

O1205 Leishmaniasis in Turkey: comparison of the microbiota of the intact skin and lesion site in patients with cutaneous leishmaniasis

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Background: Human skin is an important barrier against infectious agents and skin microbiota has been associated with inflammation, wound healing, allergies and anti-microbial defense. Commensal microorganisms may play a role in modulating the cellular responses in the skin. The aim of this study is to compare the skin microbiota of the intact skin and lesion sites of cutaneous leishmaniasis (CL) in Turkey, where CL has been endemic for centuries and has been emerging after the arrival of millions of refugees from neighboring countries lately.

Materials/methods: A total 20 CL patients in Diyarbakir, infected with *Leishmania tropica* was included in the study. Study samples were obtained by both scraping of the lesion and the intact skin, which was at least 10 cm away from the CL lesion. Samples were immediately transferred to 70% ethanol and sent to Acibadem and Celal Bayar Universities for DNA isolation. Microbiota analyses were done in Statens Serum Institute in Denmark, using Illumina MiSeq Platform and targeting both 16S and 18S rRNA genes of bacteria and eukaryotes, respectively. Bioinformatic analyses were done in Acibadem University on KNIME Analytics Platform with developed decision trees, and focused on the comparison of the microbiota of lesion and intact skin of the same CL patient.

Results: Our findings indicated a significant difference in the microbiota of lesion and intact skin of CL patients. In particular, an eukaryotic phylum, Basidiomycota, Phragmoplastophyta and a nematode were all absent on the intact skin. Opportunistic pathogens such as *Malassezia pubis* of Basidiomycota phylum were increased in lesion microbiota. In addition, three bacteria, *Microbacterium*, *Corynebacterium* and *Sediminibacterium* were found only in the microbiota of the lesion site ($p < 0.05$).

Conclusions: This preliminary study indicated an obvious difference of microbiota content of the lesion site and intact skin of the same CL patients in Turkey. *Microbacterium*, *Corynebacterium* and *Sediminibacterium*, which were identified only in the lesion site microbiota in our study, have already been associated with dermal burn injuries where same treatment agents show promising results in CL treatment. Further studies with CL patients due to *L. major* and from different regions in Turkey are planned.



