



CALL FOR PAPERS

Lots of research efforts have been dedicated to the identification of genetic mutations and understanding their consequences on phenotype (especially human health). In the recent decade, there is an emerging interest in the possibility that changes at levels other than the genetic information could also have long-lasting consequences for the phenotypes. These changes usually do not involve direct alteration of underlying DNA sequences and fall under the term “epigenetics,” which has been used to describe the study of heritable information that is not fully explained by DNA sequence variation. Thanks to the cheaper and high-through sequencing technologies, epigenetic information has been profiled at high resolution in many species recently. Their central roles in developmental processes and diseases, response to the environment, and natural variation in gene expression levels have also begun to be revealed. The main focus of this special issue is DNA methylation, which is a major type of epigenetic modification and involves covalent modification of genomic DNA.

We cordially invite investigators to contribute research papers dedicated in understanding the role of DNA methylation in regulation of gene expression and phenotypic variation as well as in development process and evolutionary mechanisms across diverse taxa.

Potential topics include, but are not limited to:

- ▶ How do epigenetic patterns, especially DNA methylation, change over evolutionary time and impact evolutionary dynamics and vice versa?
- ▶ Mechanisms revealing the regulation pattern (e.g., cis- and/or trans-acting), type of epialleles (e.g., pure, facilitated, and obligate), and stability for the transgenerational inheritance of DNA methylation
- ▶ Identifying the determinants of epigenetic patterns, such as the quantitative trait loci contributing the DNA methylation variation among natural populations
- ▶ Discovering the pattern and distribution of DNA methylation in either genomewide or targeted manner to reveal the molecular mechanisms of DNA methylation functions
- ▶ Method developments for DNA methylome profiling: cost-effective protocols and/or technologies for identifying and characterizing novel DNA base modifications

Authors can submit their manuscripts via the Manuscript Tracking System at <http://mts.hindawi.com/submit/journals/ijg/eumlh/>.

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