



## A joint effort of the Brazilian Evo-Devo community

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Thirty-five years ago, a field named ‘Evolutionary Developmental Biology’ (Evo-Devo) emerged from an interface between genetics and embryology that was settled within the current evolutionary framework. This field resurrected associations conceived more than 150 years before, and benefitted from the substantial expansion of molecular biology tools to consolidate a new approach for understanding organismal evolution. Evo-Devo has since achieved a special status in the Evolutionary Theory, with contributions for understanding themes as diverse as the molecular nature of adaptation processes, the origin of new phyla, and the emergence of evolutionary innovations. The Evo-Devo conceptual identity resides on two major theoretical categories (Minelli, 2015): 1) the concept of *genotype-phenotype maps*, which aggregates concepts such as evolvability, robustness, modularity and developmental constraints (see also West-Eberhard, 2003 and Pigliucci, 2010), 2) and the *innovation triad*, which discusses the origin of new phenotypes and evolutionary innovations and novelties (Minelli, 2015). Researchers working on Evo-Devo have established scientific societies both in Europe (Euro Evo-Devo) and America (Pan-American Evo-Devo); in Brazil, most research groups self-entitled ‘Evo-Devo labs’ have a recent history, and are mainly led by young scientists trained abroad in the field. Some of these Brazilian Evo-Devo labs often interact in the different scientific meetings held in Brazil and abroad, and the Brazilian Genetics Society (SBG) has been particularly supportive for Evo-Devo symposia in the past years. In the 2014 annual SBG meeting, the idea was conceived of launching a special series of articles on Evo-Devo in *Genetics and Molecular Biology*, GMB, the official SBG journal. The current

GMB issue comprises seven manuscripts led by Brazilian Evo-Devo labs, which encompass diverse taxa including plants (Scorza and Dornelas), basal metazoans (Lanna), flatworms (Quiroga *et al.*), arthropods (Santos and Hartfelder) and chordates (Lima *et al.*; Singarete *et al.*), and range from molecular evolution (Albuquerque *et al.*; Singarete *et al.*) and gene expression (Lima *et al.* Santos & Hartfelder) to embryogenesis and related processes (Lanna; Quiroga *et al.*; Scorza and Dornelas). This Evo-Devo article series in GMB provides a grasp on how research in Evo-Devo has grown in Brazil over the past years, often using native or so-called non-model species to address major questions in Evolution and Development.

### Synthesis of the Evo-Devo GMB article series

The current GMB issue presents seven manuscripts led by Brazilian Evo-Devo labs, as aforementioned. This section synthesizes the referred articles, which together provide an overview of the taxonomic and conceptual diversity contemplated by Evo-Devo research produced in the Country.

Two studies included in the current GMB issue approach Evo-Devo of nervous system, one focusing on flatworms (Quiroga *et al.*) and the other one in birds (Lima *et al.*). Formation of the nervous system in a neglected group of marine flatworms, the Polyclads, has been studied by Quiroga *et al.* under a phylogenetic framework, which became possible after recent advances in transcriptome analyses. These authors provide a complete histological analysis of nervous system development in twelve species of Polyclads, and include data on nerve cord arrangement and cell type evolution to offer a unique view of Polyclad

body plan organization. The other contribution for Evo-Devo of the nervous system in this GMB issue comprises vocal learning in birds (Lima *et al.*), addressing a question about the presence in the antbird *Willisornis poecilinotus* of a song nuclei circuitry that has been previously described in related bird species. The authors used gene expression and histological analyses to conclude that at least some components of the circuitry associated with evolution of vocal learning could be ancestral to the Passeriformes lineage, a very important finding given the recent publication of an avian tree of life.

Another important question addressed in Evo-Devo is whether evolution of morphological diversity imprints molecular signatures in the amino acid sequences of developmental genes. The topic was approached by Singarete *et al.* who sequenced the first exon of HoxA13 in species from three snakelike tetrapod lineages: Serpentes, Amphisbaenia and Gymnophiona. The authors identified positive selection in snakes but not amphisbaenians and caecilians, suggesting that this exon does not have limb-specific motifs. Evolution of morphological diversity has also been investigated based on the molecular nature of phenotypic plasticity, where Gonçalves-Santos and Hartfelder studied how the same genotype in honey bees produces the different phenotypes identified in caste differentiation. These authors provided an extensive morphological and transcriptomic analysis of hind leg development in Hymenoptera. As a result, several candidate genes, including transcription factors and signaling molecules, were differentially expressed in hind legs discs of workers and queens, highlighting how changes in feeding and behavior can be translated in a genetic program.

New regulators of development have been reviewed by Albuquerque *et al.*, in a manuscript that described recent discoveries of polycistronic genes in animals and plants. Polycistronic genes are unusual among eukaryotes because they encode several small open reading frames (smORFs) in a single transcript. These smORFs are translated into functional small peptides, which similarly to hormones can signal far from its producing cell. The authors discuss how the development of new bioinformatics tools and the dis-

covery of new smORFs bioactive molecules might impact future Evo-Devo studies.

Finally, two manuscripts in the current GMB issue advertise for inclusion of relegated taxa in Evo-Devo studies. Lanna claims that Brazilian non-bilateria biodiversity must be better represented in the field, especially considering recent genomes and transcriptomes of several basal metazoans that recently became available. The author explains the controversial phylogenetic hypotheses for non-bilaterians, and offers an extensive discussion about the origin of gastrulation in Metazoa. Lanna also provides an interesting discussion about the nature and evolutionary roots of the stem cell concept and the genetic programs of somatic and germ cells in basal metazoans. Another manuscript advertising for alternative biological systems for Evo-Devo presents Passiflora as a model for understanding the generation of hybrids in which androgynophore features can be analyzed (Scorza and Dornelas). Specifically, the authors analyzed the influence of auxin during flower development in the genus *Passiflora*, and showed that the addition of auxin or of its inhibitor changed the motility of the thigmotropic movement pattern of androgynophores of *P. sanguinolenta*.

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