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Emergence of novel CpG island is the key genomic change for the evolution of mammalian genomic imprinting

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Genomic imprinting is an epigenetic 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 functions in fetal and placental development and maternal behavior for 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 that evolved imprinted domains during mammalian evolution.

Biography

Shunsuke Suzuki has completed his PhD from Tokyo Institute of Technology in 2006 and Postdoctoral studies at Tokyo Medical and Dental University (2006-2009) and The University of Melbourne, Australia (2009-2012). He is now an Assistant Professor (tenure-track) at Epigenomics Division, Frontier Agriscience and Technology Center, Faculty of Agriculture, Shinshu University, Japan. His work is focused on the role of retrotransposons in the evolution of gene regulatory mechanisms in mammals.

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