

Ayelén D. Rosso<sup>1</sup>, Sofía Quesada<sup>1</sup>, Ma. Cecilia Cimolai<sup>2</sup>, Jimena Cerezo<sup>3</sup>, Claudia Milano<sup>3</sup>, Alberto Penas-Steinhardt<sup>1,2,5</sup>, Fiorella S. Belforte<sup>1,2,4</sup>.

**1** Lab. de Genómica Computacional, Dto. Ciencias Básicas, Universidad Nacional de Luján (GeC-UNLu)

**2** Programa de Estudios de Comunicación y Señalización Inter-Reino (PECSI)-UNLu

**3** Servicio de Gastroenterología, Hospital Nacional Posadas

**4** Instituto de Ecología y Desarrollo Sustentable, CONICET-UNLu

**5** Fundación Barceló - Instituto Universitario de Ciencias de la Salud, CABA

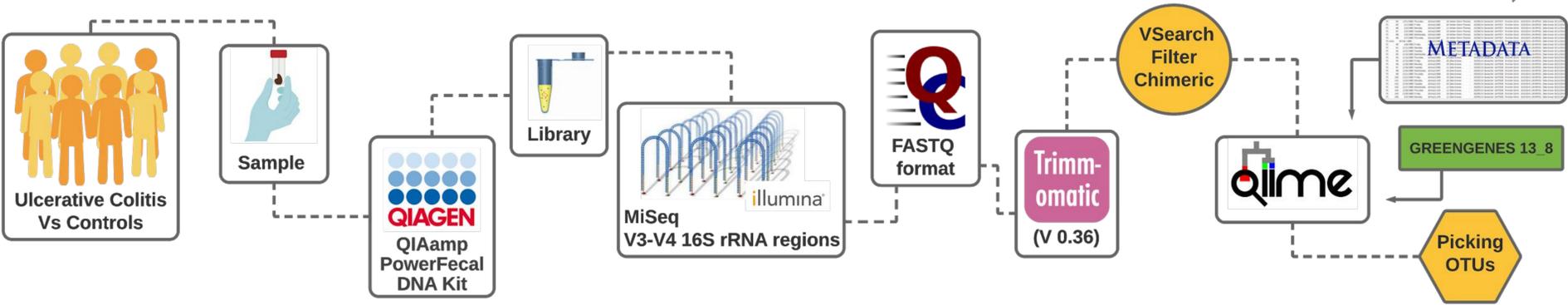
## Summary

Gut microbiota is implicated in many human disorders. Ulcerative colitis (UC) is a chronic inflammatory bowel disease. Although the specific cause is unknown, some genetic and environmental factors have been defined. The purpose of this study was to investigate whether there were differences in gut microbiota in Argentine UC patients vs non-UC controls. In this sense, 23 UC patients and 27 non-UC healthy controls matched by sex, age and BMI were included. DNA extraction was performed from 200mg of feces using Power Fecal DNA Isolation Kit (Qiagen). The hypervariable regions V3-V4 of the bacterial 16S gene was sequenced using MiSeq-Illumina system. Sequences generated were analyzed using quantitative insights into microbial ecology (QIIME) version 1.9.1 software package. To compare taxa relative abundance between groups, we performed linear discriminant analysis (LDA) effect implemented in LEfSe. Alfa diversity did not differ between CU patients and non-CU controls. However, we found that CU patients differ from non-CU controls in the observed community structure. In CU patients, the dominant phyla were Bacteroidetes (43.49±20.18%), Firmicutes (48.94±18.61%), Proteobacteria (4.13±7.12%), Actinobacteria (2.12±1.97%) and Verrucomicrobia (0.38±1.01%) while the principal phyla found in Controls were Bacteroidetes (60.06±13.540%), Firmicutes (32.82±13.51%), Proteobacteria (4.27±3.32%), Verrucomicrobia (1.45±3.18%) and Actinobacteria (0.81±1.46%). The linear discriminant analysis (LDA) effect size (LEfSe) method revealed that the genus *Bacteroides* and *Akkermansia* were higher in non-CU control and *Bifidobacterium*, *Eubacterium*, *Lactobacillus*, *Collinsella*, *Peptostreptococcus*, *Actinomyces*, *Streptococcus*, *Slackia* and *Dialister* in CU patients ( $p < 0.05$ , LDA score  $> 2$ ).

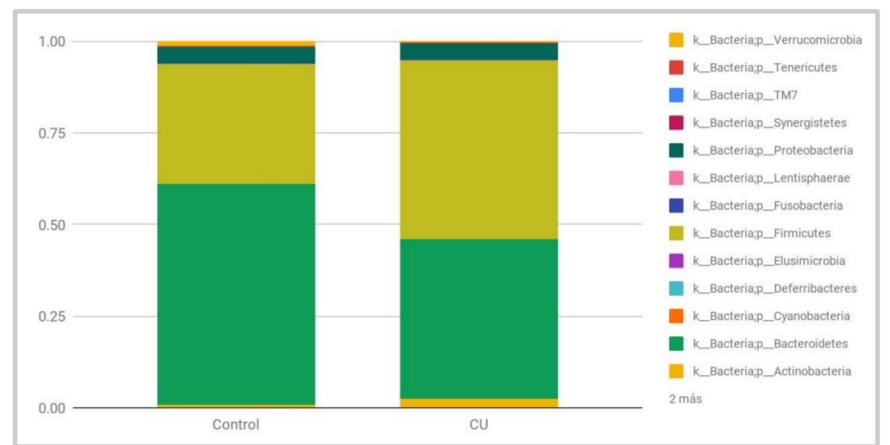
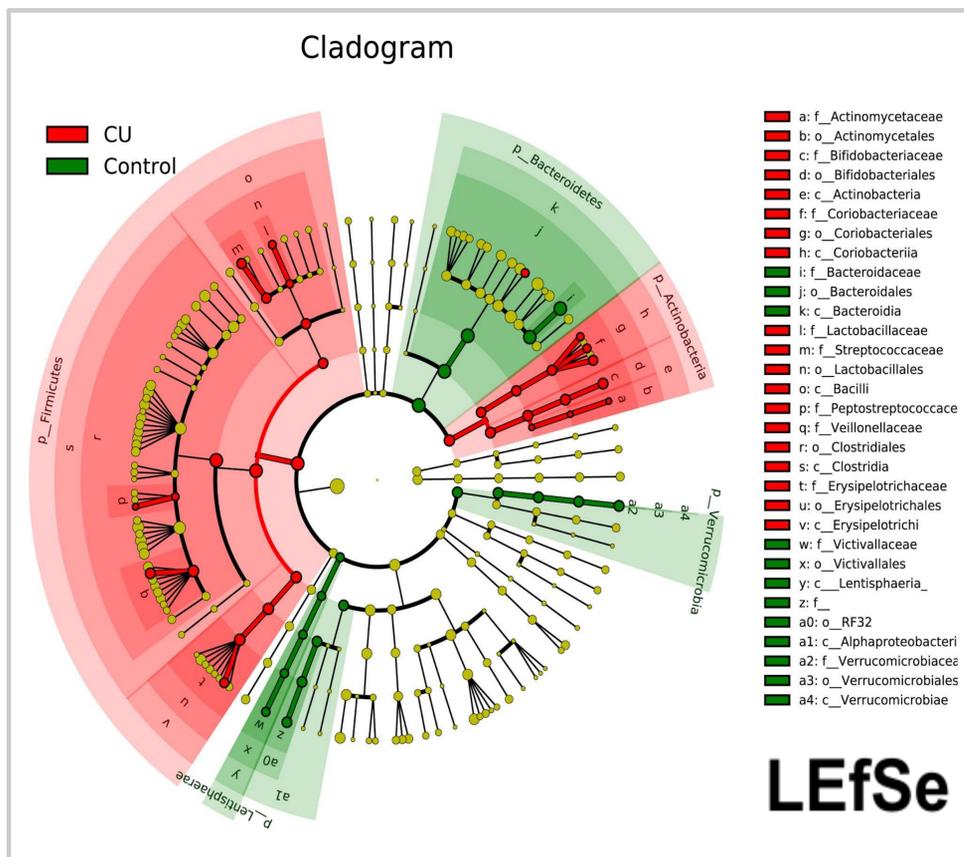
## Aim

The purpose of this study was to investigate whether there were differences in gut microbiota in Argentine UC patients vs non-UC controls.

## Workflow

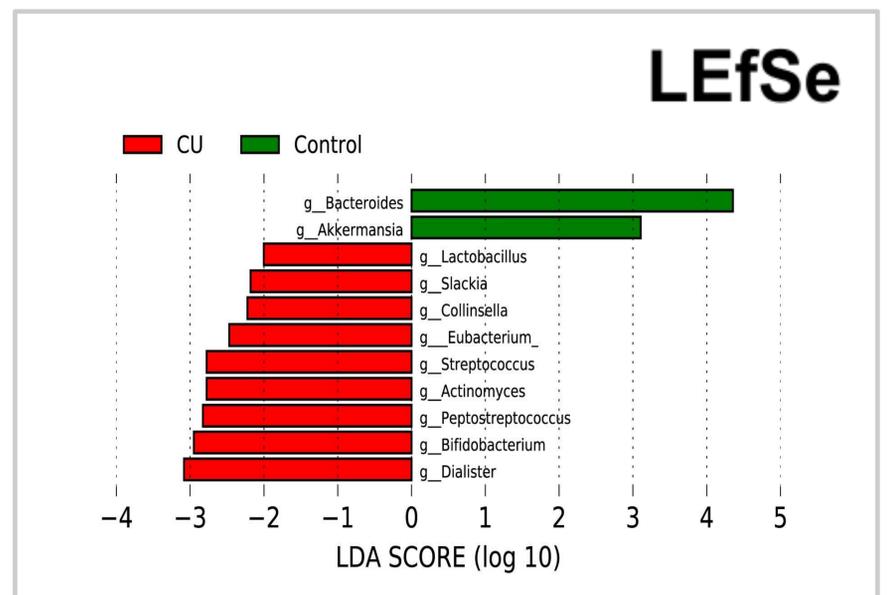


## Results



The relative abundance was greater in Bacteroidetes in Controls while in CU-Cases it was Firmicutes.

## LEfSe



We found that CU patients differ from non-CU controls in the observed community structure. Linear discriminant analysis (LDA) effect size (LEfSe) method revealed that the genus *Bacteroides* and *Akkermansia* were higher in non-CU control and *Bifidobacterium*, *Eubacterium*, *Lactobacillus*, *Collinsella*, *Peptostreptococcus*, *Actinomyces*, *Streptococcus*, *Slackia* and *Dialister* in CU patients.

## Conclusion and perspectives

Our results demonstrated that there were differences in gut microbiota in UC patients. These findings could provide the bases for further understand cause-effect relationship between microbial communities and CU in Argentine population.