Title: INTESTINAL MICROBIOTA ANALYSIS OF IMMUNOSUPPRESSED PATIENTS

Authors: SECCO, D. A^a.; PIRES, E.S^a.; MIRANDA, K.R^b.; PASQUALETTE, L.B.B.B.^a; ALVES, E.S.^a; PEIXOTO, R.J.^c; GRANATO, A.^d & DOMINGUES, R.M.C.P.^a.

Institution:

^a Laboratório de Biologia de Anaeróbios, Instituto de Microbiologia Paulo de Góes, Universidade Federal do Rio de Janeiro – UFRJ

^b Faculdade de Farmácia, UFRJ/Macaé

^c Department of Molecular and Cellular Biology, University of Guelph, Ontario, Canada

^d Division of Rheumatology, Immunology and Allergy, Brigham and Women's Hospital/Harvard Medical School, Boston, MA, USA

Abstract:

The intestinal microbiota is responsible for several key functions, such as metabolism participation, immune system modulation and colonization resistance. The use of antimicrobial, immunosuppressants and chemotherapy agents is related to microbial disbalance. Thus, the present study was aimed to analyze the effect of these agents in human intestinal microbiota. Stool samples of patients admitted to the Hematology, Oncology and Transplant wards at Hospital Universitário Clementino Fraga Filho (HUCCF / UFRJ) and samples from healthy subjects were collected from August 2013 to July 2014. All samples were submitted to microbial DNA extraction using the commercial kit QIAamp® DNA stool minikit to perform the quantitative real time PCR (RT-qPCR) assay. The individuals were divided into four groups according to the drugs used: (1) Patients under chemotherapy; (2) Patients under treatment with antibiotics, chemotherapeutic agents and imunossupressors; (3) patients under treatment with antibiotics and imunossupressors; (4) Control Group. To perform the RT-qPCR primers for Bacteriodetes, Firmicutes and Actinobacteria phyla and yProteobacteria class were used and the amplification reactions were performed using Power SYBR Green RT-PCR ™ mix and StepOnePlus Real Time PCR System equipment. The samples were analyzed by relative guantification. A decrease was observed in members of Firmicutes and Bacteroidetes phyla in groups 1, 2 and 3 compared to the control group, but this result was significant only for groups 2 and 3 in relation to the Bacteroidetes phylum (p < 0.05). An increase was observed in members of Actinobacteria phylum and yProteobacteria class compared to control group, with significant results only for group 3 in relation to Actinobacteria phylum and group 1 in relation to yProteobacteria class. Considering that Actinobateria phylum and vProteobacteria class include genus with a high medical importance, the changes introduced by chemotherapeutic, immunosuppressive and antimicrobial agents may be related to an increased susceptibility to infection by these microorganisms.

Key-words: intestinal microbiota, immunosuppression, quantitative real-time PCR

Financial support: CAPES, CNPq, FAPERJ, PRONEX