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Editorial: Women in evolutionary developmental biology 2023

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Editorial on the Research Topic

Women in evolutionary developmental biology 2023

Women pursuing a career in science face many barriers, including gender bias and discrimination, challenges in balancing work and family life, and a lack of female mentors and role models. Yet, these barriers have not stopped women researchers in the field of evolutionary developmental biology, who have lead and generated groundbreaking discoveries for decades: from Hilde Mangold, who discovered during her PhD, the Spemann-Mangold organizer in 1924, to current prominent leaders, such as Marianne Bronner, Ruth Lehmann, Cori Bargmann, Trudy Schupbach and many more. The Research Topic *Women in evolutionary developmental biology 2023* celebrates the remarkable achievements and discoveries of female scientists in the field of evolutionary developmental biology.

1 Development and evolution of *Drosophila* and other insects

The first female developmental biologist to be awarded the Nobel Prize was Christiane Nüsslein-Volhard in 1995, for her discoveries of the genes that drive early development in the fly, *Drosophila melanogaster* (Nüsslein-Volhard and Wieschaus, 1980). Three papers in this Research Topic use comparative studies of *Drosophila* and other insects, to study different aspects of development and evolution. Urum et al., investigate the development and evolution of the male terminalia (genitalia and analia) by dissecting and comparing these morphological structures in the pupas across 12 species of *Drosophila*. They discovered a substantial heterochrony in the development of pupal terminalia in different species, but were nevertheless able to align the developmental stages across species. Their detailed analyses illuminate the evolutionary origin of different substructures, identify new morphologies and suggest a possible homology of other substructures. A molecular and functional comparative study by Babišová et al. demonstrates the evolutionary conservation of the apocrine secretion across 30 species of *Drosophila* and two other dipterans from diverse habitats. Apocrine secretion is a secretory mechanism that is evolutionarily conserved in all metazoans, including the human salivary and sweat glands. Babišová et al. show that while apocrine secretion is universally used for exuvial

fluid in the 32 species they studied, not all species use exocytosis for secretion, highlighting a conserved role for apocrine secretion in providing microbial defense during pupal metamorphosis.

A mini review by Casasa discusses the regulation of phenotypic plasticity, which is the ability of organisms to change in response to their environment. This paper focuses on how insects adapt to changes in nutrition, reviewing our current understanding of the mechanisms behind this adaptability, how these mechanisms have evolved, and how multiple traits work together in response to nutrition. These studies collectively illuminate developmental processes and evolutionary adaptations in insects, demonstrating the strength of comparative analyses in understanding the mechanisms underlying these phenomena.

2 Development and evolution of sea urchins and other echinoderms

The experimental advantages of the sea urchin embryo enabled major discoveries in developmental biology, from the fundamental principles of embryology to the detailed models of the gene regulatory networks (GRNs) that drive cell fate specification (Davidson, 2010; Paganos et al., 2021). In 1983, Lynn M. Angerer revolutionized the field by using *in-situ* hybridization of RNA antisense probes to study the spatial gene expression in the sea urchin embryo (Cox et al., 1984); a method that is now widely adopted, with this paper attracting close to 2,000 citations. In this Research Topic, Lynne's former students Yaguchi and Yaguchi continue her path, and investigate the regulation of the development of the cholinergic neurons in the apical organ of the sea urchin. The sea urchin apical organ is a sensory structure located at the anterior neuroectoderm of the larva that includes serotonergic and cholinergic neurons. This study demonstrates that the transcription factor, Rx, is essential for the development of cholinergic neurons, and that the RNA-binding protein Musashi1 acts downstream of Rx and regulates the level of choline acetyltransferase. Important regulators of mRNA are microRNAs that fine-tune many developmental processes, and their dysregulation is related to a range of diseases and developmental abnormalities (Shang et al., 2023). Arnott et al. study the transcriptional regulation of miR1, miR31, miR71, miR92, miR124 and miR2012, by developmental signaling pathways and transcription factors in sea urchin embryos. Using pharmacological and genetic perturbations, the authors discovered that these microRNAs are regulated by Wnt, Nodal and Sonic Hedgehog signaling pathways and the transcription factors, Alx1, Tbr and Ets.

As more echinoderm models are developed, comparative studies illuminate the evolution of novel body plans through changes in gene regulatory networks (Gildor et al., 2019). Perrillo et al. present a new echinoderm model for comparative studies, the Mediterranean sea cucumber, *Holothuria tubulosa*. They describe a reliable method for obtaining gametes and creating embryonic cultures, as well as characterize unique larval tissues using immunohistochemistry and high-resolution microscopy. Together, these three papers exemplify how research of the

development in echinoderms uncovers the regulation of key developmental processes and provides novel insights into evolutionary developmental biology.

3 Genetic basis of phenotypic variation and adaptation in mammals

The evolution of novel traits that lead to phenotypic variation was thought to be mainly driven by changes in *cis*-regulatory elements that control gene expression (Wray, 2007). The groundbreaking work of Hopi Hoekstra revealed that a single amino-acid mutation in the coding sequence of melanocortin-1 receptor determines the coat-color of mice and allow them to thrive in different backgrounds (Hoekstra et al., 2006). Her works, and others since, have proven that phenotypic variation can be due to mutations that alter protein function (Hoekstra and Coyne, 2007). In this Research Topic, Agata et al. investigate the role of a single amino acid mutation in the transactivating domain of the transcription factor GLI3 that occurs in Neanderthals and Denisovans. They show that this mutation affects the expression of downstream genes and when introduced to mice, leads to alteration in mice skeletal morphology, implying that this mutation might have provided beneficial traits for extinct hominins.

4 Computational model of the minimal GRN that explains leaf polarity

The complexity of GRNs makes it difficult to evaluate their explanatory capacity, and various mathematical models have been used to simulate GRN function (Chaves et al., 2005; Ben-Tabou de-Leon and Davidson, 2009; Peter et al., 2012). Here, Yuste et al. used Boolean network modeling to study an experimentally based model of the GRN that controls the abaxial-adaxial polarity in *Arabidopsis thaliana* leaf primordium. They found 1,905 Boolean networks that could produce the abaxial-adaxial polarity, and among these, identified two networks that best matched perturbation data and predicted missing connections. This work highlights the ability of Boolean networks to test experimentally based GRN models and identify missing regulatory connections that need to be tested experimentally.

5 Conclusions

In conclusion, this Research Topic highlights the outstanding contributions of female scientists to evolutionary developmental biology. More broadly, the Research Topic emphasizes the importance of comparative studies and computational modeling in deciphering the regulation of fundamental biological mechanisms and gaining evolutionary insights. We commend the exceptional skill and determination of women scientists in evolutionary developmental biology who have paved the way for

future discoveries and insights, and created greater inclusivity in scientific research.

Author contributions

SB-T: Conceptualization, Writing – original draft, Writing – review & editing. MA: Writing – review & editing.

Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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