JOSÉ LUIS GÓMEZ SKARMETA   CV

PARTICIPANT AT:

CODING AND NON-CODING FUNCTIONS OF THE GENOME
BARCELONA CONFERENCE ON EPIGENETICS AND CANCER

October, 29th-30th, 2015, Barcelona

José Luis Gomez-Skarmeta, Professor, Spanish Research Council (CSIC), Principal Investigator and Scientific director of the Aquatic Vertebrate Platform at Centro Andaluz de Biología del Desarrollo, Sevilla, Spain

Professor José Luis Gómez Skarmeta has 26 years of experience in the Developmental Biology/Evolution/Genomics fields and has run an independent group since 1997. His areas of expertise are Developmental Biology (including Drosophila, Xenopus and zebrafish as animal models), Molecular Biology, Genetics, Functional Genomics and Epigenomics. In the last years he has been pioneering in combining recently developed molecular and developmental techniques to study the contribution of cis-regulatory elements and chromatin structure to development, evolution and human diseases. During his scientific career, Professor Gómez-Skarmeta has published 90 articles with a total of 3285 citations (Google Scholar). His current h-factor is 34 (Google Scholar). In the last ten years, he has directed or is directing, a total of 14 Research Grants. In 2009, he created the Aquatic Vertebrate Platform of CABD in 2009, an open research laboratory designed to facilitate the study of developmental mechanisms in lower vertebrates within a technological environment in continuous growth. This very successful Platform has been used by more than 50 national and international (Portugal, Holland, Germany, Chile, USA, UK) researched in the last 5 years.

JOSÉ LUIS GÓMEZ SKARMETA ABSTRACT

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Gene Regulation Dynamics and Chromatin Architecture During Development and Evolution

The generation of distinctive cell types that form different tissues and organs requires precise, temporal and spatial control of gene expression. This depends on specific cis-regulatory elements distributed in the non-coding DNA surrounding their target genes. We have generated maps of H3K4me3, H3K27ac, H3K27me3, ATAC-seq and DNA methylation at different developmental time-points of zebrafish embryogenesis. This study has revealed the high dynamics of the epigenome along early vertebrate development. How the huge and dynamic cis-regulatory information contained in the epigenome is organized in the genome? To address this, we have used 4C-seq to compare the regulatory landscapes of multiple genes in zebrafish and mouse embryos. Our studies demonstrate that most of them show developmental and evolutionary conserved 3D architectures that are likely essential for the correct regulation of these genes along vertebrate evolution and development. The study of the regulatory landscapes of some of these genes in the cephalochordate amphioxus and the sea urchin genome reveals that some of these 3D architectures has a evolutionary ancestral origin while other are vertebrate innovations.