

## Abstract

In plants, translation regulation plays an important role during progamic phase, fertilization and seed development. The process of translation is mostly regulated in its initiation phase, where Eukaryotic translation initiation factor 3 (eIF3) is the largest and most complex initiation factor, consisting of 12 different subunits. In plants, single eIF3 subunit mutants caused various growth and development defects, depending on the particular subunit that was mutated. However, not all the plant eIF3 subunits were characterized to this date. The objective of this work was to functionally characterize the eIF3 subunit A using *Arabidopsis thaliana* as the main model plant. We described in this work that plant eIF3A proteins share high levels of homology and domain organization with eIF3A subunits from non-plant eukaryotic species but contain regions specific only to plants. Next we described that *Arabidopsis thaliana AteIF3A* gene is transcribed in highly proliferating tissues, its protein product localizes to cytoplasm and around pollen vegetative cell nucleus and observed an increased frequency of defective pollen grains and defects in seed formation in plants with T-DNA insertion localized to the *AteIF3A* gene. We also produced stable transgenic *Nicotiana tabacum* lines expressing heterologous AteIF3A protein from Arabidopsis.