Co-evolution of genome and mobilome

Guest Editor

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Message from the Guest Editor

Dear Colleagues,

The mobilome is defined as the entire set of mobile elements of a genome, which can be categorized into four classes: self-splicing molecular parasites, plasmids, bacteriophages, and transposons. Transposons, once regarded as “junk” DNA in genome, which can move about or propagate within the genome, are the major constituents of the mobilome, and are distributed extensively in prokaryotic and eukaryotic genomes. Transposons are typically classified into two classes according to their transposition mode: RNA and DNA transposons. RNA transposons are also named as retrotransposons, which need RNA intermediate in their development cycle. Retrotransposons account for 30–50% of mammalian genomes, representing major genomic parasites of mammals, which are classified into three main groups: long interspersed nuclear elements (LINEs), short interspersed nuclear elements (SINEs), and long terminal repeats (LTRs), including endogenous retroviruses (ERVs). In general, the retrotransposon landscape of mammal genomes is dominated by LINEs and SINEs, followed by LTR retrotransposons. While multiple transposition mechanisms of DNA transposons have been defined and they can be subdivided into three major types: the cut-and-paste, peel-and-paste, and self-synthesizing transposons.

Increasing evidence indicates that mobilome plays significant roles in gene and genome evolution and is the major determinant of genome size in vertebrates and plants. They can alter the host genomic
landscape by horizontal transfer (HT) between non-mating species and are a key cause of structural variations of genomes, even resulting in the genomic rearrangement and chromosomal recombination, which are increasingly known as major factors in eukaryotic genomic evolution. One way that mobilome contributes to genome evolution is through mobilome exaptation, a process whereby mobilome, which usually persists by jumping in the genome, sometimes be beneficial at the species level by producing evolutionary innovation, such as modifying existing genes, or giving rise to novel phenotypic genes, or contributing to cis-regulatory DNA components and transcription network modifications, that may lead to key adaptive traits and potentially speciation. Thus, profiling the co-evolution of mobilome and genome will help to display the process of gene and genome evolution, promote the understanding of speciation, adaptation, and the origin of biodiversity.

In addition, studies in two closely relative research areas of co-evolution of mobilome and genome are also encouraged to submit to this special issue. One is the genetic tool development based on active transposon. Transposons, particularly cut-and-paste DNA transposons, can be considered as natural and nonviral gene delivery vehicles. Many active DNA transposons have been developed into efficient gene transfer tools and applied for germline transgenesis, insertional mutagenesis (such as gene trapping and enhancer trapping) in important model organisms, and human gene therapy. Furthermore, to overcome the main drawback of random (unspecific) integration of transposons, different strategies also have been devised to achieve enhanced specificity of transposon-mediated gene targeting. These include the fusion of transposase with different type nuclease including zinc finger proteins (ZFP), transcription activator-like effector proteins (TALE), and CRISPR-associated (Cas) protein, recombinase (such as Tn3 recombinase). Second is the genetic markers development based on retrotransposon insertion polymorphism (RIP). It is commonly accepted that RIP markers represent highly genomic coverages, large amounts, and high polymorphisms in the genomes of animals and plants, display great potential for population genetic analysis, QTL mapping, and genome selection compared with other marker systems, and Retrotransposon-based markers have been reported extensively and widely used in studies of genetic diversity, phylogeny, genetic mapping, and cultivar identification in plants and animals.

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