Comparative Microbiome Analysis of Contracted Breast Capsules : a cross-sectional study

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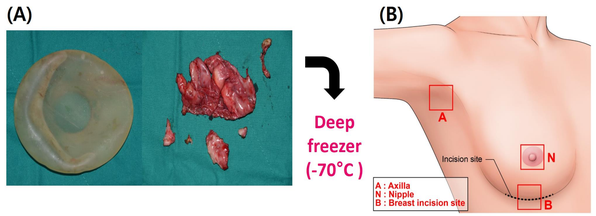
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Background

- Of all the potential etiology of capsular contracture, the leading theory of is that subclinical infection by bacterial biofilm. However, recent studies, constrained by the limitations of culture-based methods, find themselves restricted to only exploring the cultivable fraction of bacteria, thus potentially overlooking a vast and diverse array of microbial life that exists beyond the confines of laboratory cultivation.
- The aim of this study is to characterize the microbiome of the breast capsules using next generation sequencing and to estimate the origin of the bacteria found.

Methods and Materials

- 25 normal and contracted breast capsules were collected during implant removal or replacement operations. Ipsilateral skin samples were collected from axilla, nipple and breast incision site by swabbing method (Fig.1).
- We analyzed them by dividing them into 2 groups, Healthy Capsule (HC) and Contracted Capsule (CC), according to the baker classification for capsular contracture.



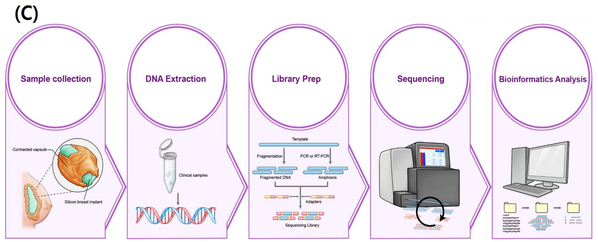


Figure 1. Collection of specimens and NGS protocols
(A) Collection of capsule specimen and storage in deep freezer.
(B) Collection of skin bacteria with swabbing methods with 3 places (3x3 cm^2 area) is shown.
(C) Overall NGS protocol with sample collection, DNA extraction, Library prepration, DNA sequencing and Bioinformatics Analysis..

Results

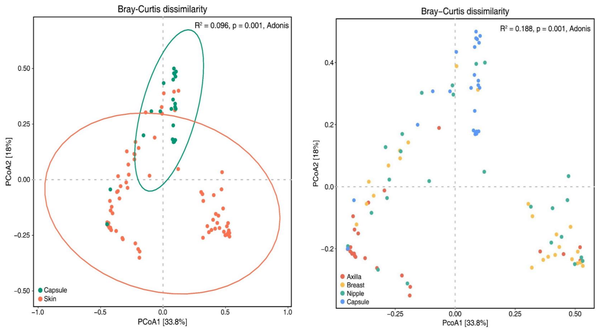


Figure 2. Beta-diversity Analysis (Skin vs. Capsule)
Beta-diversity analysis reveals that capsules are distributed in entirely separate clusters from the skin.

- Beta-diversity analysis reveals that capsules are distributed in entirely distinct clusters compared to the skin. ($p<0.05$) (Fig.2).
- In taxonomic analysis, a notable dissimilarity in bacterial composition was observed between the two specimens (Fig.3).
- In the HC, various bacteria, including those found in the breast's normal flora, were evenly distributed, whereas in in CC, colonies dominated by opportunistic pathogens (Fig.4).

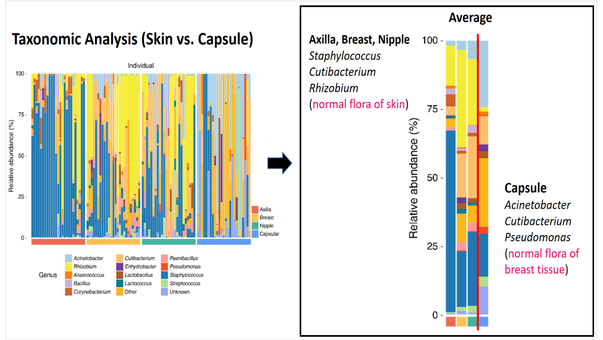


Figure 3. Taxonomic Analysis (Skin vs. Capsule)
In taxonomic analysis, bacterial composition of the two specimens were significantly different. Staphylococcus, Cultibacterium, Rhizobium were found in normal flora of skin (from axilla, breast, nipple). Otherwise, Acinetobacter, Cutibacterium, Pseudomonas were found in normal flora of breast tissue.

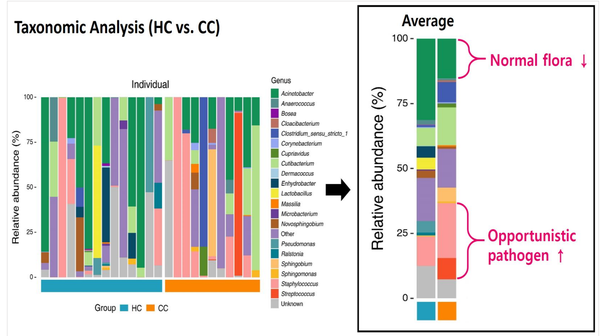


Figure 4. Taxonomic Analysis (Health capsule vs. Contracted capsule)
Various bacteria, including those from normal breast flora, were evenly distributed in the health capsule, whereas colonies were dominated by opportunistic pathogens in the contracted capsule.Z

Conclusions

- This study presented new perspectives on biofilm theory of development of capsular contracture. We suggests the possibility that the endogenous bacteria of breast tissue play a role and opportunistic pathogen dominates the microbiome as capsular contracture progresses.
- Understanding changes in the breast microbiome around the implant could potentially lead to the prevention or treatment of capsular contracture.

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