ePoster Viewing
Microbiome and resistance: what are they telling us?

STUDY OF THE DIGESTIVE FLORA OF 20 LEBANESE PATIENTS IN REMISSION OF CROHN'S DISEASE AND COMPARISON TO HEALTHY SUBJECTS

G. Rizkallah[1], R. Sayegh[2], **A. Hajj**[1], P.H. Seksik[3], G. Trugnan[3], D. Karam Sarkis[1]

[1]Molecular Microbiology Department, Saint Joseph University, Beirut, Lebanon ; [2]Service de Gastro-entérologie Hotel Dieu de France, Saint Joseph University, Beirut, Lebanon ; [3]URL U1057 INSERM/ UMR720, Paris 6 University, Paris, France

Objectives: The intestinal microbiota is an etiologic factor in inflammatory bow el disease and particularly in Crohn's Disease. The aim of this study w as to determine if the composition of the fecal microbiota of patients in remission of Crohn's disease differs from that of healthy individuals.

Methods: Tw enty remission diagnosed Crohn disease patients (R-CD) and 20 healthy subjects (HS) w ere recruited at Hotel Dieu de France Hospital in Beirut, Lebanon, from April 1st 2012 untill February 15th 2013. Exclusion criteria (ex. antibiotics and drugs containing probiotics consumption for at least 3 months before enrolment) and inclusions criteria helped to avoid possible multi-factorial distortions in the microbiota composition. Fecal samples w ere collected and conserved at -80°C, than sent to the Paris for analysis. The forty fecal samples w ere analyzed by quantitative real-time polymerase chain reaction. Bacterial counts for *Faecalibacterium prausnitzii, Escherishia coli, Coccoides, Bacteroides, Lactobacillus, Clostridium leptum* and *Bifidobacterium* w ere transformed to logarithms (Log$_{10}$). The results obtained w ith the 2$^{-\Delta\Delta Ct}$ method w ere used to compare the abundance of each of these seven bacterial species among these tw o groups (Mann-Whitney tests). The study w as approved by the local ethical committee and all subjects gave an informed w ritten consent.

Results: *Bifidbacterium*, *Lactobacillus*, *Clostridium leptum*, *Faecalibacterium prausnitzii* and *Clostridium coccoides* w ere less abundant in the tw enty R-CD patients group w hen compared to the 20 HS. *Bacteroides* levels show ed no quantitative differences among these tw o groups. *Escherichia coli* levels w ere higher in the R-CD group compared to the HS group. How ever, these quantitative differences did not reach statistical significance.

Conclusions: In the present study, the composition of the fecal microbiota of R-CD patients did not significantly differ from that of healthy individuals. How ever, our results remain original for different reasons.

In fact, this study constitutes the first Lebanese research describing the intestinal microbiota of healthy subjects and that of patients in remission of Crohn's disease. The absence of statistical significance might be explained either by a low statistical pow er or by the fact that the microbiota of R-CD patients is quite similar to that of healthy subject. Further studies including a larger number of patients are needed to investigate the difference betw een the tw o groups in order to determine w hether bacterial fecal dysbiosis is a predictive indicator of a higher-relapse risk in Crohn's Disease.

In addition, and to our best know ledge, this is the first study examining the composition of intestinal microbiota in R-CD patients, as most of the studies explored it in patients w ith active inflammatory bow el diseases (Wang2013, Machiels2013, Galecka2013). Finally, the methods used in our study are similar to those used in several international publications on Crohn Disease; it might be therefore helpful for comparison betw een Lebanese and other populations' digestive microflora.
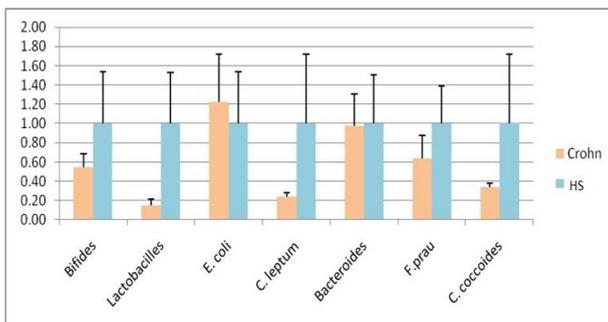

Figure 1