

Intestinal Microbiome Shows Altered Diversity and Enterobacteriaceae Overgrowth in Carriers of Fluoroquinolone Resistant *E. coli*

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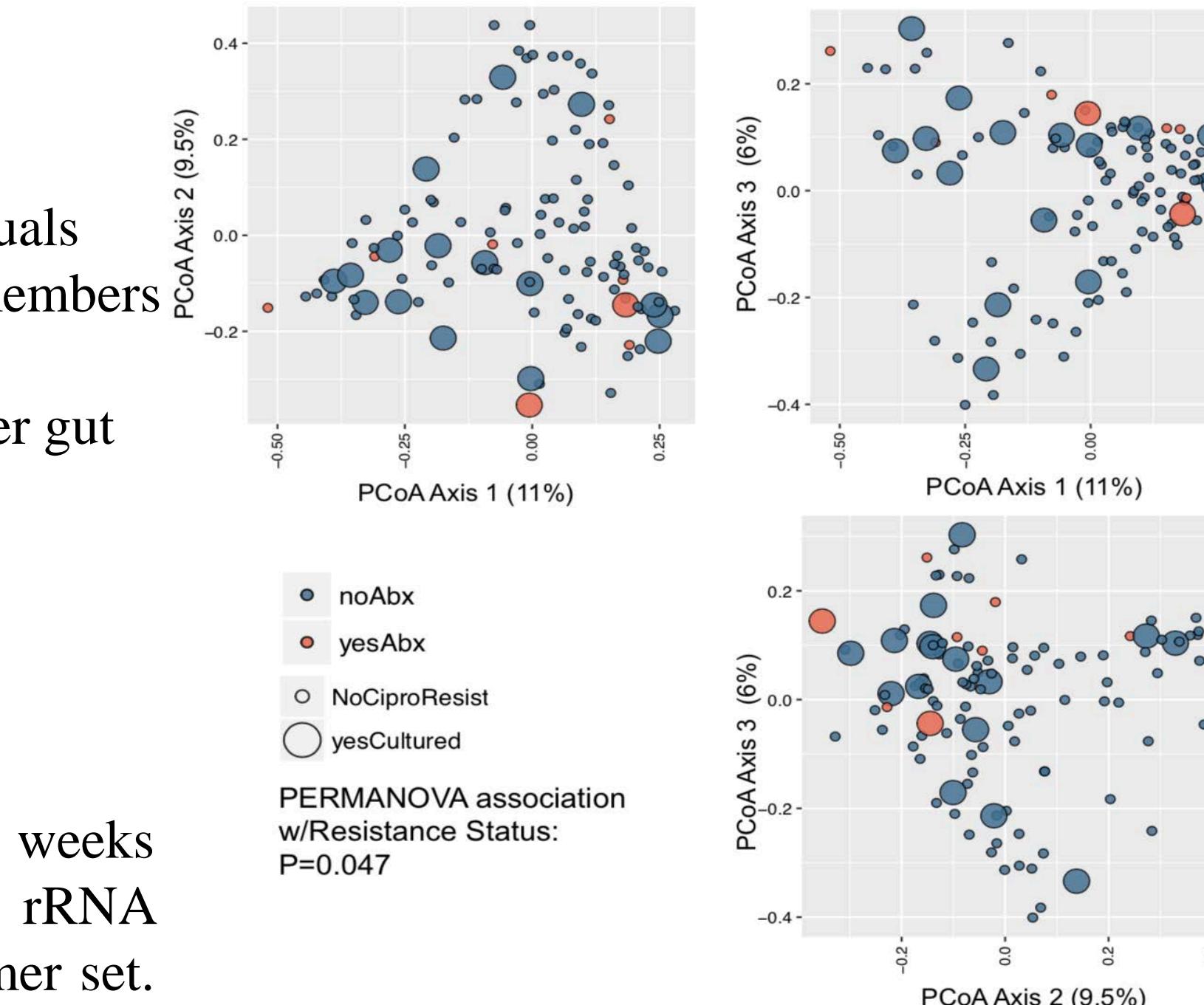
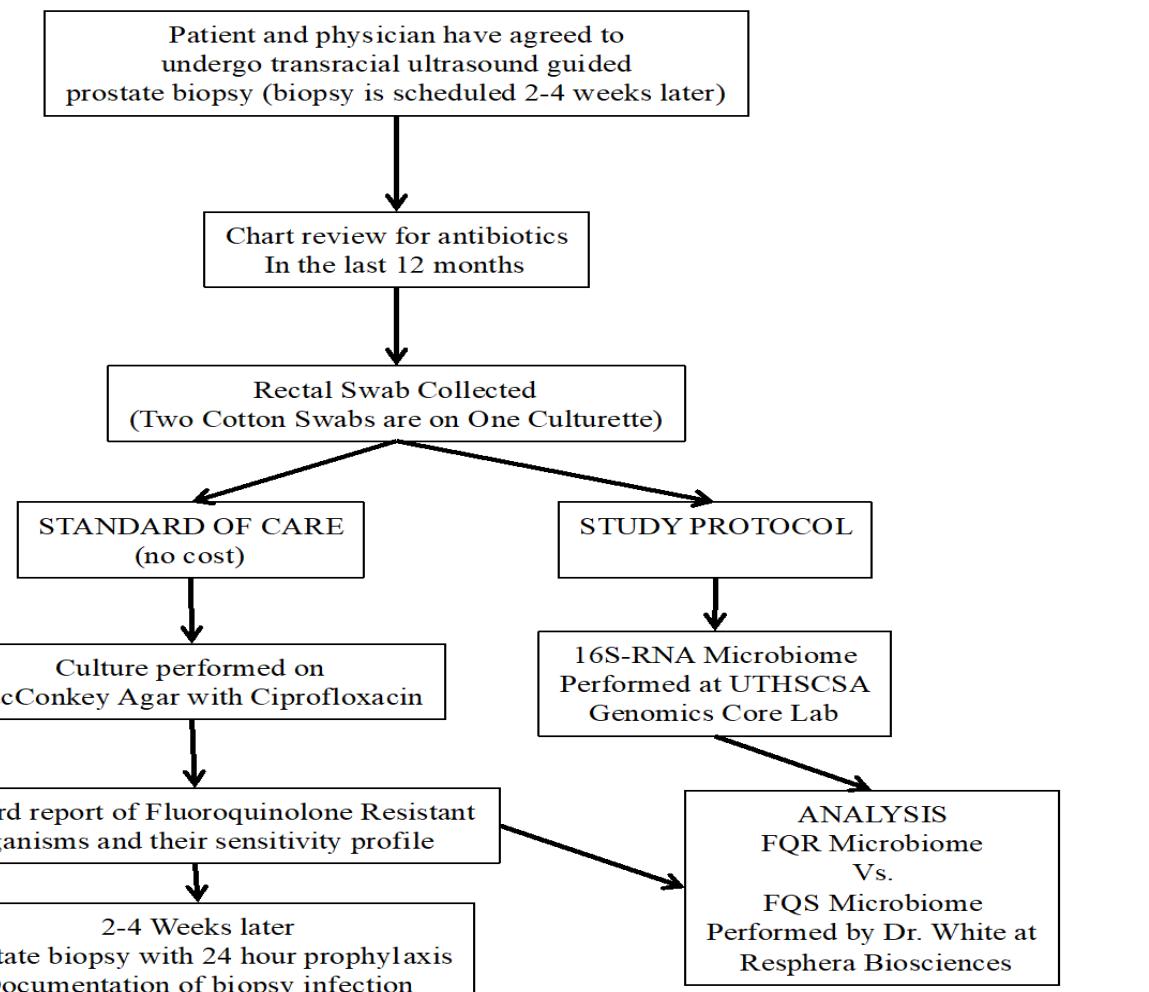
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Introduction/Objective

- Fluoroquinolone resistant (FQR) *E. coli* = prostate biopsy infections
- Our objective is to evaluate the gut microbiome of individuals positive or negative for FQR *E. coli* to identify bacterial members associated with resistance to FQR colonization
- Potentially for development of non-antibiotic means to alter gut flora prior to prostate biopsy

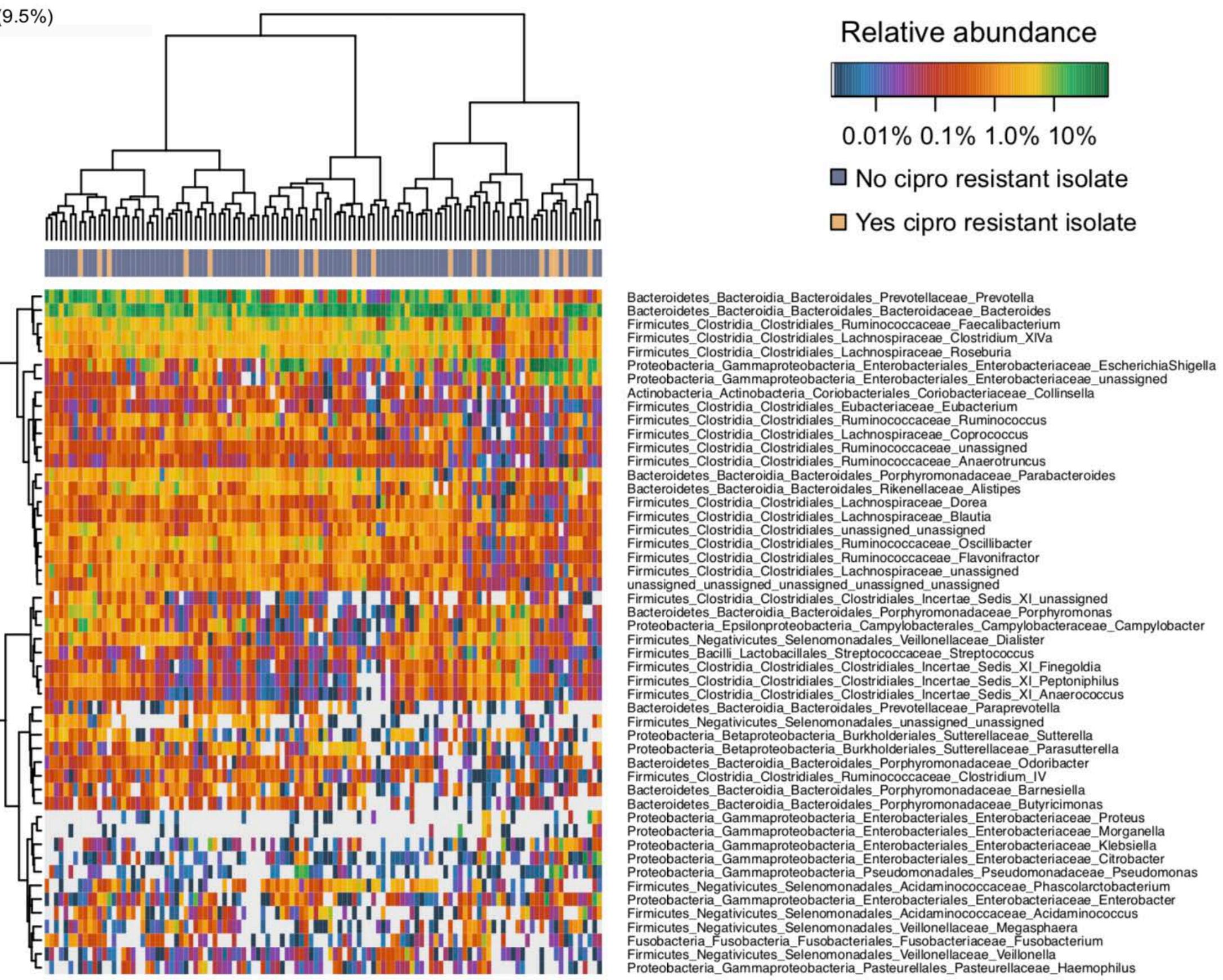
Methods

We prospectively collected 116 rectal swab samples at least 2 weeks prior to transrectal prostate biopsy, and performed 16S rRNA amplicon sequencing (MiSeq paired-end) using the V1V2 primer set. Taxonomic assignment was performed using Resphera Insight, and alpha and beta-diversity analysis was performed using QIIME. PERMANOVA was employed to evaluate statistical significance of beta-diversity distances within and between groups of interest. Differential abundance analysis utilized the nonparametric difference test for alpha diversity measures and the negative binomial test for taxonomic count data with P-value correction using the False Disco



Results

Of the clinical cultures we identified 18 isolates (16%, 18/116) were FQR *E. coli* positive. Men positive for *FQR E. coli* maintained relative reduced alpha diversity compared to non-FQR subjects (inverse simpson; $P=0.05$). The association of microbial community membership with FQR status was found to be significant for Bray-Curtis ($P=0.047$) and weighted-UniFrac measures ($P=0.01$). Enterobactericeae relative abundance was significantly overrepresented in the FQR subjects (adj. $P=0.03$), while the bacterial family Aeromonadaceae was absent in the culture group despite low relative abundance in non-FQR subjects (adj. $P<0.001$). At the species level, *Prevotella disiens* was significantly enriched in FQR negative subjects (adj. $P = 0.012$), while *Shigella flexneri* and *Proteus mirabilis* were significantly higher in the FQR positive group (adj. $P=0.017$ and adj. $P=0.028$, respectively).



Conclusions

Men colonized with FQR bacteria have:

- Less diverse bacterial communities (dysbiosis)
- Higher levels of Enterobacteriaceae
- Reduced levels of *Prevotella disiens*.
- Implications in pre/probiotic intervention

