# Functional conservation of Nascent polypeptide associated complex in plants

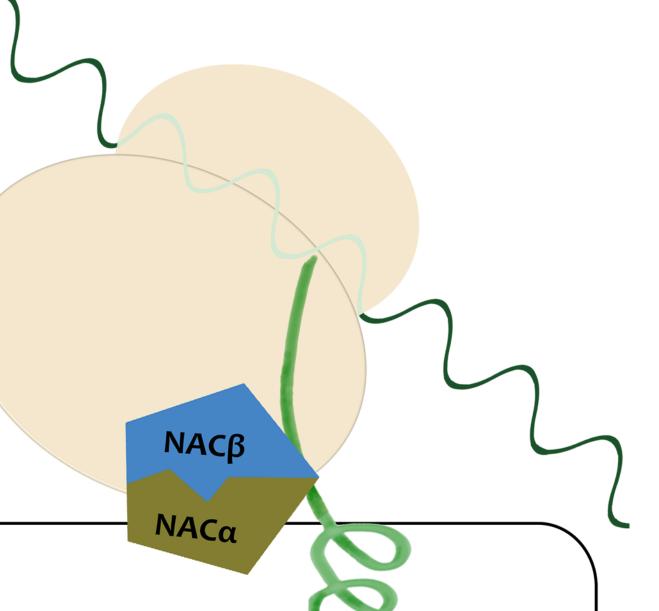


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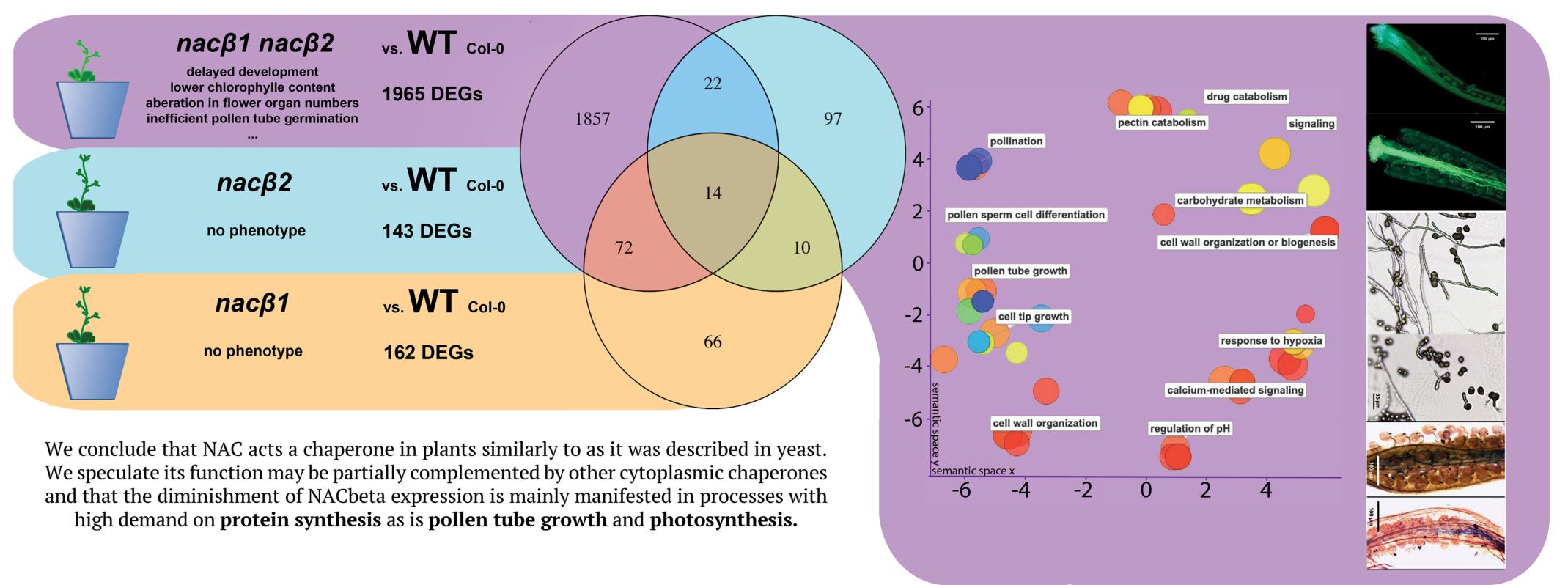
### INTRODUCTION

Nascent polypeptide associated complex (NAC) was first described as a heterodimer with ribosome binding capacity in yeast S. cerevisiae. Upon binding to the ribosome, NAC is supposed to form a protective tunnel-like structure, that shields the nascent polypeptides and assists in their folding, being thus categorized as a **cytoplasmic de novo chaperone**. The heterodimer consists of NACbeta and NACalpha subunits, but mainly the NACbeta subunit was studied in plants. It was proved to influence stress tolerance and plant reproduction. We acquired the **A. thaliana** double homozygous mutant of both NACbeta subunits. By analysing its defective phenotype and using further molecular approaches, we confirmed its possible role in translation, plant reproduction and other important processes. Due to its chaperone function, NAC most likely represents an important regulator with a pleiotropic effect on **plant development**. To distinguish the role of individual subunits and to monitor their evolutionary conservation, we focused on annotating NAC subunits in basic land plant **Marchantia polymorpha**, which possess only sole NACbeta and NACalpha subunits in its genome which share high sequence similarity to **A. thaliana's** NACs.



## NACbeta SUBUNITS INFFLUENCE TRANSLATION IN ARABIDOPSIS

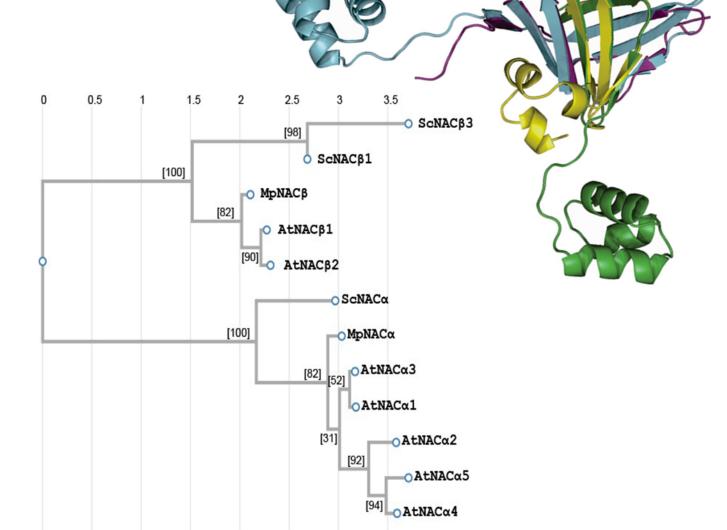
According to localization studies, both NACbeta subunits are present in cytoplasm. Knock-down of NACbeta subunits in A. thaliana led to lower chlorophyll content and defects in **pollen germination and pollen tube growth**. The flower organ numbers of the mutant plants are distorted and irregular. Proteomic analyses of mutant flower buds proved the observed phenotype showing downregulation of photosynthetic and pollen tube growth-connected proteins. Based on the transcriptomic analysis, we concluded that NAC represents a part of a broader cytoplasmic chaperone system and may also influence stress responses. Furthermore, the knock-out of the beta subunits led to down-regulation of numerous genes connected to male-germ line development.<sup>1</sup>



# NAC SUBUNITS SHARE A HIGH SEQUENCE SIMILARITY BETWEEN A. THALIANA AND M. POLYMORPHA

The sequences of genes encoding NAC subunits are well conserved between organisms especially in the region of **NAC domain**, a beta-barrel like structure responsible for NAC's dimerization. Thus, we hypothesize the NAC function between A. thaliana and M. polymorpha is conserved and the proteins will be able to complement its function. Then, due to the high similarity of NAC domain sequence, we hypothesize, that the NAC subunits from these two organisms will be able to form heterodimers together.





# **FURTHER PROSPECT**

We aim to create Marchantia knock-out mutant of each NAC subunits by CRISPR-Cas9 genome editing system. Further, cellular, and molecular aspects of NAC subunits will be analysed and compared to results acquired from A. thaliana. Together, we will provide a comparative analysis of NACsubunits in plant evolution and analyse its function in plantdevelopment with focus on reproduction.

