A distinct cutaneous microbiota profile in bullous pemphigoid patients

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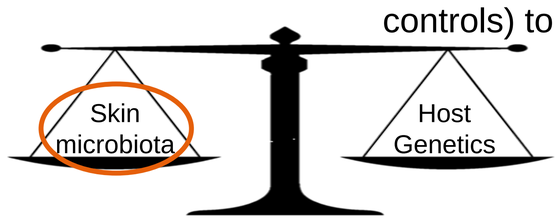
Background

Bullous pemphigoid (BP) represents the most common autoimmune blistering disease in Europe. Whereas some progress has been achieved in defining genetic risk factors for autoimmune blistering diseases, the role of environmental agents is not as well defined. Emerging evidence suggests that host immunity influences the skin microbiota while the latter modulates cutaneous immunity.

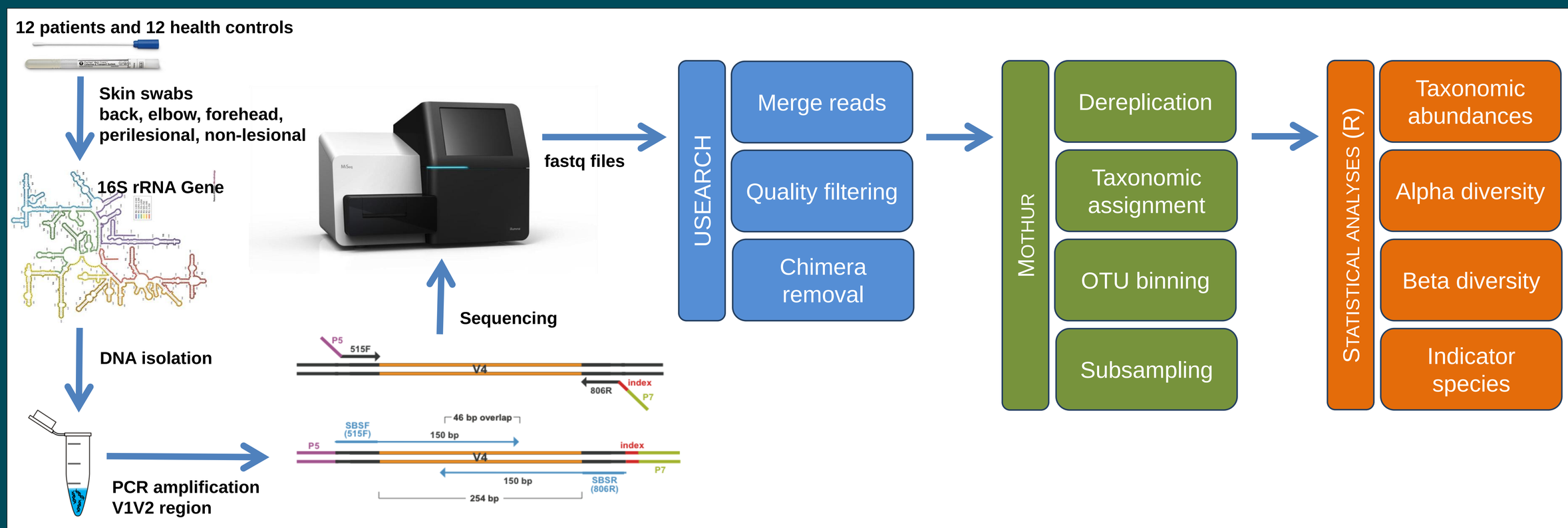


Conclusion

We were able to show the existence of a distinct cutaneous microbiota profile in bullous pemphigoid. Moreover, these results raise the possibility that the cutaneous microbiome may contribute to the pathogenesis of bullous pemphigoid, with important implications for treatment methods.

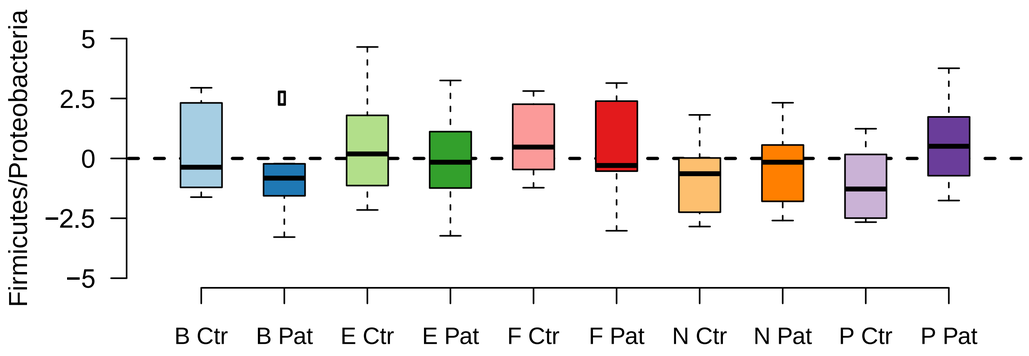
In the future, we will increase the sample size (450 patients and 450 controls) to investigate the found differences more thoroughly.

Methods



Results

The relative abundance at phylum level was significantly different at perilesional vs. non-lesional sites in bullous pemphigoid patients. We observed a clear shift from Proteobacteria within control samples towards the Firmicutes phyla in patients at the same anatomic locations.



Constrained analysis of principle coordinates (CAP) of Bray-Curtis dissimilarity was performed using all sampled sites. Samples cluster by sample location. Additionally, perilesional sites of patients and controls show a distinct separation, whereas the other sample locations are not distinct separated between patients and controls. For better visualization only elbow, forehead and perilesional sites are shown.