cis-Regulatory Control of Three Cell Fate-Specific Genes in Vulval Organogenesis of *C. elegans* and *C. briggsae*

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Martha Kirouac

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ABSTRACT

The great-grandprogeny of the *Caenorhabditis elegans* vulval precursor cells (VPCs) adopt one of the final vulA, B1, B2, C, D, E and F cell types in a precise spatial pattern. Formation of the pattern of vulval cell types is likely to depend upon the *cis*-regulatory regions of the transcriptional targets of these intercellular signals in vulval development. The outcome of such differential activation will result in individual cell types. *egl-17*, *zmp-1*, *cdh-3* are expressed differentially in the developing vulva cells, providing a potential readout for different signaling pathways. To understand how different signaling pathways interact to specify unique vulval cell types in a precise pattern, I have identified upstream *cis*-regulatory regions that are sufficient for their ability to confer vulval cell type-specific regulation when fused in *cis* to the basal *pes-10* promoter. In the *egl-17* promoter, I have identified a 143 base pair (bp) region that drives vulC and vulD expression, and a 102 bp region that is sufficient to drive the early expression in presumptive vulE and vulF cells. In the *zmp-1* promoter, I have identified a 300 bp region that is sufficient to drive expression in vulE, vulA and the anchor cell. In the *cdh-3* promoter, I have identified a 689 bp region sufficient to drive expression in the anchor cell and vulE, vulF, vulD and vulC, a 155 bp region sufficient to drive only anchor cell expression, and a separate 563 bp region that was also sufficient to drive expression in these vulval cells. I have identified the *C. briggsae* homologs of these three genes, and the corresponding control regions, and tested these regions in both *C. elegans* and *C. briggsae*. I find that these regions of similarity in *C. elegans* and *C. briggsae* upstream of *egl-17*, *zmp-1*, and *cdh-3* promote expression in vulval cells and the anchor cell. Using

the regions defined by the sufficiency analysis and phylogenetic footprinting, I have been able to isolate over-represented sequences that may play important roles in conferring vulval and anchor cell expression.

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