Editorial

Invertebrate epigenomics: the brave new world of the spineless

Epigenetics was initially defined more than 50 years ago by Conrad Waddington as: ‘the branch of biology which studies the causal interactions between genes and their products which bring the phenotype into being’ [1, 2]. Whereas this original definition of epigenetics was used to describe a sequence of irrevocable developmental decisions undertaken by the cells in the embryo to narrow their developmental choices, the word epigenetics has since evolved to define various, often heritable, DNA sequence-independent changes that can result in altered transcriptional outputs. More precise definitions of the word epigenetics were proposed throughout recent years [3, 4] even though a consensus on its precise meaning has not yet been reached. Nonetheless, Conrad Waddington was right in identifying that embryogenesis is governed by a series of signals that progressively define cell fate and shape the embryo. Nowadays, we know that such signals consist of regulatory mechanisms such as DNA methylation, histone modifications, long non-coding RNA and others.

Myriad studies carried out throughout the past decades transformed our understanding of the role of epigenetic processes in embryonic development and evolution. More recently, the use of massively parallel DNA sequencing in numerous epigenome profiling techniques has yielded a vast wealth of epigenomic data that have allowed us to gain profound insights into the nature of these processes. However, studies in vertebrates, and in particular mammalian models, have garnered most attention, often marginalizing equally important reports from invertebrate models. In this special issue of Briefings in Functional Genomics, we will provide an overview of recent epigenomics studies conducted in key invertebrate models and discuss the implications of epigenetic mechanisms in invertebrate development, caste specification, homeostasis and evolution.

To begin with, Maleszka and colleagues put forward an exciting theory of how genomic and epigenomic regulatory degeneracy may have played a role in generating organismal complexity and enhancing evolvability. This enticing theory is supported by numerous examples ranging from Caenorhabditis elegans to humans, thereby emphasizing the universal nature of such regulatory organization. Nowadays, it is believed that the massive phenotypic disparities observed between organisms with similar gene numbers are generated through regulatory differences. A more nuanced understanding of species-specific, epigenomic adaptations will be needed in order to start addressing such intriguing conundrums. One interesting example of such a specific adaptation mechanism is highlighted in the review by Duffy and colleagues. The unique organizational features of the Plasmodium falciparum genome appear to hold a key to understanding the pathogenic processes associated with malaria. During its intra-erythrocytic lifecycle, this pathogenic protist maintains an unusual chromatin conformation with the majority of its genome retained in the euchromatin compartment. Furthermore, P. falciparum employs a range of epigenetic mechanisms to control its var virulence genes through a complex repertoire of histone variants and chromatin remodeling activities. The authors discuss the current and future therapeutic use of histone modifying enzyme inhibitors in treating malaria.

Moving up the phylogenetic ladder, Gavery and Roberts review the current knowledge regarding DNA methylation in bivalves and explore its putative role in these molluscs, offering unique perspectives on this modification in both evolutionary and ecological contexts. Using the pacific oyster (Crassostrea gigas) as an example, the authors discuss the possible functions of gene body DNA methylation in stochastic and targeted gene regulation. Gene body DNA methylation appears to be the ancestral form of this modification as both vertebrates and invertebrates share this common genomic pattern. Interestingly, many invertebrate organisms appear
to have suffered from an evolutionary loss of DNA methylation. One such organism is the nematode *C. elegans* which, due to its precise developmental lineage map, relatively small genome and amenability to genetic manipulation, has become one of the all-time favorite epigenetic models. The review by González-Aguilera and colleagues explores numerous epigenetic mechanisms used throughout the *C. elegans* lifecycle. The authors highlight the role of histone modifications in the anchoring of chromatin to the nuclear periphery and discuss the implications of histone modifying enzymes in *C. elegans* longevity. The inclusion of *C. elegans* in the modENCODE consortium [5], and the increased frequency of its use in epigenomics studies, paints a bright future for the exploration of epigenomic modifications in the form and function of this lovable nematode.

A highly intriguing aspect of epigenomic regulation in the animal kingdom is the generation of different phenotypes by the same genome. One such phenomenon that is often associated with labor division (e.g. workers and queens) and found in insect societies is called polyphenism. R. Bonasio reviews the role of epigenetic control in ant polyphenism with a specific emphasis on DNA methylation and histone modifications. Whereas the exact function of epigenetic mechanisms in the context of caste specification is still not clear, the almost exponential increase in DNA sequencing power together with novel genome manipulation tools will soon allow us to tackle these issues in a range of different species and yield more definitive insights. Finally, in the last review article of this issue, N. Iovino discusses oocyte development and early *Drosophila melanogaster* embryogenesis from an epigenetic perspective, with a particular focus on posttranslational histone modifications.

In this special issue, we review the roles of epigenomic phenomena in various invertebrate organisms. This compilation of recent findings can be considered a treasure-trove of novel epigenetic paradigms that can be explored only in certain organisms, some of which are still not well established and widely used, but from which important insights may be gleaned that have far reaching implications beyond these only spineless species. Major technological advances are now allowing a thorough epigenomic exploration of more exotic organisms, casting a wider net in our search for the roles of these important regulatory processes, likely leading to a better general understanding of processes related to embryonic development, disease etiology and evolution.

Ozren Bogdanovic

AR Centre of Excellence in Plant Energy Biology
The University of Western Australia, Perth, WA 6009, Australia

o.bogdanovic@gmail.com

References