

# Crohn associated microbial communities associated to colonic mucosal biopsies in patients of the western Mediterranean

Vidal, Roberto

Ginard, Daniel

Khorrani, Sam

Mora-Ruiz, Merit

Munoz, Raul

Hermoso, Marcela

Díaz, Sara

Cifuentes, Ana

Orfila, Alejandro

Roselló-Móra, Ramon

© 2015 Elsevier GmbH. Next generation sequencing approaches allow the retrieval of several orders of magnitude larger numbers of amplified single sequences in 16S rRNA diversity surveys than classical methods. However, the sequences are only partial and thus lack sufficient resolution for a reliable identification. The OPU approach used here, based on a tandem combination of high quality 454 sequences (mean >500 nuc) applying strict OTU thresholds, and phylogenetic inference based on parsimony additions to preexisting trees, seemed to improve the identification yields at the species and genus levels. A total of thirteen biopsies of Crohn-diagnosed patients (CD) and seven healthy controls (HC) were studied. In most of the cases (73%), sequences were affiliated to known species or genera and distinct microbial patterns could be distinguished among the CD subjects, with a common depletion of Clostridia and either an increased presence of Bacteroidetes (CD1) or an anomalous overrepresentat