little-studied bilaterian group that includes annelids, flatworms and molluscs (Fig. 1). The researchers found that the anticipated dorsal–ventral homeobox pattern was rarely observed, even in part, in the nervous systems of these species, including in an annelid closely related to *P. dumerilii*. These results suggest that even closely related species that have similar nervous-system architectures can deploy ancient genes very differently.

Previous studies in acorn worms[8] (hemichordates) and flatworms[9] found no dorsal–ventral homeobox-gene expression in their trunk nervous systems. This absence was previously interpreted as a secondary loss of an ancestral neural patterning system. But in light of Martín-Durán and colleagues' data, this condition could, in fact, reflect the ancestral nephrozoan state. It now seems that the 'typical' dorsoventral gene network was not deployed in the nervous system of the last common ancestor of bilaterians or nephrozoans. Rather, the developmental mechanisms that pattern the neural cords in mice, flies and *P. dumerilii* might have evolved convergently.

Martín-Durán and colleagues' work paints a complex and nuanced picture of nervous-system evolution. Their data raise the possibility of multiple origins of animal nerve cords, and suggest that a suite of genes that pattern the dorsal–ventral axis has been repeatedly co-opted into nervous-system development. Indeed, the authors show that the relationship between an animal's morphology and the expression of particular developmental genes might not always be tightly linked. These insights raise exciting questions about the mechanisms of evolutionary change that underlie the development of morphological diversity, including why convergently evolved nervous systems sometimes use highly conserved suites of genes, and what developmental constraints govern variations in these mechanisms across animals.

A frequent criticism of the study of key model organisms such as fruit flies, mice and nematode worms is that these species are highly derived — that is, they contain many traits unique to them — and thus are unlike any distant ancestor. But all living species are highly derived, being shaped by natural and sexual selection on evolutionary timescales to maintain adaptation to varying ecological niches. What Martín-Durán and co-workers have highlighted is not that these model organisms are inappropriate 'reference species'[10]. Rather, they demonstrate the importance both of developing reference species for multiple groups within a robust phylogenetic framework, and of consistently examining close relatives of the reference species before drawing conclusions about the evolutionary history of shared features. ■

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