Special Issue

Evolution of Root Nodule Symbioses

Message from the Guest Editor

In the last two years, the increased application of phylogenomics approaches enabled by the growing number of sequenced genomes of host plants has led to breakthroughs. Large-scale analyses of epigenetic changes and of non-coding RNAs have been added to the arsenal of researchers. Nevertheless, there are still a lot of open questions which should be answered based on the available tools: What is the basis for symbiotic efficiency—the adaptation of a particular microsymbiont to a particular host is an ongoing evolutionary process, but what are the molecular players? What is the molecular basis for the induction of legume nodules without infection threads formed in root hairs? Which host features are responsible for the accommodation of rhizobia in symbiosomes instead of fixation threads? What are the signal factors of *Frankia* strains? What are the reasons for the loss of the symbiosis in the majority of plant lineages derived from the common ancestor of Fabales, Fagales, Cucuribtales, and Rosales? The forthcoming Special Issue aims to present a platform for the discussion of these new developments in root nodule symbioses.

Guest Editor

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Deadline for manuscript submissions

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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?

Editor-in-Chief

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