CHRD 2024: Abstract Submission Form

Presenter Name Claire Risbey

Role in the project Design Analyze Data Write Abstract **Presenter Status** Undergraduate Students

Research Category Clinical

Title

The concordance of clinically diagnosed symptomatic bacterial vaginosis (BV) and molecular BV

Background

Bacterial vaginosis (BV) is common and is associated with numerous poor reproductive health outcomes and increased risk of STIs. The role of specific bacterial taxa in BV symptoms and how well they are detected by diagnostic tools remains unclear.

Objective

This analysis uses samples collected from participants in the local THRIVE BV study and hypothesizes that unique bacterial species will associate with specific symptoms and diagnostic tools.

Methods

Vaginal swabs from 64 females (26 BV positive; 40 BV negative) aged 18-50 were processed using 16S rRNA sequencing to generate microbiome data. Participants recorded symptoms on baseline surveys and physicians provided gram stain, whiff test, pH and Nugent score results. We identified significant (chi-squared, Fisher's exact, Kruskal-Wallis, Mann Whitney) associations between microbiome dominance or specific bacterial taxa with BV symptoms and different diagnostic tools.

Results

Vaginal microbiome profiles were categorized as Lactobacillus dominant (LD), if their profile was 50% or more Lactobacillus species, otherwise they were considered non-Lactobacillus dominant (nLD). More nLD participants experienced discharge (padj=0.043) and odor (padj=4.10E-3). As well, nLD were significantly (p<2E-8) identified as positive using whiff tests, Gram stain, pH and Nugent scores. Using bacterial strain level identification, Parvimonas and Gardnerella were associated with bleeding (padj<0.025), Sneathia sanguinegens and Ruminococcaceae were positively linked to odor and yeast overgrowth (p<0.01), and Porphyromonas was strongly associated with UTI symptoms (padj=0.001). Interestingly, five bacterial taxa were associated with symptoms including bleeding, itching, yeast overgrowth, UTI symptoms, discomfort, pain, odor while evading all diagnostic tools.

Conclusion

Certain bacterial strains associate with different BV symptoms. Some bacterial strains associate with symptoms but not clinical diagnostic tools (Nugent, whiff, pH), indicating these bacteria may play a role in misdiagnosing patients. Whether these strains can be treated with common BV therapies or if novel treatments are required need to be investigated.

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No

Authors

Name	Email	Role	Profession
Claire Risbey	risbeyc3@myumanitoba. ca	Presenting Author	Medical Student
Samantha Knodel	sxh1141@case.edu	Co Author	Biostatistician
Tobi Taylor	txt326@case.edu	Co Author	Research Assistant
Samantha Bailey	sab277@case.edu	Co Author	Research Assistant
Christina Farr	cxf288@case.edu	Co Author	Assistant Professor
Vanessa Poliquin	vpoliquin@sharedhealth mb.ca	Co Author	Associate Professor
Adam Burgener	adam.burgener@case.e du	Co Author	Associate Professor
Alicia Berard	alicia.berard@umanitoba .ca	Co Author	Assistant Professor