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.