

The difference in numbers of *Hox* groups and clusters between *Drosophila* and other invertebrates, on the one hand, and vertebrates, on the other, indicates a major increase in the degree of control over developmental processes between primitive metazoans and advanced chordates. Comparison between *Drosophila* and mammals suggests that a hypothetical common ancestor would have had approximately six *Hox* genes arranged in a single cluster. Other metazoan groups share a more recent common ancestry with vertebrates than they do with modern arthropods. Echinoderms appear to have nine genes in one cluster, but paralogues of groups 1–3, which control development of the head region in other metazoans, have not been recognized (Ruddle et al. 1994a). Among chordates, the hemichordate *Saccoglossus kowalekii* has representatives from each of groups 1–9 among vertebrates, which are probably arranged in a single cluster (Pendleton et al. 1993). The urochordates, which have been thought to be more closely related to vertebrates than are hemichordates, actually have fewer *Hox* genes, although the number and the identity of these genes differs from one urochordate group to another. Ruddle et al. (1994a) argued that this probably reflects an irregular pattern of gene loss in this group, which suggests significant divergence of the urochordates from the lineage leading to vertebrates. Holland et al. (1994) determined that the cephalochordates, characterized by *Branchiostoma* (commonly referred to as amphioxus) has ten *Hox* genes arranged in a single cluster. The relative similarity of the genes in *Branchiostoma* to the first ten *Hox* groups in vertebrates shows that the linear sequence is the same in the two taxa. The three most posterior *Hox* groups present among vertebrates (*Hox* 11–13) have not been recognized in *Branchiostoma*.

There is thus a major difference in the number of gene clusters and the total number of *Hox* genes between the cephalochordates and most jawed vertebrates. This may be bridged to some extent by the condition in the living jawless vertebrates, the hagfish and lampreys. Nineteen *Hox* genes have been identified in the lamprey, and others would be expected from groups 11–13, for which a probe was not then available. The known *Hox* genes may be arranged in as few as two clusters, although a higher number cannot be ruled out (Pendleton et al. 1993).

Current evidence suggests two major episodes of *Hox* gene duplication in the early evolution of vertebrates: one between cephalochordates and jawless vertebrates, and another between jawless and jawed vertebrates (Holland et al. 1994). There was a much greater change in both developmental patterns and adult structures between cephalochordate and jawless vertebrates than occurred between jawless and jawed vertebrates. Presumably this was related to much more significant changes in the number and arrangement of the genes controlling developmental processes.

The origin of craniates

Although cephalochordates had achieved the primary characters of chordates – notochord, dorsal hollow nerve cord, and pharyngeal gill slits – as well as a post-anal tail and segmental muscles throughout the trunk and tail, they lack many other features that characterize vertebrates. The differences in the head region are par-