

Special Issue on Genomics of Nonmodel Invertebrates

CALL FOR PAPERS

The advent of Next-Generation Sequencing (NGS) technologies has significantly improved sequencing throughput, while greatly reducing costs. Multiple joint efforts have been launched aiming at sequencing the genome and/or transcriptome of different animal species. Understandably, the selection of the taxonomic groups targeted is largely biased by the agricultural or medical relevance of the species included.

About 95% of all animals in our planet are invertebrates: they play crucial roles in the functioning and maintenance of ecosystems, and many of them have a direct impact on our lives, being cultured and harvested for food, being used in pharmacological research, or being involved in human health issues (e.g., parasites and vectors), among other things. However, despite their importance, most invertebrate species have been largely overlooked by the big sequencing consortia. Only the recently formed GIGA (Global Invertebrate Genomics Alliance) community has focused its efforts on the sequencing of invertebrate genomes, with an emphasis on marine taxa because of their outstanding phyletic diversity.

The goal of this special issue is to get a better understanding of ecological and evolutionary aspects of nonmodel invertebrates using a variety of genomic tools.

Potential topics include but are not limited to the following:

- ▶ Genome and/or transcriptome sequencing efforts of nonmodel invertebrates: genome structure, function and evolution, epigenetics, and growth-, immune-, stress-, developmental-, and tissue-specific patterns of gene expression. Annotation of coding and noncoding sequences, new methods and/or software for genome/transcriptome in silico functional annotation, orthology detection, and comparative studies
- ▶ Gene expression: evolution, development, epigenetics, growth, immune system, stress, tissue-specific patterns of gene expression, and interaction with the environment, symbionts, or hosts
- ▶ Metaomics of environmental samples: community-level and molecular-based approaches; metagenomics, metabarcoding, metatranscriptomics, development of new or improved methods for reducing bias and accurately annotating bulk community data, and development and comparison of taxonomic and phylogenetic diversity indexes. Population genomics, diversity, and structure: adaptive molecular variation, population demography, and evolutionary history. Population dynamics of invasive/endangered species and effects and consequences of invasions on biodiversity
- ▶ Phylogenomics: reconstruction and clarification of evolutionary relationships between different taxonomic groups and application of genomic approaches to evolutionary biology
- ▶ Genomics of aquaculture: linkage mapping, identification and analysis of genes related to economically important traits, molecular marker assisted selection, and domestication process
- ▶ Genomics of nonmodel invertebrates involved in human disease and health issues such as parasites, vectors, or emerging human pathogens

Authors can submit their manuscripts through the Manuscript Tracking System at <https://mts.hindawi.com/submit/journals/bmri/evolutionary.biology/gmi/>.

Papers are published upon acceptance, regardless of the Special Issue publication date.

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Submission Deadline

Friday, 27 October 2017

Publication Date

March 2018