

Translation of mRNA Subsets by eIF4E-Family Members in *Caenorhabditis elegans*

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Abstract

eIF4E is a translational initiation factor that recognizes the 7-methylguanosine-containing cap of mRNA. Although most studies to date have been of the translational roles of eIF4E, it is becoming apparent that eIF4E participates in all stages of the mRNA "life cycle" – transcription, splicing, nucleo-cytoplasmic transport, translation, movement into P-bodies, and degradation. Another relatively new development is that all eukaryotic organisms examined to date (except *Saccharomyces cerevisiae*) have been found to express multiple eIF4E-family members (up to eight). A major focus of our laboratory is to understand the physiological rationale for multiple eIF4E-family members. We use for these studies a powerful model organism, the nematode *Caenorhabditis elegans*. We have identified five eIF4E-family members, IFE-1 through IFE-5. Surprisingly, the knockout of individual IFE genes impairs translation of specific mRNA subsets. We are using bioinformatics tools to gain insight into mechanism for this specificity.