

Alternations in the skin microbiota are associated with symptom severity in mycosis fungoides

Yumeng Zhang, Lucia Seminario-Vidal, Leah Cohen, Mohammad Hussaini, Jiqiang Yao, David Rutenberg, Youngchul Kim, Anna Giuliano, Lary A. Robinson, Lubomir Sokol

Moffitt Cancer Center and University of South Florida

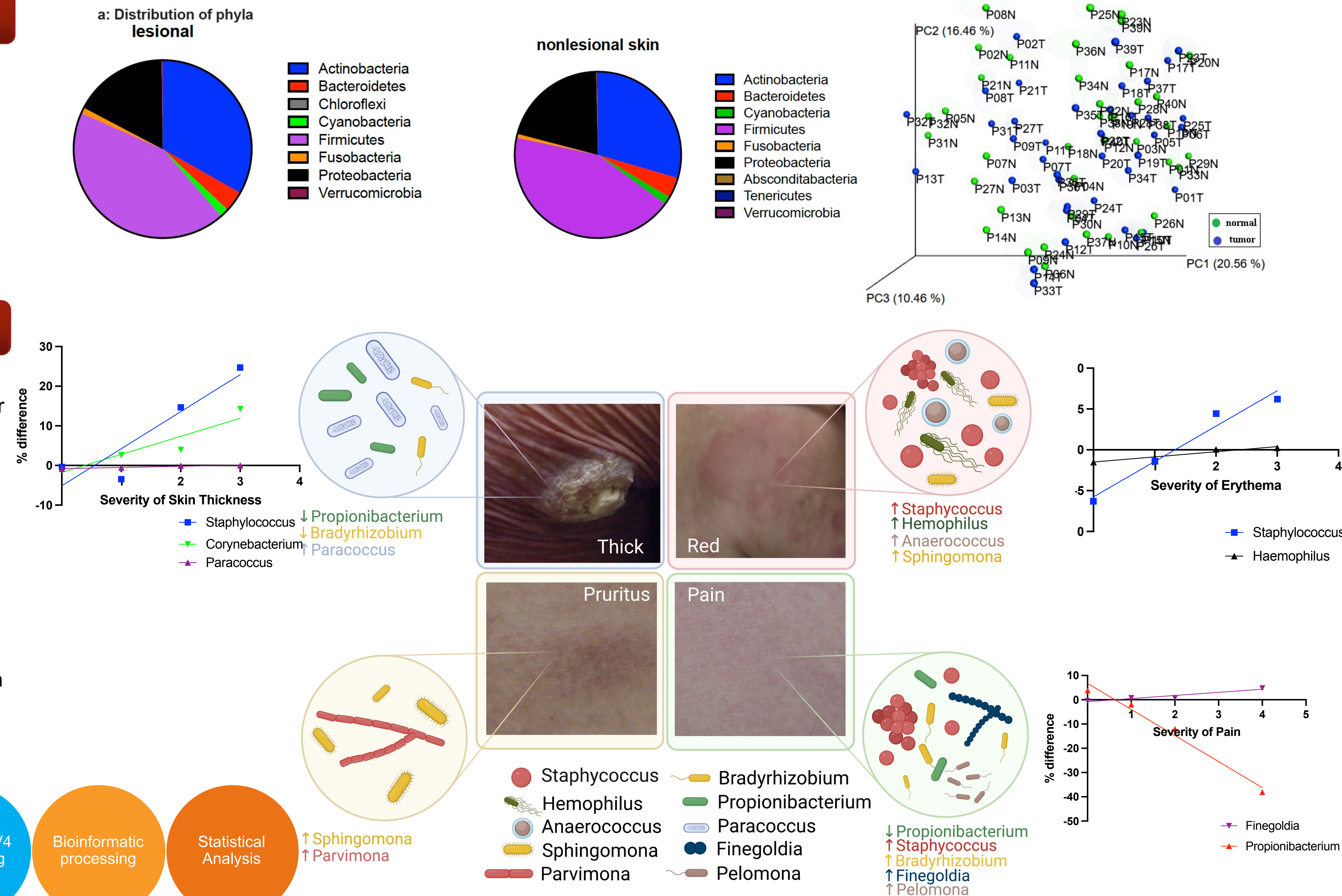
Background

Mycosis fungoides (MF) is the most common subtype of cutaneous T cell lymphoma (CTCL). Recently *Staphylococcus aureus* colonization of the cutaneous lesions has been implicated in the pathogenesis. The role of skin microbiota in the symptom's manifestation of CTCL remains unclear.

OBJECTIVE: to characterize the regional skin microbiota changes in patients with MF and to identify skin microbial signatures associated with various symptoms and their severity.

Design and Main Outcomes

Prospective pilot cross-sectional study of 39 patients with MF treated at CTCL interdisciplinary clinic at Moffitt Cancer Center from March 2019 to June 2019. Skin microbial samples were taken from the lesional skin and the contralateral nonlesional healthy skin from the same patient. 16s ribosomal RNA sequencing was performed on the samples. Alpha diversity was measured using Shannon entropy and compared using the Wilcoxon signed rank test. Beta diversity was visualized with a principal components' analysis. The relative abundance of the OUT was compared between lesional and matched nonlesional skin using T test. The difference in genus-relative abundance in skin microbiota between the lesional and nonlesional skin were used to reflect changes. The changes in genus-relative abundance were correlated with the scores for symptoms.



Result

Lesional skin appeared to have less bacterial diversity and richness than non-lesional skin, although differences were not statistically significant.

Principal coordinate analysis plots of Weighted UniFrac distance for beta diversity showed that interpersonal variability in skin microbiota is greater than the intrapersonal changes caused by cancer involvement. Microbiota signatures associated with different symptoms or signs were identified.

An increase in *Staphylococcus* in lesional skin was especially associated with pronounced erythema, and a decrease in *Propionibacterium* in lesional skin was associated with increased pain and skin thickness.

Conclusion

We identified microbial signatures associated with different symptoms, signs, and treatments.

Our findings suggest a potential microbial role in changing disease phenotypes among patients with CTCL.

Larger studies of skin microbiota of patients with MF may further characterize these differences and support antibiotic treatments to mitigate CTCL symptoms and perhaps prevent disease progression.

Funding

This work was supported through NIH/NCI grant titled Infection and Cancer Research: A New Frontier in Cancer Prevention and Control (5K05CA181320) and a grant received from the University of South Florida, Graduate Medical Education Office.

