

# 3<sup>rd</sup> International Conference on Clinical Microbiology & Microbial Genomics

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## Genomics and metagenomics for clinical microbiology diagnostics

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Bacterial genomics and metagenomics are new and powerful tools that can help in diagnostics processes. Bacterial genomics have already demonstrated its usefulness in the detection and management of outbreaks in the community and in hospital facilities. Traditional microbial genome sequencing relies upon clonal cultures, but the new era of genomics is facing a new challenge: the metagenomics analysis. In the next few years it is probable that metagenomics will be used in clinical diagnostic settings. Thus, metagenomics has the potential to revolutionize pathogen detection in laboratories by allowing the simultaneous detection of all microorganisms in a clinical sample. For viruses is useful for directly detecting pathogenic viruses without advance genetic information. The use of metagenomics for virus discovery in clinical samples can help in the understanding the etiology of unexplained illness. For bacteria, it should be reminded that only a small fraction of the phylogenetic diversity of Bacteria and Archaea is represented by cultivated organisms. Metagenomics will probably serve to identify new pathogens, and new infections caused by consortiums. Microbiome analysis will be an important field of research to define and validate new analytical tests based in the metagenomics analysis of different human microbiomes. Metagenomics has brought new challenges to bioinformatics. Cloud computing can solve the problem and publicly available software solutions would be needed to extend the use of cloud for the analysis of huge metagenomics and genomics data sets in a way designed to facilitate clinical microbiology diagnostics.

### Biography

Eduardo Pareja is a Medicine Doctor that begun working in transplant Immunology and did his PhD thesis about human HLA-DR antigens in 1981 while working as a professor of Biochemistry at The University of Cordoba. After that, he went to work at a regional hospital as Head of the Section of Immunology where he run a Transplant Immunology Unit and very soon he pioneered in Spain the application of Molecular Biology to clinical immunological environments. At the same time he worked in Bioinformatics and Theoretical Biology developing programs for tissue typing and genomic typing. In this period, he published different papers in International Journals, he directed several PhD thesis and designed innovative genomic typing methods for HLA-DR genes. The last years in the hospital he was in charge of Web Applications area in The Medical Informatics Department. In 2005, he with Raquel Tobes founded Era7 Bioinformatics ([www.era7bioinformatics.com](http://www.era7bioinformatics.com)). Working as the CEO of Era7, he has built a multidisciplinary team and led the company to the position in which Era7 Bioinformatics is the Next Generation Sequencing leader in Spain and an international company with presence in the USA offering a wide portfolio of Cloud Computing based bioinformatics solutions.

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