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What microbial ecology can do for biotechnology: Looking at uncultured microbes in nature, a new gold mine

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Traditionally, research institutions or companies that bioprospect new microbial compounds with biotechnological applications start with the isolation of a microorganism in a Petri dish. However, Microbial Ecology in the last two decades has shown that cultivation techniques do not recover the vast majority of uncultured bacteria in nature, which means that 99% of microbes living out there remain totally unknown. That culture bias impacts severely on Biotechnology since an incredible number of metabolic pathways, enzymes, proteins and different microbial compounds with unquestionable biotechnological potential are still waiting for being discovered. To circumvent that limitation, metagenomics (i.e. sequencing of DNA directly extracted from the uncultured microbial community) has significantly and unquestionably broadened our knowledge in the last 10 years leading to the discovery of innumerable genes and pathways with biotechnological application. In metagenomics, like in a puzzle, genetic information is fragmented in millions of small pieces of DNA that somehow has to be afterward recomposed to make biological sense. Very recently, a new approach called Single Cell Genomics has emerged as a new and powerful strategy in Microbiology, opening thus new avenues to disentangle the genomic information and metabolic and biotechnological potential of most uncultured microbes. In Single Cell Genomics, we are able to sequence the DNA from a single, individual cell directly separated from the sample leading thus to a new manner of bioprospection. So, for instance, a lab searching for new glycosidases, proteases, lipases, or theoretically interested in almost any target chemical substrates might now use Single Cell Genomics. In the talk, the author will focus on the biotechnological application of this new approach and show several examples of the usefulness of Single Cell Genomics, such as in biofuel production or bioprospection of new enzymes and compounds.

Biography

Manuel Martinez-Garcia received his PhD in Molecular Microbial Ecology from University of Alicante, Spain in 2005. In 2006, he joined the Division of Microbiology as assistant lecturer of Microbiology. During that period he focused on the study of the diversity and function of uncultured marine microbial symbionts in addition to the study of extremophile microorganisms by using different molecular and physiological techniques. He conducted three postdoctoral short stays in Europe: the Max Planck Institute for Marine Microbiology (Bremen), Ludwig-Maximilians University (Munich) and the Laboratory of Photosynthesis at the Academy of Sciences of the Czech Republic. During 2009-2011, he moved to USA, where as a Postdoctoral Researcher at the Single Cell Genomics Center (Bigelow Laboratory Maine, USA), he was developing cutting-edge techniques of Single Cell Genomics combined with Metagenomics and new sequencing platforms (Illumina and PacBio) to study the metabolic capabilities of uncultured marine and freshwater microbes.

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