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O0748 Changes in gut microbiome composition in patients undergoing HSCT colonised by ESBL bacteria and treated with carbapenems

Silvia Corcione*[1], Benedetto Bruno[2], Alessandro Busca[3], Ilario Ferrocino [4], Gabriele Bianco[5], Lucia Brunello[3], Chiara Dellacasa[3], Giovanni Di Perri[1], Rossana Cavallo[6], Francesco Giuseppe De Rosa[1]

[1] University of Turin, Dept of Medical Sciences, Infectious Diseases , Turin, Italy, [2] Department of Oncology, Stem Cell Transplant Center, University of Turin, Turin, Italy., Turin, Italy, [3] Department of Oncology, Stem Cell Transplant Center, AOU Città della Salute e della Scienza, Turin, Italy., Turin, Italy, [4] DISAFA - Microbiology and food technology sector, University of Turin , Turin, Italy, [5] Microbiology and Virology Unit, Laboratory of Microbiology and Virology, AOU Città della Salute e della Scienza",Turin, Italy., Turin, Italy, [6] Department of Public Health and Pediatrics, Laboratory of Microbiology and Virology, University of Turin, Turin, Italy., Turin, Italy

Background: Several studies have shown loss of diversity of the gut microbiome in association with significant gut injury following hematopoietic stem cell transplantation (HSCT). Prolonged broad spectrum antibiotic use further promotes loss of microbiome diversity and increases the risk of intestinal colonization by multi-drug-resistant (MDR) bacteria. Aims of this study were to prospectively evaluate the overall changes in gut microbiome composition after HSCT and differences in patients colonized by MDR bacteria and treated with carbapenems.

Materials: We performed a prospective observational study evaluating the gut microbiota of 20 hematological patients undergoing HSCT, from admission (T0) through day +28 (T5). Fecal microbiota was assessed by 16S amplicon-based sequencing. Clinical, and microbiological data as well as fecal samples were collected every 7th day from admission.

Results: One-hundred fecal samples were analyzed**.** Overall, we found a progressive decrease of bacterial richness from T0 to T5, with a significant reduction of Blautia, Ruminococcus and Dorea species, which are strictly associated with the production of short chain fatty acids (SCA). Moreover, in the 30% (no.6) of patients who were colonized by ESBL bacteria, we observed a significant reduction of Clostridium spp and Bifidobacterium species. As for antibiotic therapies, carbapenems were used as second line treatment of febrile neutropenia in 50% (no 9) of cases, usually associated with aminoglycosides. In patients treated with meropenem, a strong decline of Blautia and Ruminococcus species was observed. This finding suggests a correlation between carbapenem regimens and increase of pro-inflammatory bacterial strains in the gut.

Conclusions: Our data support the hypothesis that loss of intestinal commensals that produce short-chain fatty acids may increase dysbiosis. Moreover, for the first time we report significant and progressive alterations in the composition of Blautia, Ruminococcus and Bifidobacterium species in patients treated with meropenem and colonized by ESBL bacteria, respectively. Our findings offer potential modifiable targets to reduce risk of colonization by MDR bacteria and to promote a carbapenem-sparing approach in the HSCT setting.