



Emerging Trends in Human Skin Microbiome in Diabetic and Non-diabetic Subjects

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Introduction

- The human epidermis naturally contains a wide variety of micro-organisms¹
- Alterations in the cutaneous microbiome disrupt the host-microbe relationship and permit unchecked colonization by pathogens resulting in clinical infection²
- Comorbidities such as diabetes mellitus (DM) may also contribute to these transitions to clinical infection^{3,4}
- Foot infections and ulcerations are serious clinical problems for patients with diabetes
 - Up to 85% of all non-traumatic lower extremity amputations are a direct result of diabetic foot ulcers (DFUs)⁴
- Differences in pathogenic organisms populating the cutaneous microbiota of the feet of diabetic patients versus nondiabetic ones, may represent an increased risk for development of foot infections and DFUs

Objectives

- Use Next Generational Sequencing (NGS) to identify and quantify all bacterial and fungal sequences found in skin swabs collected from plantar surfaces and interdigital spaces of persons with and without DM
- Determine if NGS shows a difference between groups in diversity, quantity or antibiotic resistance of pathogenic organisms found in collected samples
- Determine if differences found represent an increased risk for development of foot infections and chronic DFUs

Methods

- Single center, cross-sectional
- Two study groups: patients with (N=50) and without DM (N=50)
- No amputations, wounds or active dermatological conditions on the right foot
- Foot-washing \geq 6 hours prior to sample collection
- After informed consent, swabs were collected from the interdigital space and plantar forefoot of each subject's right foot
- Samples sent for NGS analysis to Zymo Research Corp. to identify and quantify all bacterial and fungal species present

Results

- 100% of samples in both groups had bacterial dermal pathogens; 90% had fungal pathogens at different degrees of relative abundances.(Figure 1)
- A large variety of bacterial and fungal pathogens found on the diabetic subjects were not found on non-diabetic subjects (Figure 2)
- 73% of samples showed either a bacterial or fungal overgrowth, where one species represented more than 50% of the bacterial or fungal composition, (37% and 17% respectively), or overgrowth in both (20%)
- Most abundant bacterial species were *Staphylococcus pettenkoferi* (29.7%) and *Staphylococcus hominis* (7.9%)
- The two most abundant fungal species, Ascomycota sp. (13.6%) and Fungi sp. (12.5%), have not been previously described and could only be identified to the phylum and kingdom level, respectively

Figures

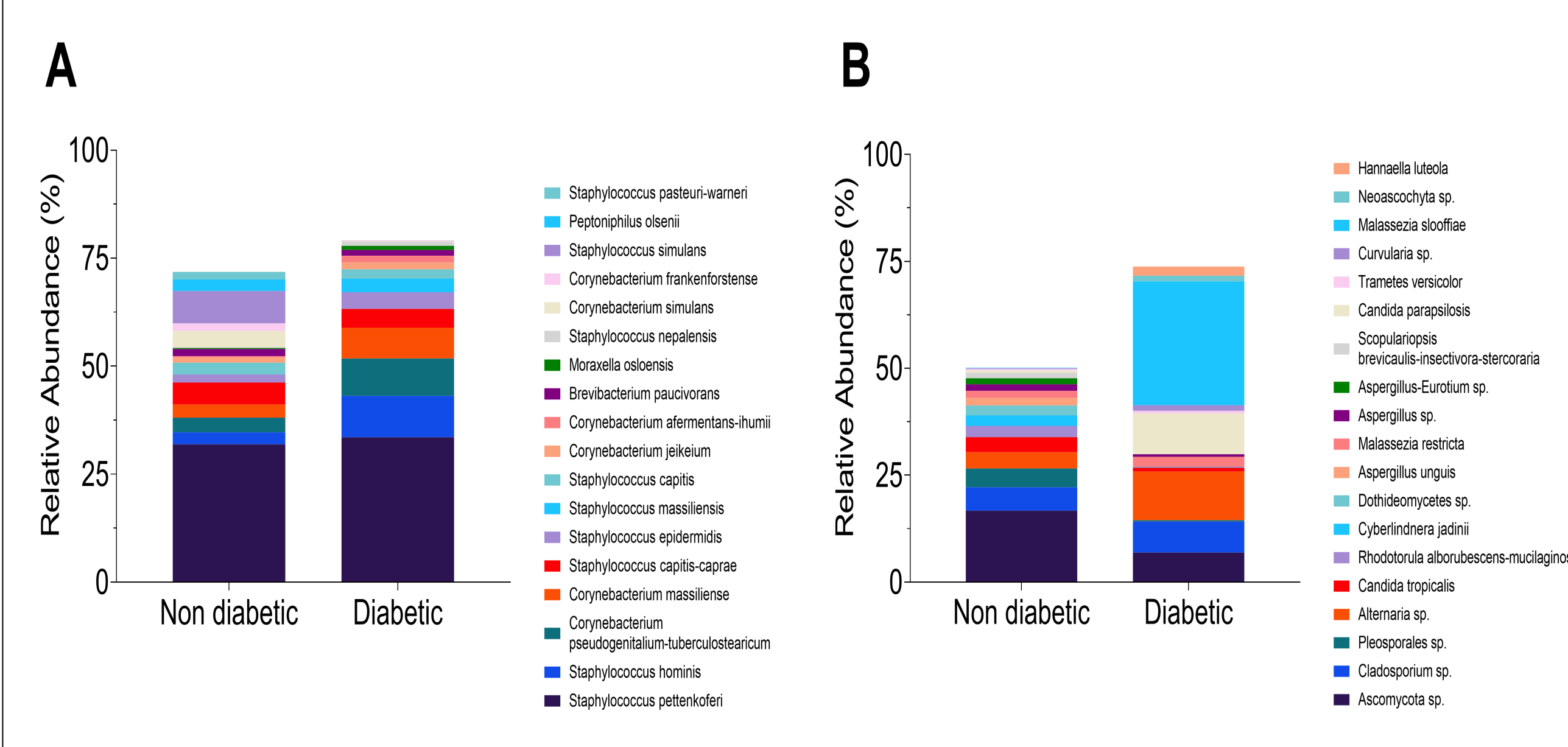


Figure 1 Most abundant bacterial and fungal species in the cutaneous microbiome of nondiabetic and diabetic subjects

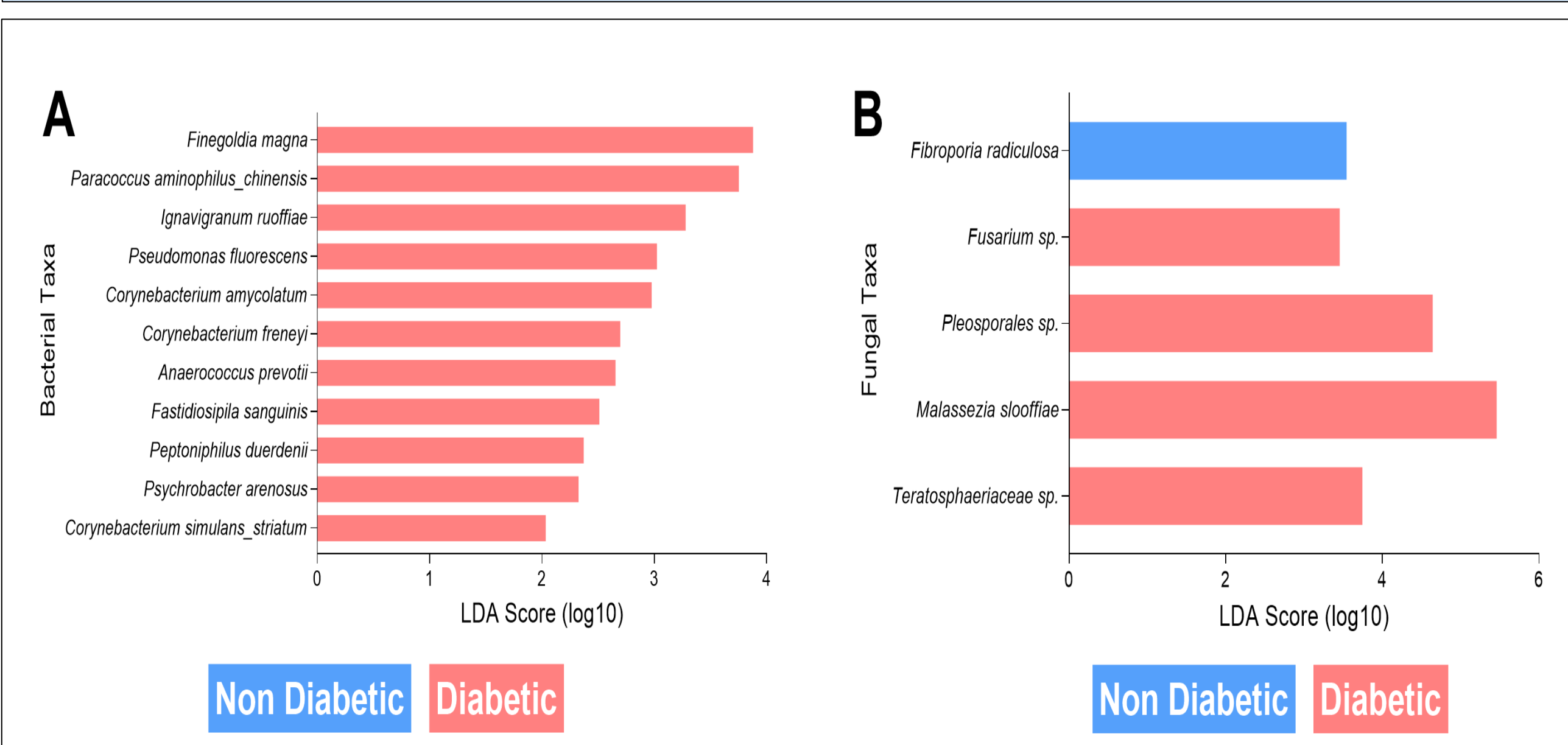


Figure 2 Species with significantly different abundances and frequencies between the diabetic and nondiabetic cohorts (P<0.05)

Discussion

- This study highlighted the complexity of the human cutaneous microbiome
- In gastrointestinal health, a high degree of diversity is a marker for a healthy microbiome¹
- In this data set, most samples lacked diversity, with one species dominating bacterial or fungal composition
- Having a pathogen present in the microbiome, did not indicate a disease state or warrant antibiotic treatment

Conclusion

- Further understanding of the human cutaneous microbiome will improve our understanding of skin health management strategies
- More work is needed to interpret the findings and compare them to current literature to best determine if the significant differences detected could be contributing to the development of chronic skin and soft tissue infections in persons with diabetes

References

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