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Evolutionary analysis of A-to-I RNA editing across 12 vertebrate species

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Adenosine-to-Inosine (A-to-I) editing is a widely observed co-/post-transcriptional mechanism across metazoan, which contributes to the transcriptome diversity and flexibility without altering genomic sequences. Although great attention has been paid to identification and biogenesis of A-to-I RNA editing, the questions where and when this modification occurs remain mostly unclear. In this study, we described a pipeline to detect high-confidence editing sites using clustering and conservation strategies based on RNA sequencing data alone, without using single-nucleotide polymorphism information or genome sequencing data from the same sample. This pipeline consistently achieved high accuracy, regardless of sequencing depth, the number of compared samples, species or where the editing sites were located. We then applied this method to identify RNA editing events in 12 vertebrate species (from zebrafish to human), thereby constructing an evolutionary landscape of editomes. Our result revealed that highly clustered and conserved editing sites tended to have a higher editing level and a higher magnitude of the ADAR motif. We showed that the ratio of the frequencies of non-synonymous editing to that of synonymous editing remarkably increased with increasing the conservation level of A-to-I editing, indicating that the highly conserved editing events occurred more frequently at non-synonymous sites than at synonymous sites. These results thus suggest potentially functional benefit of highly clustered and conserved editing sites. Our study thus provides an evolutionary aspect of A-to-I RNA editing across vertebrate species, expanding this important but understudied class of non-genomically encoded events for comprehensive characterization.

Biography

Te-Lun Mai has completed his PhD from Department of Physics, National Taiwan Normal University. He is currently a Postdoctoral Fellow at Genomic Research Center, Academia Sinica. He has published seven papers in peer-reviewed journals in computational biology concerning folding and evolution of membrane proteins, synchronized activities of neuronal networks, RNA editing and circular RNA.

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