B·DEBATE International Center for Scientific Debate BARCELONA

CRG Centre for Genomic Regulation

RAGNHILD ESKELAND

CV

PARTICIPANT AT:

CODING AND NON-CODING FUNCTIONS OF THE GENOME

BARCELONA CONFERENCE ON EPIGENETICS AND CANCER

October, 29th-30th, 2015, Barcelona

Ragnhild Eskeland, Project leader, Department of Biosciences, University of Oslo, Norway and Associate Professor II, Department of Molecular Biology, University of Bergen, Norway

Background in Molecular Biology and Biochemistry (Cand. Scient., Molecular Biology, Sars International Centre for Marine Molecular Biology and University of Bergen, Norway and PhD in Biology, University of Munich, Germany). Project leader of the Chromatome Team, Department of Biosciences, University of Oslo. Her main research interests are the regulation of gene expression through higher order chromatin structure and nuclear organization during stem cell differentiation and in cancer cells. Her team focuses on the role of histone variants and protein complexes in regulation of chromatin structure during embryonic stem cell differentiation and in cancer cells. She is also interested in the effects of drug exposure on the epigenetic landscape in human embryonic stem cells and is a member of PharmaTox Strategic Research Initiative, UiO.

B·DEBATE IS AN INITIATIVE OF:

biocat "la Caixa" Foundation

B·DEBATE International Center for Scientific Debate BARCELONA

CRG Centre for Genomic Regulation

RAGNHILD ESKELAND

ABSTRACT

PARTICIPANT AT:

CODING AND NON-CODING FUNCTIONS OF THE GENOME

BARCELONA CONFERENCE ON EPIGENETICS AND CANCER

October, 29th-30th, 2015, Barcelona

Ragnhild Eskeland, Project leader, Department of Biosciences, University of Oslo, Norway and Associate Professor II, Department of Molecular Biology, University of Bergen, Norway

The Role of Two Isoforms of Histone H2A.Z in Embryonic Stem Cells

Changes to the composition of nucleosomes, such as histone variant replacements, are important mechanisms for chromatin-based gene regulation. Histone variant H2A.Z is essential in mammals, and has been linked to both transcriptional activation and repression. In differentiated cells, H2A.Z containing nucleosomes are enriched with H3K4me3 around the transcriptional start sites (TSS) of active genes. However, in embryonic stem cells (ESCs) H2A.Z also co-localizes with the repressive mark H3K27me3 at developmentally regulated genes. There are two genes encoding H2A.Z (H2AFZ and H2AFV). The promoters of these genes are significantly different, but their protein products differ in only three amino acids and no variant-specific antibody is available. We have therefore utilized the CRISPR/Cas9 genome editing technology to endogenously tag the two H2A.Z genes in murine ESCs. The resulting cell lines express the targeted H2A.Z variant with an N-terminal TY1-tag. These cell lines provide us with important tools for investigating the characteristics of H2A.Z.1 and H2A.Z.2, such as their genome-wide enrichment by ChIP-seq, variant specific changes in protein levels upon differentiation, posttranslational modifications and interaction partners.

B·DEBATE IS AN INITIATIVE OF:

biocat "la Caixa" Foundation