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TITLE OF PRESENTATION: *The information hidden in the human genome: from the history of populations to adaptation and disease*

Abstract of presentation

Studying genomes allows us to understand, based on the differences between them, the evolutionary processes that have occurred in the past and is currently the most powerful tool for reconstructing evolution, and in particular human evolution. On the other hand, it allows us to recognize where natural selection has been and where we have a whole new vision of the adaptation process. Last, but not least, these views have consequences on the disease risk that may be calculated at the individual level.

Biographical note

Professor of Biology at the Pompeu Fabra University (Barcelona). Group leader in the Evolutionary Biology and Complex Systems Program in this University. Promoter of the Institute for Evolutionary Biology, IBE (UPF-CSIC). His research field is in different aspects on the study of the human genome variation and diversity: human population genetics, molecular evolution, comparative genomics and the interaction between human evolutionary biology and other fields, including medicine, genetic of complex diseases, statistical genetics and others. Recent publications are mainly on the footprint of natural selection in the human genome and the emerging field of Evolutionary Systems Biology, with the relationship of molecular networks and adaptation in genome-wide perspective. He has published over 350 research papers, most of them since his major dedication to genome studies (since 1992). Director of ICREA (Institució Catalana de Recerca i Estudis Avançats) till 2015.