CANCER MICROBIOME

If you missed out our October Awareness month posts on Linked In, now the time to catch-up! Post were addressing the role of microbiota in cancers, from his emerging role in Tumor Microenvironment to his singularity in Breast Cancer tissue.

Phylogene is proud to participate in raising awareness of breast cancer during Breast Cancer Awareness Month!

Exploring the Emerging Role of the Gut Microbiota and Tumor Microenvironment in Cancer Immunotherapy

The tumor microenvironment (TME) is a complex ecosystem, which includes many different types of cells, abnormal vascular systems, and immunosuppressive cytokines. TME serves an important function in tumor tolerance and escapes from immune surveillance leading to tumor progression (1).

In few words:

- Gut microbiota can shape TME by regulating the immune and hormonal factors of the whole host, in other words, host gut microbiota is emerging as a critical modulator of the TME.
- An in-depth understanding of TME, its role and related molecules will provide important insights into the biological behavior of different tumor types.
- The Cancer Microbiome: Distinguishing Direct and Indirect Effects Requires a Systemic View

Excellent review asking pragmatic questions regarding the role of microbiome in cancers and the need to use multiomic approaches for better data integration (2).

"Outstanding Questions":

- What other members of the human microbiome beyond bacteria –archaea, fungi, and viruses (including bacteriophages) are important for cancer?
- How can we integrate microbial composition and function with other relevant data such as habitat, host information, and other variables quantified by omic approaches?
- Does the human microbiome play a role in the link between migration and cancer incidence?
- Why does the success of microbiota transplants vary from patient to patient?
- Can the ability of gut microbes to influence the central nervous system be leveraged to manage pain in cancer patients or even cancer development?
- Can we engineer microbiomes to turn immunotherapy nonresponders into responders?

The human microbiome is a mysterious treasure of the body playing endless important roles in the host's metabolism, digestion, immunity and well-being. On the other hand, it actively participates in the development of a variety of pathological conditions including Cancer (3).

This review highlights few interesting findings regarding microbiota in breast cancer:

- Breast cancer tissue contains its own unique microbiota
- Preclinical data indicates that breast microbiota dysbiosis contributes to breast cancer initiation and progression
- Differences in breast microbiota composition have been found between breast cancer subtypes and disease severities that may contribute to immunosuppression
- Interactions between breast microbiota, gut microbiota, and immune system (Breast Gut Axis)

Microbiome and Breast Cancer: New Role for an Ancient Population

The human microbiome is a mysterious treasure of the body playing endless important roles in the host's metabolism, digestion, immunity and well-being. Although the multiple evidences liking the microbiome to Breast Cancer (BC) are undeniable, there are essential questions to be answered to unlock the exact role of the microbiome in the development and treatment of BC (4).

This review aimed at evaluating:

- The role of the microbiome as a risk factor in the occurrence of BC investigating and assessing the impact of the altered composition of breast, guts, and milk microbiome in the physiological status of normal breast as well as cancerous or non-cancerous breast lesions.
- The role of microbiome in the development and maintenance of inflammation
- Clinical and therapeutic applications of the microbiome- e.g., probiotics, microbiome genome modulation, and engineered microbiome enzymes in the management of BC

What is the role of microbiota in cancers? Protectant or enhancer of the disease?

With Phylogene you can characterize bacterial populations in Tumor microenvironment and elucidate metabolic pathways. Just think out of the box!

- Bacterial 16s rDNA and fungal ITS sequencing with OUT-based estimation to investigate microbial diversity and determine taxonomic composition.
- *High-resolution nano LC-MS/MS quantitative metaproteomics and HolXplore™ data processing, for host-microbiota interactions discovery.*

(1).https://www.frontiersin.org/articles/10.3389/fimmu.2020.612202/full

(2).https://www.cell.com/trends/cancer/fulltext/S2405-8033(20)30017-0

(3).<u>https://doi.org/10.1016/j.ajpath.2021.02.020</u>

(4).https://www.frontiersin.org/articles/10.3389/fonc.2020.00120/full

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