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REFORMED TAXONOMIC GROUPING OF *GARDNERELLA VAGINALIS* BASED ON COMPUTATIONAL AND FUNCTIONAL CHARACTERIZATION OF CARBOHYDRATE METABOLISM

Niamh O'Grady

Mentor: Amanda Lewis

Bacterial Vaginosis (BV), a shift from a *Lactobacilli* dominated vaginal flora to a polymicrobial imbalance involving Gram-variable and Gram-negative bacteria, is a common vaginal condition for women of reproductive age. BV predisposes women to several adverse reproductive health outcomes including higher risk of sexually transmitted infections, pelvic inflammatory disease, infertility, and preterm birth. *Gardnerella vaginalis*, one of the most frequently isolated bacterial species from women with BV, is poorly understood in the possible roles it plays in the condition. Although there have been attempts to classify *G. vaginalis* in the past, currently available methods remain inadequate for distinguishing *G. vaginalis* from related bacteria and differentiating between strains. In this work, I report a new method of combining bioinformatic analysis of genomes and experimental validation of predicted functions of genes across the strains of *G. vaginalis* in the areas of 1) core genes, already established in identifying different clades of *G. vaginalis*, 2) sialic acid liberation and foraging from sialoglycans, theorized to be involved in the degradation of mucus in the vagina during BV, and 3) broader carbohydrate metabolism, to group *G. vaginalis* strains in appropriate clades. From this classification, clades 1, 2, and 3 emerge as sialic acid consumers through sialylate lyase, while only selected strains from clades 1 and 2 are equipped to cleave sialic acid from glycans using a sialidase. Clade 1 strains also appear to have the capability to consume carbohydrates on a broader scope as compared to the other clades. Overall, the unification of functional and genomic studies of *G. vaginalis* improves on the classification from the conventional methods in microbiology, leading to better distinctions between strains. Further, this approach suggests that *Gardnerella* have varied metabolic adaptations, which may be helpful to understand the broader biology and pathogenesis of *Gardnerella*.