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# Mechanisms and impact of ribosomal RNA methylation in plants

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Ribose methylation (2-*O*-Me) is the most common modification of ribosomal RNAs (rRNA) in various life forms and are pivotal for ribosome assembly and translation. These 2-*O*-Me modifications are guided by small nucleolar C/D-box RNAs (C/D snoRNA) and are deposited by the methyltransferase FIBRILLARIN (FIB). Our work, performed in the plant model *Arabidopsis thaliana*, highlights that rRNA 2-*O*-Me is a dynamic process. To understand the impact of such modulation of rRNA 2-*O*-Me on translation, we examined *Arabidopsis* plants lacking the major nucleolar protein Nucleolin 1 (NUC1). Depletion of NUC1 (*nuc1*) resulted in decreased rRNA 2-*O*-Me levels(1) and, hence, in ribosome hypomethylation. Our findings suggest that reduced rRNA 2-*O*-Me in *nuc1* may be triggered by defects in the assembly of the C/D snoRNP complex. Ribosome hypomethylation leads to an accumulation of polysomes detectable in their polysome profiles and a stalling of ribosomes at the start codon shown in 5'Pseq analysis. We are now trying to elucidate if this stalling could be either inferred to the formation of the 80S complex or to difficulties in interacting with translation initiation factors. All in all, our results underscore the crucial role of rRNA methylation and the heterogeneity of ribosomes in their assembly and translation processes. (1) *Azevedo-Favory J et al. (2021) RNA Biology 18:11, 1–18*

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