

Local Breast Microbiome in Implant-based Reconstruction and Change over Time with Antibiotics

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Background

High rates of post-operative infections in women who undergo mastectomy with immediate prosthesis placement (in spite of peri-operative and post-operative antibiotics)

- 5.8-28% of patients develop implant infection^{1,2}
- Antibiotic use in the post-operative period is not well-studied or supported by data

The breast microbiome of breast cancer patients differs from healthy controls^{3,4} → microbiome differences may play a role in regulating the local immune system. 16s rRNA sequencing allows us to define the local breast microbiome, which is described in terms of:

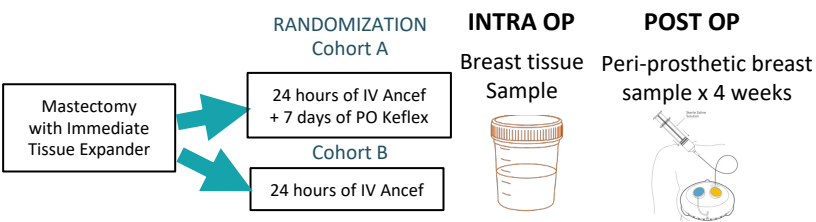
- Species Richness: number of species in a community
- Shannon Diversity Index: accounts for species evenness

Objective

We aimed to define the breast microbiome and its change over time with the use of post-operative antibiotics

Methods

We designed a two-armed, randomized controlled trial in patients undergoing mastectomy with immediate tissue expander reconstruction, ultimately aiming to enroll 100 patients per cohort

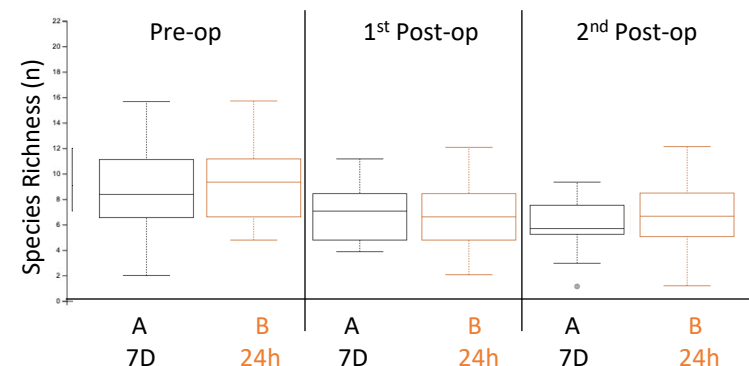


Results

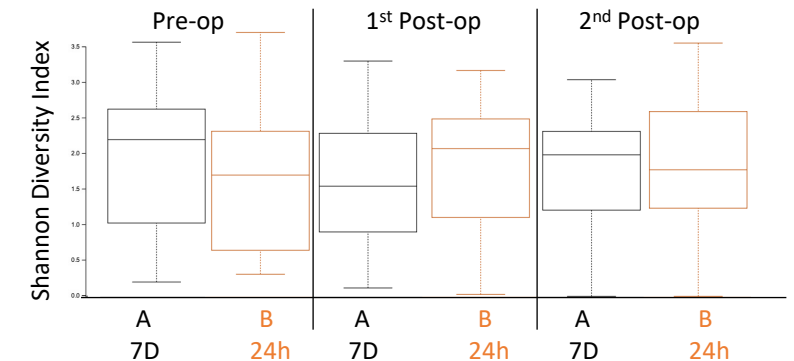
- Nineteen patients received 24 hours of IV antibiotics + 7 days of PO antibiotics (Cohort A), while 20 received only 24 hours of antibiotics (Cohort B)
 - No significant differences between pre-op cohorts in microbiome measures
- Significant differences in following species percent representation seen from Pre-op to Post-op in Cohort A (7 days) – not seen in cohort B

Genus	Pre-op A	1 st Post-op A	2 nd Post-op A	P value
Finegoldia	3.92	0.061	0.000	p=0.032*
Corynebacterium	2.07	0.000	0.000	p=0.016*

- Species Richness: Significant differences between 1st Post-op A (p=0.009) and 2nd Post-op A (p=0.002) compared to Pre-op A; Significant differences between 1st Post-op B (p=0.006) and 2nd Post-op B (p=0.007) compared to Pre-op B



- Shannon Diversity Index: No significant differences seen from Pre-op to 1st or 2nd Post-op samples in cohort A or B



Conclusions

- Breast species richness did decrease with both courses of antibiotics.
- Breast diversity did not change with the differing lengths of antibiotics courses
- Finegoldia and Corynebacterium have been implicated as causative organisms in breasts abscesses
 - Their presence in these samples and decrease is still of unclear significance
- Future directions: we will be expanding our study cohort to power our data so that we can better understand what constitutes an optimal breast microbiome from the infection prevention standpoint.

References

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