Genomics-2013
International Conference on
OMICS Group Conferences
Accelerating Scientific Discovery
Functional and Comparative Genomics & Pharmacogenomics
November 12-14, 2013 DoubleTree by Hilton Hotel Chicago-North Shore, USA

Retrotransposons as the Key for the Evolution of Genomic Imprinting in Mammals

Shunsuke Suzuki

Shinshu University, Japan

Abstract

Genomic imprinting is a unique epigenetic regulatory mechanism which induces parent-of-origin-dependent expression to subset of genes. In higher vertebrates, genomic imprinting has been found only in viviparous mammals (the eutherians and marsupials) and some imprinted genes have essential roles associated with fetal and placental development and post-natal care. Therefore, how genomic imprinting arose during mammalian evolution is of great importance to understand its relevance to the evolution of these mammalian traits. Parent-of-origin-dependent expression of imprinted genes is mostly associated with parental allele-specific DNA methylation of the CpG islands called differentially methylated regions (DMRs). Although the essential role of DMRs for genomic imprinting mechanism has been well established, little is known about how they evolved. Comparative genome analysis in the *SGCE-PEG10* domain revealed that *PEG10*, a retrotransposon-derived imprinted gene essential for placental development, was acquired in the common ancestor of marsupials and eutherians. Furthermore, in the tammar wallaby, both imprinting and differential methylation were restricted to *PEG10* unlike eutherians, suggesting that the insertion of *PEG10* was the origin of imprinting in this domain. Also, comparative genome analyses in other imprinted domains showed that most DMRs have emerged as novel CpG islands during mammalian evolution. I suppose that the emergence of novel CpG island consequent of retrotransposon insertion was the key genomic change for the acquisition of DMRs which evolved imprinted domains in mammals.

Biography

Shunsuke Suzuki has completed his PhD at the age of 27 years from Tokyo Institute of Technology and postdoctoral studies from Tokyo Medical and Dental University and The University of Melbourne. He is the assistant professor of Epigenomics Division, Frontier Agriscience and Technology Center, Faculty of Agriculture, Shinshu University, Japan. Currently his researches focus on functional and dysfunctional roles of retrotransposons for the regulation of gene expression in the human genome.