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Mobile Elements in Phylogenomic Reconstructions

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Deadline for manuscript submissions:
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Message from the Guest Editors

Retrotransposed elements (REs), a special class of transposable units that arise via reverse transcription of RNA intermediates and subsequent insertion, comprise a substantial proportion of eukaryotic genomes. Their insertion, while not continuous over time, is largely random and virtually homoplasy-free. Their presence/absence patterns provide historical evidence of speciation events, making them excellent phylogenomic markers.Depending on the ancestral timeframe of speciation events of a given lineage, incomplete lineage sorting may somewhat confound these patterns, necessitating special multidirectional screening strategies to clarify evolutionary reconstructions. Today, however, many such computational tools exist and are available to evolutionary scientists everywhere to partially automate these screenings. REs have now been used to significantly resolve the conundrums present in many phylogenetic trees. This Special Issue will be unique in presenting methodologies and strategies of exploring phylogenetically diagnostic REs and their usefulness in revealing new phylogenies.

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Message from the Editor-in-Chief

Genes is central to our understanding of biology, and modern advances such as genomics and genome editing have maintained genetics as a vibrant, diverse and fast-moving field. There is a need for good quality, open access journals in this area, and the *Genes* team aims to provide expert manuscript handling, serious peer review, and rapid publication across the whole discipline of genetics. Starting in 2010, the journal is now well established and recognised. Why not consider *Genes* for your next genetics paper?

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