Investigation of the Gut Microbiota Composition and Activity in Acute Myeloid Leukemic Patients: First Results of the MicroAML Study

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Introduction: The gut microbiota, a key regulator of host metabolism and immunity, is affected in preclinical models of leukaemia and cachexia. Reversing these changes in the gut microbiota can provide benefits to the host. To evaluate the translational value of pre-clinical studies, a multi-centric, prospective, observational study was initiated: MicroAML. The main objective of this study is to assess the composition and activity of the gut microbiota in patients diagnosed with acute myeloid leukaemia (AML).

Methods: Patients newly diagnosed with AML were recruited (n=30). Biological samples and clinical data were collected before any therapeutic intervention. Patients' food habits and cachectic hallmarks (e.g. appetite, muscle strength, body composition) were also collected. Control subjects from the general population were matched (1:1) for age, sex and BMI. Blood, faeces and urine were analysed using 1H-NMR metabolomics. The gut microbiota composition was assessed using shotgun metagenomics.

Results: Compared to control subjects, AML patients at diagnosis do not show significant difference in body composition and quality of their diet. The gut microbiota of AML patients shows some specific changes. AML patients also display clinical and metabolic alterations (inflammation, hyperglycaemia, anorexia, muscle weakness). We are now investigating the contribution of the gut microbiota to those metabolic changes by integrating metabolomics and metagenomics data.

Discussion: Our first results show significant changes in the composition of the gut microbiota as well as early signs of metabolic alterations in AML patients at diagnosis. Using a multi -omics strategy, we are now investigating whether these signs are related to changes in gut microbiota composition and activity. ClinicalTrials.gov Identifier: NCT03881826