

Genetic control of the cephalic furrow morphogenesis in *Drosophila*

The evolution of distinct head and trunk domains revolutionized animal morphology. Sophisticated anterior structures evolved to sense the environment while powerful posterior appendages propelled bilaterians to diversify and occupy every ecosystem on the planet. Pioneering work on developmental genetics revealed that the head and the trunk identities are specified by distinct regulatory landscapes early in embryogenesis. However, the developmental mechanisms that establish the boundary between such territories remain poorly understood. Here I investigate this key bilaterian trait using as a model the cephalic furrow – an understudied structure that demarcates the embryonic head/trunk boundary in the fly *Drosophila melanogaster*. The cephalic furrow is one of the first morphogenetic events during gastrulation. It begins when a single row of lateral cells undergo cell shortening forming a deep invagination in the embryonic epithelium. However, the specification of these initiator cells and the signaling cascade controlling the cephalic furrow morphogenesis remain unclear. To uncover potential regulators, I compiled a genome-wide list of candidate genes expressed at the cephalic furrow, and I am screening for genes that are disrupted in the only mutant strains known to affect the furrow, *buttonhead* and *even skipped*. To understand how the molecular patterning relates to the morphogenetic movements, I am using lightsheet microscopy to visualize the tissue and protein expression dynamics *in toto* between wild type and mutant embryos. This approach will reveal new patterning genes and their role in the cephalic furrow formation in *Drosophila*, bridging the gap between molecular patterning and morphogenesis, and help to uncover the developmental mechanisms that establish the embryonic head/trunk boundary, a key trait for bilaterian evolution.

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