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The Role of Metal Response Elements in Predicting Genes in C elegans Zinc Metabolism

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Zinc is an essential mineral for humans, so understanding zinc metabolism is relevant to human health. There is currently an incomplete knowledge of zinc transcriptional control. The Kornfeld lab used *C. elegans*, a nematode worm that has many conserved properties with mammals and responds transcriptionally to dietary zinc, to identify zinc-regulated genes. Four genes were identified that are induced by dietary zinc at the transcriptional level and contain a fifteen base pair element called the metal response element (MRE). When this element was removed, the zinc-inducible expression of one of these genes was reduced. Bioinformatic approaches were used to identify additional candidate genes in the *C. elegans* genome containing a MRE. Based on these observations, we proposed that genes containing the MRE are induced by dietary zinc and may play a role in zinc metabolism. The goal was to determine if candidate genes containing the predicted MRE are induced by dietary zinc. This can elucidate mechanisms of transcriptional regulation and identify genes that mediate zinc metabolism. I cultured worms in low and high-level zinc environments, extracted the worm RNA, and quantified transcript levels of candidate genes by qRT-PCR to determine if the gene was significantly induced. We can say with confidence that the F35E8.11 gene is induced by dietary zinc. F20C5.5, K01A12.4, and MO2D8.6 are likely induced. The RNA fold change for other genes tested did not significantly differ from basal levels to be determined as affected by zinc. Further experiments, such as using fluorescence microscopy to visualize transgenic worms with GFP or genetic analysis using loss of function mutations and RNA interference, are needed to confirm inducibility and the role of the MRE in zinc induction.