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Marine Genomics

Special Issue
Marine genomics for evolution and development

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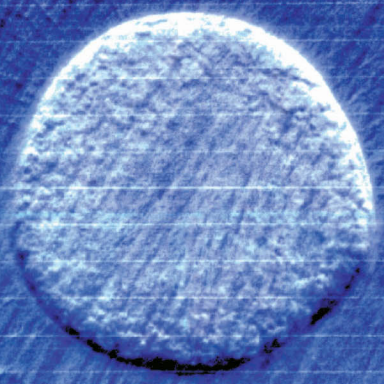

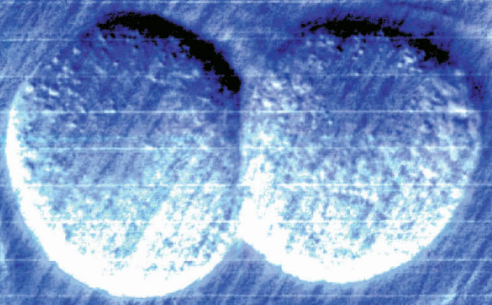

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Editorial

Genomics going wild: Marine sampling for studies of evolution and development

Comparative genomics and comparative developmental biology are strongly connected fields that synergistically influence each other. In order to understand the evolution of animal forms, it is necessary to understand how the genomic information is translated into morphology during the development of an organism. The continuous progress in sequencing technology accelerates the collection of genomic information of animals and facilitates the genomic sampling of many species. Albeit still facing difficulties with heterozygosity, large genome sizes and repetitive regions, the transition of animal genome sequencing to a laboratory routine is foreseeable.

The major challenge we face is to understand the connection between changes in genomic sequences and changes in morphology. The key to disclose the relationship between genotype and phenotype is a deep comprehension of the developmental processes and their evolutionary modifications. Genomics and transcriptomics have entered the toolkit of comparative developmental biologists and these methods continue to become more automated and improve in quality over time. However, bioinformatics alone cannot explain the essential evolutionary changes in embryos and have to be followed up with organismal work. Although recent bioinformatic attempts promise solutions for long held problems in animal evolution, they remain just hypotheses when they are not verified with organismal approaches (Hashimshony et al., 2014). These approaches offer a hint to where changes in genomic and transcriptomic regulation might be connected to morphology and thus can only provide a starting point for investigations. Moreover, the insights gained when quantitative embryonic gene expressions turn into differently shaped hourglasses are questionable, since these approaches largely neglect the diversity of embryonic development and the different roles genes can play during development (Kalinka and Tomancak, 2012).

One of the reasons that organismal verifications of recent bioinformatic approaches are still lacking is that working with embryos is an extremely difficult task. There are currently over 200 sequenced animal genomes; these genomes outnumber by far the species in which developmental studies are currently being conducted (Dunn and Ryan, 2015). This discrepancy between sequenced animal genomes and the number of species in which developmental studies are actually performed will increase. Since evolutionary biology is a comparative approach, it cannot be restricted to just a handful of model species. Even when some nematodes, insects and vertebrates are investigated in the greatest detail, their common evolutionary ancestry would remain obscure when developmental biology does not sample species that separate these groups in the animal tree.

There is a clear need to study the embryogenesis of many more species with modern tools targeting preferably marine species, since major events in animal body plan evolution happened in the ocean. The animals need not only to be found in the field at the right time during their reproductive season, but also needs to be convinced to give embryos to the investigator who has to know what tools can be applied to study them. The embryos – when successfully obtained – are 'wild' and this approach differs a lot from the work with domesticated species. In other words, for each species an attempt has to be made that is comparable to Thomas Hunt Morgan's first establishment of *Drosophila melanogaster* as laboratory animal. But many species simply cannot be cultured in the laboratory and will have to be collected from the field. There is no automation or scalability of this work foreseeable and this hands-on approach is needed to pioneer marine embryos. The current hype of the CRISPR/Cas9 genome editing technology, is turning out to be very difficult to implement in most animal species and will not be amenable for conducting this approach to study their embryogenesis, simply because these species cannot be cultured in the laboratory. However, the approach to study embryos in a comparative way is clearly High Risk–High Gain: Broadening the taxon sampling for embryological studies will deliver solid insights into the evolutionary processes that shape organismal forms. It is a necessary next step that cannot be replaced by the study of established domesticated species. Comparative genomics in this respect can be considered as a tool that will facilitate the study of embryos. The grand challenge for the evolutionary developmental biology (EvoDevo) community will therefore be to follow up this influx of genomics and transcriptomics data with experimental embryology and functional genomics to validate and further understand the biological processes that are occurring.

The European society for Evolutionary Developmental Biology (EED) aims to promote EvoDevo by regularly organizing meetings on this subject in Europe. Among many others, two symposia organized within the 5th EED meeting in Vienna (Austria) in 2014 addressed in part the above illustrated issues: The symposium "Uncovering the genomic bases of phenotypic change in the NGS era" discussed about the progress made by using Next Generation Sequencing technology in comparative genomics of non-model systems. The symposium "The evolution of sensory systems in the marine environment" addressed the importance of studying the enormous variety of organisms that evolved in the marine environment. From the many contributions to the meeting, we have assembled this Special Issue of Marine Genomics, consisting of three reviews and four full-length research articles, to give an overview of recent advances in the genomics and transcriptomics of marine 'non-model' systems for evolutionary developmental biology.

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