29th ECCMID Amsterdam, Netherlands 13 – 16 April 2019

The congress of ESCMID

P2400 Gram-negative bloodstream infections as an outcome of gut domination: an observational cohort study

Igor Stoma*[1,2,3], Eric Littmann[3,4], Emily Fontana[4], Sejal Morjaria[3,4,5], Ingrid Leiner[3], Ying Taur[3,4,5], Eric G. Pamer[3,4,5]

[1] Belarusian state medical university, Minsk, Belarus, [2] Minsk scientific practical center of surgery, transplantation and hematology, Belarus, [3] Infectious Disease Service, Department of Medicine, Memorial Sloan Kettering Cancer Center, New York, United States, [4] Lucille Castori Center for Microbes, Inflammation & Cancer, New York, United States, [5] Weill Cornell Medical College, New York, United States

Background: Rapid spread of Gram-negative bacteria (GNB) has become a major healthcare threat in the last decade, despite the implementation of infection control strategies. Hematopoietic stem cell transplantation (HSCT) is a potentially curative treatment for various hematologic malignancies, while bacterial bloodstream infections (BSIs) remain an important cause of morbidity and mortality, occurring approximately in 20–34% of allogeneic HSCT recipients. Earlier studies have shown the protective effect of diverse gut microbiota against development of infectious complications in allo-HSCT patients, including protection against highly antibiotic-resistant bacteria. Therefore, in this observational cohort clinical study we characterized the effect of gut microbiota composition on the risk of BSIs in allo-HSCT patients.

Materials/methods: Adult patients undergoing allo-HSCT during the period from 2011 to 2017 were included in the study. Participants were enrolled in a fecal collection protocol, where fecal samples were collected during the initial transplant hospitalization and stored within 24 hours in a biospecimen bank. Among the inclusion criteria for the study were: patients with at least three sequenced fecal samples during the period from pre-HSCT admission day to the engraftment day. DNA was extracted and purified from each fecal sample, and the V4 to V5 region of the 16S rRNA gene was PCR-amplified using modified universal bacterial primers. Purified PCR products were sequenced using the MiSeq Illumina platform.

Results: A total of 765 patients have met the study criteria, and were selected for analysis. There were totally 785 procedures of allo-HSCT performed in the study participants. Of all included patients, 5988 fecal specimens were collected, with an average of 34.845 high-quality 16S rRNA bacterial sequences per specimen. In the Cox proportional hazards regression model of microbiome composition, it was shown that the predictive effect of Gram-negative intestinal domination on BSI risk is most frequently based on E. coli and Klebsiella spp. domination, having their effect sustained on various taxonomic levels.

Conclusions: In this study, we have evaluated the effect of gut microbiota composition on risk of BSIs caused by GNB in a large cohort of allo-HSCT patients, showing that preceding gut domination is a predictive factor for a subsequent BSI.