## Towards understanding the role of heterogeneous ribosomes in Arabidopsis. Characterization of the ribosomal protein family eL24

Duarte-Conde, JA (2); Toribio, R (3); Villar-Arcas, B (2); Sans-Coll, G (2); Castellano, MM (3); Merchante, C (2)

(2)Instituto de Hortofruticultura Subtropical y Mediterránea "La Mayora", Universidad de Málaga-Consejo Superior de Investigaciones Científicas (IHSM-UMA-CSIC); (3)Centro de Biotecnología y Genómica de Plantas (CBGP-UPM-INIA/ CSIC)

Duarte Conde, JA

## Abstract:

Translation and its regulation play an important role in plant adaptation. Despite being the key molecular machines that synthesize proteins, ribosomes have traditionally been considered passive molecular players in determining which mRNA to translate. This view is changing due to studies showing that ribosomes can have an active role in regulating the translation of different mRNA subpools in mammals and bacteria (*Genuth & Barna., 2019*). In plants, the potential specialization is significantly greater, as each ribosomal family is encoded by two to seven paralogs. Moreover, several indications in the literature point towards differential roles among these paralogs. However, whether this heterogeneity provides selective translation of specific mRNAs under particular cell conditions has yet to be demonstrated.

To address this question, we are characterizing the ribosomal family eL24, composed of two paralogs, eL24z and eL24y. Both are ubiquitously expressed in *Arabidopsis* at a very similar level. It was described that the *el24y* displayed important growth retardation and

auxin-defective phenotypes, while little was known about the eL24z paralog (*Nishimura et al., 2005; Park et al., 2017*).

By characterizing mutants in both paralogs, we have provided evidence that both eL24y and eL24z are are involved in the assembly of the 80S ribosomes, are constituents of actively translating ribosomes, and exert common functions in translation. However, our sequencing studies also indicate a greater impact on the translational machinery in el24y. Since we also show evidence that overall translation is unaffected in any of the mutants, the phenotypic differences between them may be due to the specific function of the paralog y in translation reinitiation (Zhou, Roy, and Arnim., 2010), a process in which paralog z seems to be less important according to our results. Our ongoing experiments are designed toward definitively answering the question of whether the two paralogs within this family play different functions in translation.

## **References:**

Genuth, N. R., & Barna, M. (2019). Nat Rev Genet, 19(7), 431–452; Nishimura et al. (2005). Plant cell, 17, 11; Park et al. (2017). Biochem Biophys Res Commun, 16, 494; Zhou et al. (2010). BMC Plant Biology, 10, 19.

## Funding Acknowledgement:

This work is funded by Grants BIO2017-82720-P, PID2021-123240NB-100, and RYC-2017-22323 from the Ministerio de Economía, Industria y Competitividad and a UMA20-FEDERJA-100 grant from Junta de Andalucía to C.M.; a PRE2018-083348 fellowship from Ministerio de Ciencia, Innovación y Universidades to JADC, and the Plan Propio de investigación from the University of Málaga, Campus de Excelencia Andalucía Tech. We are grateful to Dr. Eduardo de la Peña (IHSM) for his help in the statistical analysis of the polysome profiles.