

OeGHO - Förderpreis Onkologie 2021

LCBiome Study – Lung Cancer microBiome *Deciphering the host-microbiome crosstalk in lung cancer*

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Background: Within the tumor microenvironment (TME) of lung cancer, the local microbiota is believed to tightly interact with the heterogenous cell populations of the host, particularly the immune cell compartment, potentially modulating (anti-tumor) immune reactivity. Both the tumor microbiota composition and the mechanisms behind this host-microbiome interaction is poorly understood.

Aim: To in-depth map the microbiome composition together with the TME (of both the tumor tissue and the respective bronchoalveolar space) on a genomic level and to compare this to healthy tissue. This approach will help to identify potential bacterial patterns that directly influence the TME.

Methods: We will use a multi-omic approach by applying next generation sequencing techniques to analyze both tumor and healthy lung tissue as well as bronchoalveolar lavage fluid in 5 patients with early stage non-small cell lung cancer. The analyses include single cell RNA sequencing (host TME), whole genome sequencing (microbiota) and whole exome sequencing (tumor antigenicity). These in-depth data will be combined by bioinformatic analysis to decipher a potential host-microbe crosstalk in non-small cell lung cancer (NSCLC).