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EDITORIAL

Causa formalis—detail matters

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Science is the art of explanation. To explain something means to draw a model of it, such that the implications of the model predict what will happen in reality. This procedure requires to deduce a consequence from causes. However, we use more than one type of causality, as pointed out more than two millennia ago by Aristoteles in his Physics (Aristoteles 347 B.C.). He discriminated four types of causality, explanations on the level of material (*causa materialis*), of effect (*causa efficiens*), of purpose (*causa finalis*), and of form (*causa formalis*). Different disciplines of biology focus on different types of causality: while molecular biology tries to deduce the behavior of life forms mainly from specific properties of molecules (such as DNA or proteins) and their interactions, evolutionary biology mainly considers whether a trait is useful for survival. For cell biology, it is organization in space and emergence of shapes (*causa formalis*) what matters. In this endeavor, cell biology follows two streams that are quite antagonistic: on the one hand, from its very beginning as a scientific discipline marked by the famous cell theory by Schwann and Schleiden (1838), cell biology had been searching for general laws that are valid for all life forms, thus paving the way for molecular biology. On the other hand, cell biology had been intrigued by diversity, describing meticulously the numerous details, where life forms are unique. Both streams are important, and their cross-connection has been fruitful. In a time, where biodiversity is facing the risk of irreversible extinction, investigating cellular aspects of diversity is more important than ever. The study of the *causa formalis* helps to understand the morphogenetic principles underlying taxonomy, to integrate otherwise mysterious peculiarities into a common rule, and to describe variabilities of shape in the language of unifying principles that can be quantified. Three contributions in the current issue illustrate for animal systems, why and how detail matters.

The contribution by Lewandowski et al. (2017) in the current issue describes the expression pattern of two transcription factors, paxilline 3 and 7, during myogenesis of the grass snake (*Natrix natrix*). The motivation for this work lies in an evolutionary question: while being important transitions for the evolution of terrestrial animals, the reptiles display a great diversity with respect to muscle development, which may reflect the diversity in their modes of locomotion. As a consequence, it is difficult to define a typical model for myogenesis. In their previous work, authors have carefully characterized myogenesis in different snakes, such as cobras (Khannoon et al. 2016). Now, they ask the question, whether the cellular details of myogenesis in the grass snake follow the pattern seen in fish and frogs or whether they resemble those seen in amniotic vertebrates. They can show that, while early muscle development is of the amniotic type, the later stages deviate from the common amniotic pattern, especially with respect to the presence of slow muscle fibers of the so-called white type that are filled with lipid droplets. These peculiarities might be linked with adaptation to the respective ecological niche, specifically with the need to hibernate. This would mean that ecological adaptations would leave their footprint even in the cellular details of myogenesis.

The correlation between functional adaptation and cellular details is not trivial, though. This is seen in the contribution by Santos et al. (2017) in the current issue. The authors have been using ultrastructural analysis to address phylogenetic issues of insect evolution, such as the Archaeognatha (Rost-

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Roszkowska et al. 2010). In their current work, they investigate the digestive tract of Heteroptera with different feeding habits comparing zoophagous and phytophagous species and compare features of secretory, absorptive, transport, storage, and excretory cells by transmission electron microscopy. Since the Heteroptera are considered to be a monophyletic group, this comparison would allow to conclude, to what extent feeding habit, and to what extent phylogenetic relationship shape the ultrastructure of the cells involved in the central region of the gut, where nutrients are absorbed. The study arrives at two conclusions—on the one hand, the details of the midgut digestive cells do not differ between zoophagous and phytophagous species including specific details such as the presence of spherocrystals or a perimicrovillar membrane, which prevents digestive enzymes from dilution in the large quantities of sap. These details seem to depend mainly on phylogeny, not on function. On the other hand, the authors demonstrate multifunctionality of the digestive cells that are not only capable of absorption but also of other activities such as secretion, transport, or storage. It might be this multifunctionality which allows to cope with different feeding habits, such that there was no strong selection pressure towards divergent differentiation. As a consequence, the features of the common ancestor for recent Hemiptera had been preserved.

While cell biology is often perceived as the science of beautiful images, functional analysis cannot come along without quantitative data. However, shape is often complex and variable, which is especially true, when it comes down to shapes of individual cells. This issue is especially accentuated in cells with amoeboid motility, where cell migration is accompanied by seemingly amorphous changes of shape. Even standard approaches of quantifications, such as classification systems, arrive at their limits with such cell types. In their contribution to the current issue, Karetin and Pushchin (2017) propose and test a novel approach to morphological quantification, using the highly "volatile" coelomocytes of a sea star, *Aphelasterias japonica*, as a challenging experimental system. Unlike other systems of classification, they use a non-biased approach, describing the observed shapes by fractal geometry and then analyzing the resulting multidimensional character set by different clustering algorithms, considering also cross-correlations between parameters by statistical methods, such as principal component analysis. They arrive at four distinct cell types that have been overlooked previously. The advantage of this approach is to be seen in the possibility to classify complex cell shapes by objective parameters, i.e., without bias of the observer. This typization can pick up differences that had been overlooked so far but may be functionally relevant. Moreover, the method might be useful also for other amoeboid cell types, for instance the mobile cells of the mammalian immune system.

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