

A Treasure Trove for Future Discoveries: The Female Urogenital Bacterial Collection (UroGenBC)

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The female urogenital microbiome (FUM) harbours a unique and dynamic microbial community that can impact human biology and health. Whole-genome shotgun metagenomics is the most advantageous method to provide a complete picture of the genome content of FUM and achieve accurate functional assignments. This can only be warranted if metagenome sequences can be interpreted to reveal all the species and strains present, and a positive control (mock community with a known polymicrobial profile) is included to assess biases and accuracy of the experimental and computational procedure from low microbial biomass samples (urinary microbiome). Thus, understanding FUM functions requires cultivated bacteria for experimental validation, and reference bacterial genome sequences to interpret metagenome datasets and guide functional analyses. Currently, none of the recognized culture collections has devoted time and effort to advancing FUM's research and innovation.

Under the UroGenBC project, CCP aims to: i) present the first female urogenital bacteria culture collection, a comprehensive set of complete bacterial genome sequences from female midstream urine and vaginal samples; ii) develop DNA and whole-cell mock communities; and iii) build a consortium for a Horizon Europe project.

The Culture Collection of Porto-Faculty of Pharmacy, University of Porto (CCP; <https://ccp.ff.up.pt/>) holds a private collection of almost 2000 bacterial strains isolated from midstream urine and vaginal samples, at two distant time points (within 2.5-year interval), from 20 reproductive-age asymptomatic women (DOI: 10.1186/s12866-021-02123-3, DOI: 10.1128/spectrum.01308-22). The strains were previously identified by MALDI-TOF MS and gene markers sequencing, and represented almost 50 genera (mostly belonging to Bacillota and Actinobacteria phyla, followed by less prevalent Proteobacteria, Bacteroidetes, and Fusobacteria). The focus on high-resolution identification of Lactobacillaceae family, Corynebacterium and Gardnerella genera allowed our group to unveil 13 new bacterial species (3, 8 submitted to IJSEM for validation, and 2 under review, respectively) (DOI: 10.1099/ijsem.0.003901, DOI: 10.1099/ijsem.0.004726, DOI: 10.3390/microorganisms11020388). CCP believes that further exploration of the remaining genera will depict new species inhabiting the urogenital sites of female body. Moreover, we revealed that the healthy FUM is a source of potentially pathogenic and antibiotic resistant Escherichia coli strains, including those causing urinary tract infections, and diverse E. coli lineages were observed per individual and urogenital sample type (DOI: 10.3390/microorganisms10010027). The future strategy of CCP is to achieve the proposed goals, crucial for fully understand the association of urogenital microbiome with urinary/vaginal diseases and disorder, underpinned by the United Nations for Sustainable Development Goal 3, in partnership with other European culture collections.