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Characterization of Four Novel Nonsense Mediated Decay Homologs in *Tetrahymena thermophila*

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The nonsense mediated mRNA decay (NMD) pathway is a ubiquitous post-transcriptional mRNA surveillance pathway in eukaryotes, including *Tetrahymena thermophila*. This pathway is implicated in the degradation of cytoplasmic mRNA containing a premature termination codon (PTC), which would otherwise lead to expression of aberrant proteins. While genes in this pathway are well characterized and studied in organisms such as Drosophila, mice, and even humans, such research has yet to be conducted in *T. thermophila*. To determine the temporal expression pattern of uncharacterized genes in *T. thermophila* NMD (*NMDP1*, *NMD2*, UPF1, and *UPFL1*), we generated cDNA for each gene throughout multiple time points in the *T. thermophila* life cycle. The gene was then attached to a YFP plasmid and transformed into *T. thermophila*, with subsequent visualization of the protein's localization. We identified 4 novel genes, *NMDP1*, *NMD2*, UPF1, and *UPFL1*, putatively involved in *T. thermophila* NMD. With an RNase and EST1 RNA binding domain, *NMDP1* appears to mediate the cleavage of target mRNA strands. The *NMD2* gene containing MIF4G domains is homologous to *UPF2* and may function to recruit proteins to the NMD complex during growth. Both *UPF1* and *UPFL1* possess ATP dependent RNA helicase function, and may be essential for the formation of the NMD complex to degrade PTC-mRNA at different points in the *T. thermophila* life cycle. All 4 genes in the present study appear to be involved in *T. thermophila* NMD. However, our data fails to identify the exact mechanism these genes interact with each other, if at all, to promote the degradation of PTC-containing mRNA. Future experimentation can identify the recruitment process of the NMD complex to facilitate nonsense mRNA decay in *T. thermophila*.