Identification of cancer type specific gut microbiota shifts in paediatric oncology patients with pre-transplant treatment

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Bone marrow transplantation (BMT) in cancer is lifesaving. Preconditioning regime causes massive gut microbiota depletion and differences in gut microbiota are supposed be associated with post-transplant complications. This study aimed to determine the association of type of cancer diagnosis and related gut microbiota composition alterations in patients undergoing BMT including acute lymphoblastic leukaemia (ALL;n=8), acute myeloblastic leukaemia (AML;n=5) and other cancer diagnosis (OCC;n=8) compared to healthy controls (CTRL;n=14). Stool samples were collected before BMT at Transplantation Unit at University hospital (2018-2020). *16S rRNA* shotgun sequencing (Illumina MiSeq, 2x300bp) was performed. Data were analysed by QIIME2. In each cancer type specific gut microbiota pattern was identified. Significant abundance changes of bacterial OTUs; 74(AML), 37(ALL) and 66(C) were detected compared to CTRL (higher abundance of *Faecalibacterium, Blautia, Agathobacter, Dialister*). In ALL changes in *Firmicutes/Actinobacteria* (*Firmicutes/Collinsella*) while in AML *Proteobacteria/Bacteroidota/Firmicutes* (*Enterobacter/Bacteroides/Firmicutes*) were observed. OCC were associated with changes in *Firmicutes/Bacteroidota* (increase of *Prevotella, Alistipes*). In conclusion, changes in gut microbiota caused by preconditioning regime effect more patients with AML and other cancer types than with ALL. Furthermore, a specific gut microbiota composition shift between diagnosis even after intensive antibiotic treatment predict higher vulnerability of AML and patients with solid tumours to post-transplant immune complications.