AAI
Associazione Antropologica Italiana

ALMA MATER STUDIORUM
UNIVERSITÀ DI BOLOGNA

21° CONGRESSO
dell'Associazione Antropologica Italiana

Towards a Next-Generation Anthropology: challenges & synergies

Bologna and Ravenna
September 3-5, 2015

P. 24

EXPLORING MICROBIOTA BIODIVERSITY THROUGH MASSIVE PARALLEL SEQUENCING WITH THE ION TORRENT PGM PLATFORM

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Keywords: *Microbiota, Human Evolution, Massive Parallel Sequencing, Microbiome and Human Genome Co-Evolution*

The totality of microbial communities that share the human gastro-intestinal tract as ecological niche is called "microbiota" and, recently, several studies had highlighted the close relationship between its composition and various human conditions. Nevertheless, the evolutionary history of this interaction remains still unexplored. Massive parallel sequencing of the human intestinal microbiome provides a new approach to explore the correlation between changes in microbiota composition and the host physiological status.

Recently, a new kit for metagenomic analysis has been developed for the Ion PGM platform. The "*Ion Torrent Metagenomics 16S kit*" allows analyzing most part of the various hypervariable regions which characterize this gene and which are commonly used for bacterial identification. Furthermore, the "*Ion 16S Metagenomics Analysis Module*" within the Ion Report software provides a specific support for analysis of 16S results. We tested the efficiency of this kit on 20 human samples belonging to two groups exposed to different exogenous compounds.

Preliminary results showed an evident difference in the microbial composition between the two groups and a different performance efficiency of the investigated hypervariable regions. These findings also suggest that some regions are particularly indicated in the analysis of gastro-intestinal microorganisms biodiversity than others.

This metagenomic approach is still rarely applied in anthropological studies, although recent researches showed that some key passages of our evolutionary history, as the divergence from African apes or the Neolithic transition, have deeply influenced our microbiota composition and biodiversity. Therefore, investigating the microbiota composition in relation with human genetics promises to shed new light on the underlying complex co-evolutionary processes.