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# CHARACTERIZATION OF FOUR NOVEL NONSENSE MEDIATED DECAY HOMOLOGS IN *TETRAHYMENA THERMOPHILA*

Joyce Chung, Jason Kunisaki, Kelsey Pitts, and Joshua Sands

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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*.