

Identification and characterization of translation re-initiation factor (EAD1/2) targets in uORF containing sequences of *Arabidopsis thaliana*

Katie Vollen

Though 30-50% of plant genes contain upstream open reading frame (uORFs) sequences, very little is known about the mechanics and contexts in which plants employ this mode of translational regulation (1, 2). Generally, uORFs are thought to decrease the translation of a main ORF, leading to lower protein levels. The objective of this project is to clarify the role of translation re-initiation factors in facilitating the translation of a main ORF. Translation re-initiation machinery has been identified and partially characterized in humans, drosophila, and yeast species (MCT-1/DENR, TMA 20 & 22). Ethylene and auxin defect 1 & 2 (EAD) have been identified by the Alonso-Stepanova lab as potential orthologs in the plant model, *Arabidopsis thaliana* (*A. thaliana*). Previous work in the lab shows that EAD1/2 are required for the translation of a subset of uORF containing mRNA transcripts. This project will focus on what differentiates EAD mRNA targets from non-targets in uORF containing sequences. A greater understanding of EAD regulation and transcript targets can help clarify a novel mechanism of translational regulation & potentially inform the engineering of more effective crops.

1. Lei, L. *et al.* Ribosome profiling reveals dynamic translational landscape in maize seedlings under drought stress. *The Plant Journal* **84**, 1206–1218 (2015).
2. Liu, M.-J. *et al.* Translational landscape of photomorphogenic *arabidopsis*. *The Plant Cell* **25**, 3699–3710 (2013).