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P 006 – ID 021 - Role of the environmental microbiome on preterm newborns colonization: a pilot study by NGS

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Introduction: Extremely preterm infants, due to their characteristics, represent an extremely at-risk group of contracting healthcare-associated infections (HAIs). Late-onset sepsis is a major cause of morbidity and mortality in newborns admitted to neonatal intensive care units (NICUs). In this study we characterized the colonization by environmental microbiome on preterm infants, by analyzing nasal swabs from preterm infants at the time of birth and during the permanence in the NICU.

Materials and Methods: A total of 55 nasal swabs were collected from 30 newborns admitted to NICU, independently from their clinical conditions. The study time-course of samples collection included: 30 swabs at the time of birth (group N), 18 after 9 days (group S) and 7 after 13 days (group SA). At the same time points, samples from the environment have been collected including sinks, footboards of the beds, and floors. Microbiome analyses were simultaneously performed by NGS and by a custom real-time PCR (qPCR) microarray kit.

Results: In nasal swabs, the bacteria most frequently detected with the NGS method were: *Corynebacterium spp.* (N: 40%, S: 56%, SA: 57%), *Staphylococcus spp.* (N: 53%, S: 94%, SA: 100%), *Streptococcus spp.* (N: 53%, S: 61%, SA: 71%) and *Escherichia-Shigella spp.* (N: 33%, S: 61%, SA: 100%). Other bacteria detected frequently were *Acinetobacter spp.*, *Pseudomonas spp.*, *Klebsiella spp.*, *Enterobacter spp.*, *Cutibacterium spp.* and *Rothia spp.* The qPCR analysis allowed the identification of bacteria up to species level. To be noted, within the genus *Staphylococcus* the main species were *aureus* (N: 3%, S: 33%, SA: 43%) and *epidermidis* (N: 27%, S: 89%, SA: 100%). Instead, within the genus *Streptococcus* the most frequently detected species were *pneumoniae*, *infantis*, *oralis* and *salivarius*, with higher identification rates in the SA group. This method also allowed the identification of the fungus *Candida albicans* in group S (6%) and SA (43%). Environmental NGS analysis of the NICU showed the presence mainly of *Staphylococcus spp.*, *Streptococcus spp.*, *Corynebacterium spp.*, *Cutibacterium spp.*, *Acinetobacter spp.*, *Escherichia-Shigella spp.* and *Pseudomonas spp.* Interestingly, the similarity between the microbiome of nasal swabs and the environmental one increased with the stay of the newborns in the ward.

Discussion and Conclusions: Based on molecular analyses, our study highlights the importance of routine screening to assess the rate and type of colonization of fragile newborns by the environmental microbiome. The introduction of this new approach may be important for environmental monitoring and for consequent clinical management of newborns admitted to NICU ward.