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MESH MICROBIOME AND ITS CLINICAL IMPLICATIONS

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Introduction:

Changes in the vaginal and urinary microbiome have been related to different disease conditions(1-3). Little is understood about the mesh microbiome, or its relationship with the urinary or vaginal microbiome, and mesh complications. This study aimed to characterise the microbiome of explanted midurethral slings, and its association with mesh complications.

Methods:

Women (n=74) provided samples of mesh, urine and swabs from the vagina and skin of the groin or suprapubic regions (n=397), and were allocated to an associated clinical group: chronic pain, vaginal mesh exposure, lower urinary tract (LUT) perforation or recurrent incontinence considered our control group. Any cases of frank clinical mesh infection were excluded. Samples were analysed via amplification of the v4 region of 16S rRNA gene, and next-generation DNA sequencing.

Results:

Relative abundances at the genus level by each type of sample are represented in Figure 1. Mesh samples had a higher species diversity compared to vaginal (p<0.0001) and groin (p<0.0001) swabs, but not urine. Mesh samples from those with exposure carried greater species diversity (p=0.0201) and change in community (p=0.0204) with more Actinomyces, Bifidobacterium, Dialister, Fusobacterium, Gardnerella, Oriibacterium and Peptostreococcus. Vaginal swabs from those with mesh exposure also corresponded with greater species diversity (p=0.006) and change in community, p=0.014. Mesh arms associated with pain sites carried lower species diversity (p=0.0104) and change in community (p=0.003). There was also a change in the skin bacterial community in corresponding pain sites (p=0.024). LUT perforation resulted in a significantly different urinary microbiome (p=0.011), with more Peptonophiilus.

Conclusion:

Unexpectedly, the microbiome of mesh was most similar to the LUT, not the vagina. This is possibly because incontinence at time of implantation changes the vaginal microbiome. The variation found in diversity in both mesh and skin samples within individuals with pain may indicate a microbial cause of mesh complications.

References

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