Translation regulation of uORFs-containing genes in Arabidopsis

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Translational regulation has long been recognized as a vital process in the cell responses to the environment and in the execution of developmental programs, yet still little is known about the selective translation of specific mRNAs and its regulation. By the implementation of the Ribo-Seq technology in Arabidopsis [1], we uncovered a translation regulation module in response to ethylene that involves the key-signalling gene *EIN2*, the 3´UTRs of *EBF1* and *2* and the NMD machinery [2]. We now focus on the *ead1,2* mutants, which present altered responses to ethylene and auxin. The two corresponding genes represent the likely orthologs of translation factors from yeast and humans, and this, together with their inferred roles in multiple response pathways, offer an excellent opportunity to investigate the role of signal integration at the translational level. EAD1 and 2 interact and Ribo-seq on *ead1* revealed an accumulation of translating ribosomes in the 5´UTRs of uORF-containing genes and reduction in the levels of ribosomes in the main ORF. *ead1* is also impaired in the translation of GFP when fused to WT 5´UTR of potential EAD1 targets but not when fused to uORF-less versions of the same 5´UTRs. Our hypothesis is that, under certain hormonal and/or environmental conditions, EAD1/2 work as a complex required for the efficient translation of mRNAs that have common structural and functional features. Our progress towards the identification of the conditions where the EAD1 regulation of translation is required will be presented.

[1] Merchante C *et al*. *Bio-Protocol*, *6*(21), 1–34.
[2] Merchante C *et al*. (2015) Cell, 163(3): 684-697