

Oral Communication 3

Insights into the phylogeny, resistome, virulome and host adaptation from *Gardnerella* genome analysis

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Abstract

Background: *Gardnerella* spp. is often seen as evidence of vaginal pathologies, although members of this genus can also be found in the urinary and vaginal microbiota of asymptomatic women [1,2], making its role in the urogenital tract unclear. **Objective:** To assess phylogenomic and functional analysis of *Gardnerella* genus. Resistance (ARGs) and virulence genes (Vg) was also explored to unveil their role in health and urogenital disease development. **Methods:** Twenty-nine *Gardnerella* isolates from urine (U, n=22) and vaginal swabs (VS n=7) of women [24 asymptomatic, 5 with overactive bladder (OAB)] were identified by cpn60 and WGS (NovaSeq 6000; Illumina). Together with 118 genomes from public databases (from U (n=35), VS (n=82) blood (n=1), and unknown samples (n=2)), we used TYGS platform and fastANI for species identification. Phylogenomic and pangenome analyses were performed using anvi'o v7.1 and Roary. Vg were annotated with COG and KEGG databases, and ARGs with AMRFinder Plus. Vg presence/absence outputs were analyzed with R. **Results:** 4 species and 10 genomic species were identified, 41% of the collection being comprised by *G. vaginalis*. ANI and dDDH values are insufficient for distinguishing *Gardnerella* species. Pangenome was composed by 4537 gene clusters and the core genome of by 514. Differences in carbohydrates and amino acid metabolism and absence of correlation of functions with human body sites or disease were observed. The virulome and *Gardnerella* species/genomospecies exhibit are intertwined. ARG to aminoglycosides (*aph(3')-Ia*), macrolides (*mefA*, *msrD*, *ermX*), tetracyclines (*tetM*, *tetL*), lincosamide and streptogramins (*lsaC*) were detected in several isolates. Open pangenomes were observed in *G. vaginalis*, *G. leopoldii*, *G. swidsinskii* and GG3. **Conclusions:** *Gardnerella* comprises 4 species and 10 genomic species. Core genome analysis, ANI and dDDH are recommended for appropriate species assignment. *Gardnerella* species/genomospecies are associated with a particular set of VFs and metabolic functions. ARGs with clinical relevance were also observed in different *Gardnerella* species.

Keywords: *Gardnerella*; pangenome; urogenital; microbiome

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