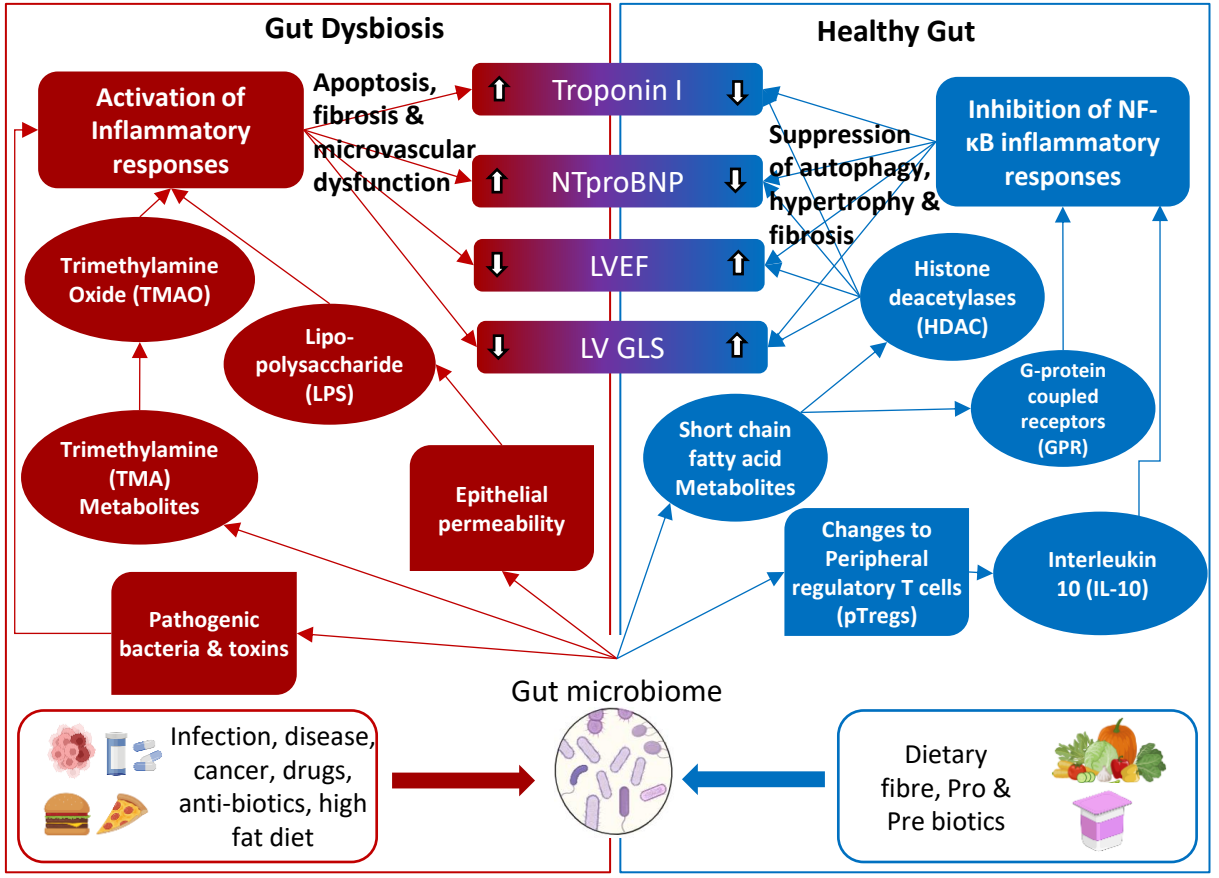
1. Introduction: The CARDIOCARE project Prospective Clinical Study (NCT06334445) is examining genomic, transcriptomic and metagenomic factors in therapy-induced cardiotoxcity in breast cancer patients. Specifically, associations of the gut microbiome and established biomarkers of cardiotoxicity (LV-GLS, LVEF, Troponin I and NTproBNP).

2. Methods: 98 women >55 years of age diagnosed with breast cancer at three cancer treatment centres:

- European Institute of Oncology, Italy
- Bank of Cyprus Oncology Centre, Cyprus
- National and Kapodistrian University Athens, Greece

Faecal samples and measurements of LVEF, LV-GLS, Troponin I, NTproBNP were collected prior to treatment.

Spearman's correlations of the relative abundances of bacteria from 16S rRNA metagenomics analysis and cardiotoxicity biomarkers with significance assessed via permutation testing.



3. Results: The relative abundance (RA) of family *Bacteroidaceae* was positively associated with LV-GLS (r_s=0.39, p<0.00032) and Troponin I (r_s =0.21, p<0.042), similar also at the genus level (r_s =0.40, p<0.00022; r_s =0.21, p<0.043). Significant associations (p<0.05) were also found at species level, between LV-GLS, LVEF, Troponin I and NTproBNP with several *Bacteroides* species.

4. Conclusions: The RA of certain *Bacteroides* species prior to treatment was correlated with cardiovascular parameters linked to an increased risk of breast cancer treatment-induced cardiotoxicity.

Bacteroides are prevalent commensal gut bacteria with effects on inflammation via regulation of T lymphocytes within the gut mucosa.

Bacteroides have been associated with other cardiovascular diseases.

Bacteroides could be candidates for modulating the gut microbiome to protect against cardiotoxicity during cancer treatment.

5. Future/Upcoming work: