High relative abundance of bacillales is associated with Epidermolysis Bullosa (EB) at different stages of wound healing

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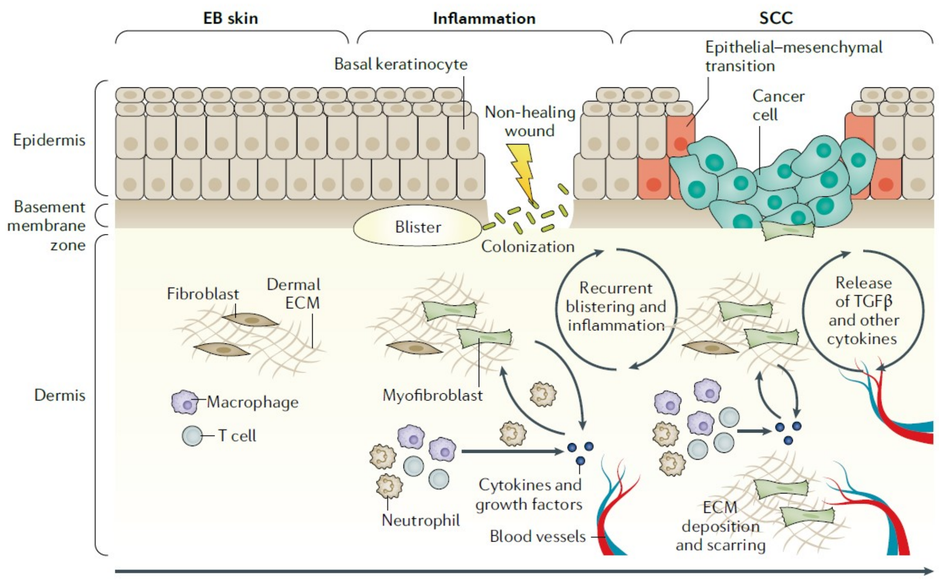
What is Epidermolysis Bullosa (EB)?

EB
Epidermolysis Bullosa is a group of **rare** genetic skin disorders

- Incidence of 19.6 per million live births
- Mucocutaneous fragility and blister formation
- Affects internal organs
- At least 16 genes involved
- There is no cure

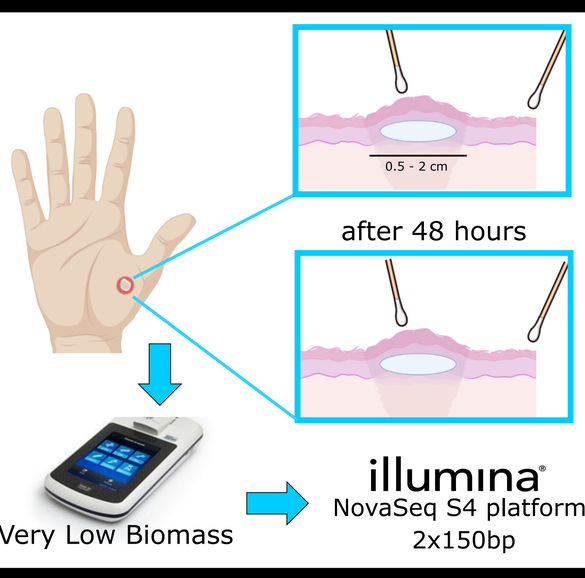
EB is classically grouped into four major types according to the level of skin cleavage: EB simplex (**EBS**), junctional EB (**JEB**), dystrophic EB (**DEB**), and Kindler EB (**KEB**). A heterogeneous phenotypic spectrum exists with: persistent blistering, inflammation, scarring, delayed re-epithelisation, abnormal wound healing, and infection.
It can cause disability and death. Understanding the **skin microbiome** and its relationship to the **inflammatory-immune response** are fundamental prerequisites for developing novel therapies.



Certain types of EB are associated with an increased risk of developing cutaneous squamous cell carcinoma (SCC)[1].

The study aims to characterise, for the first time, the skin microbiome of blisters and unaffected skin of EB patients employing a metagenomic approach.

Methods



[2]

-Blister between 0.5 and 2 cm
-30 seconds skin swab
-Swabs from blistered skin
-Swabs from healthy skin sourrounding the blister

References

1) Bardhan A, et al, Epidermolysis bullosa. Nat Rev Dis Primers. 2020 Sep 24;6(1):78.
2) Meyer F, et al., The metagenomics RAST server – a public resource for the automatic phylogenetic and functional analysis of metagenomes. BMC Bioinformatics. 2008 Sep. 19; 9:386.

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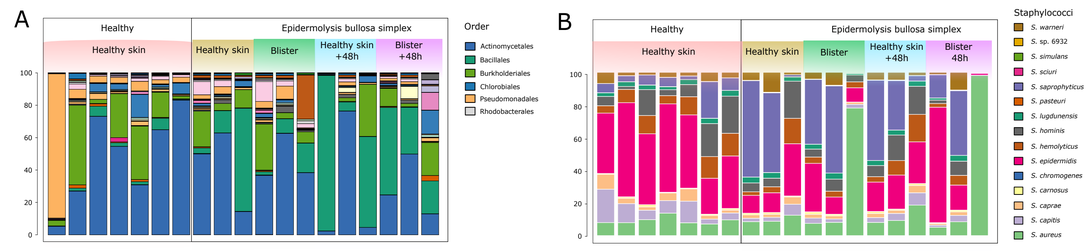
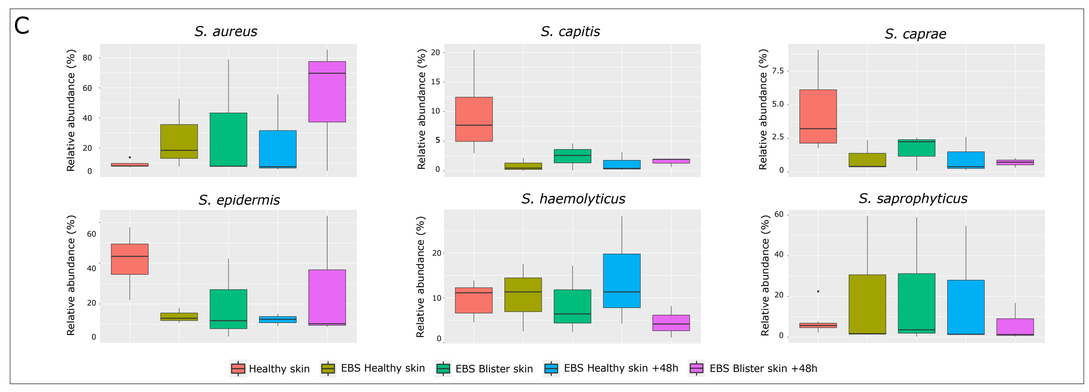
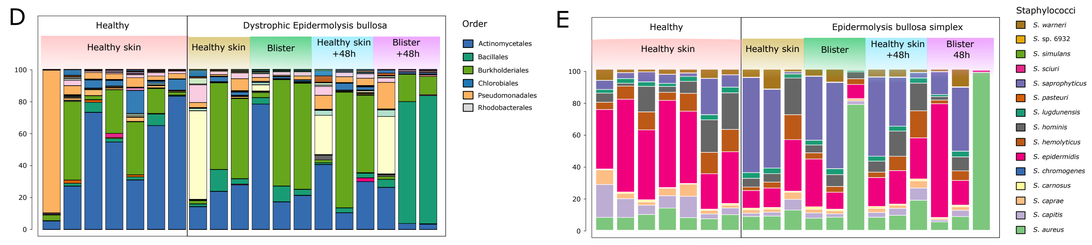
Results

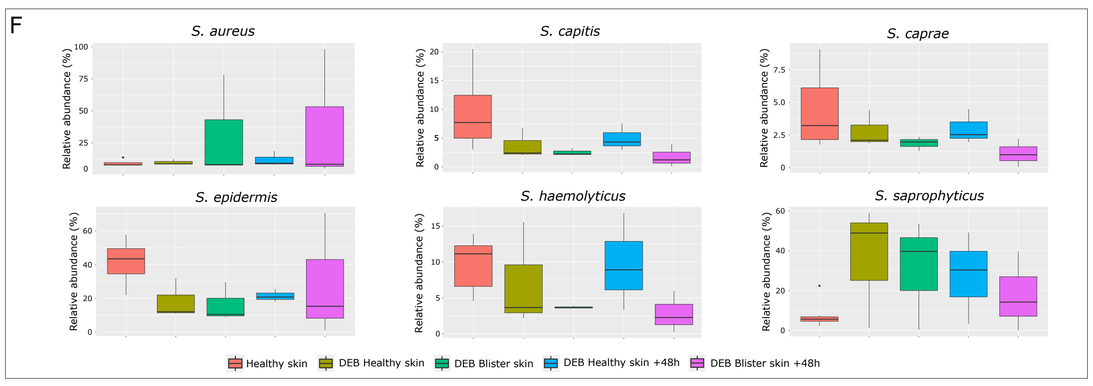
Epidermolysis Bullosa simplex



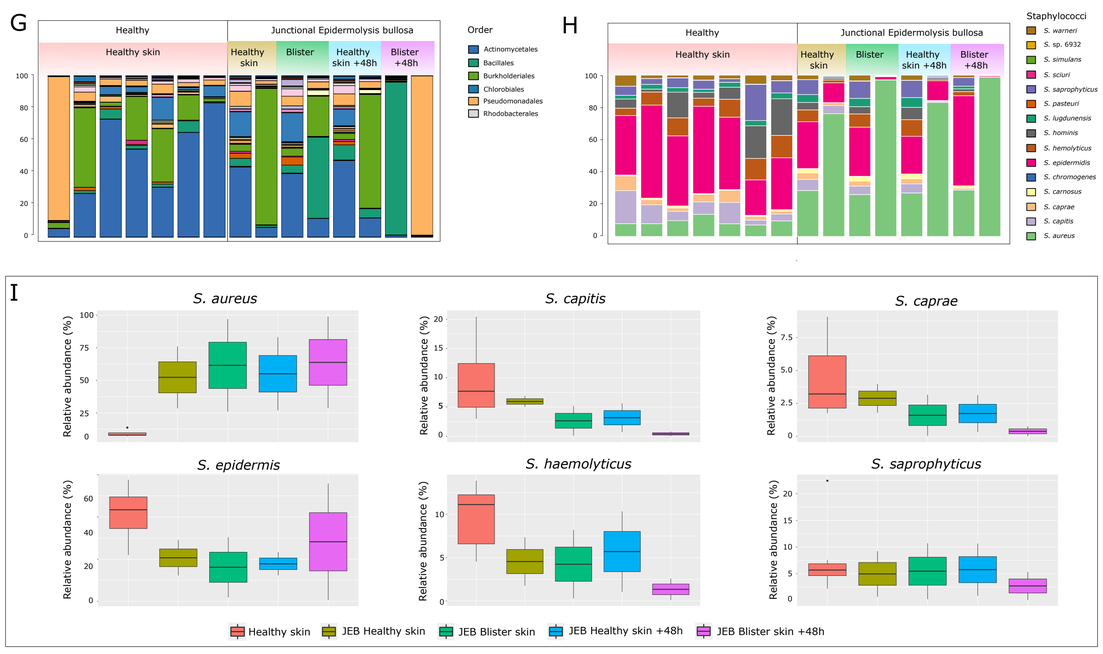


Dystrophic Epidermolysis Bullosa





Junctional Epidermolysis Bullosa



Bacterial relative abundance in healthy individuals (n=7) and people affected by EB simplex (n=3) (A,B,C), Dystrophic EB (n=3) (D,E,F), and Junctional EB (n=2) (G,H,I). A,D,G) Individual content of bacteria; most abundant bacteria are shown in the legend with order as taxonomical level. B,E,H**)** Relative abundance of *Staphylococci* species. C,F,I) Relative abundance of the most abundant species of *Staphylococci*.

Conclusion

-The skin microbiome of EB patients has a **high** relative abundance of **Bacillales**.
-Composition of the skin microbiome in EB patients varies **during wound healing**; in particular, the *Staphylococci* showed species-specific and EB type-specific abundancies.
-We observed a **decrease** of ***S. epidermis*** in all EB samples.
-In **EBS**, ***S. aureus*** showed an **increase** of the relative abundance of blistered skin after 48 hours of blister formation.
-In **DEB**, we observed a **high** relative abundance of ***S. saprophyticus***, with progressive decrease over time.
-In **JEB**, ***S. aureus*** mantained a **high** relative abundance in EB patients skin samples.
-These results suggest that there is **association** between shifts in the microbiome and **wound healing** in EB patients subtypes, which can be **exploited therapeutically**.