Open PhD position 2026/2027

Institute of Experimental Botany
of the Czech Academy of Sciences

Epitranscriptomic control of mRNA fate in pollen

Project Description

Introduction

Epitranscriptomics has emerged as a crucial regulatory layer of gene expression, modulating RNA fate without altering nucleotide sequence. Chemical modifications of RNA, most prominently N6-methyladenosine (m^6A), regulate transcript stability, localization, translation efficiency, and decay. These reversible modifications enable cells to rapidly adjust gene expression programs in response to developmental cues and environmental changes.

The male gametophyte of flowering plants (pollen and pollen tubes) provides an exceptional system to study epitranscriptomic regulation. Pollen development involves tightly controlled transitions between proliferation, differentiation, and functional maturation, while later stages rely predominantly on post-transcriptional regulation due to reduced transcriptional activity. Large pools of stored mRNAs are selectively utilized during pollen germination and pollen tube growth. Although recent studies have identified roles for epitranscriptomic reader proteins in pollen, the dynamics of RNA modifications themselves, the balance between writer, reader, and eraser enzymes, and their functional relevance for developmental fitness and stress responses remain poorly understood.

Importantly, epitranscriptomic regulation has been implicated in plant stress responses, including temperature stress. Since heat stress strongly compromises pollen viability and fertility, understanding how RNA modifications contribute to adaptive gene regulation in male gametophytes is of both fundamental and practical importance.

Aims

The primary aim of this PhD project is to elucidate how epitranscriptomic RNA modifications regulate gene expression dynamics during male gametophyte development, maturation, and function. The project will focus on the dynamic balance between RNA modification writers, resders, and erasers and their impact on specific transcript populations.

Specific objectives include:
(i) characterization of spatial and temporal **dynamics of selected RNA modifications** during pollen development and germination,
(ii) functional analysis of key **epitranscriptomic regulatory proteins** in the male gametophyte,
(iii) integration of epitranscriptomic changes with **mRNA stability, translation, and developmental transition**s, and
(iv) evaluation of the role of RNA modifications in **pollen responses** to environmental stress, particularly **heat stress**.

This work will move the field beyond descriptive studies toward a functional and dynamic understanding of epitranscriptomic regulation in plant reproduction.

Methods and experimental approach

The project will primarily use the model plant Arabidopsis thaliana. Mutant and transgenic lines affecting selected epitranscriptomic regulators will be analyzed. RNA modification mapping will be performed using next-generation sequencing–based approaches (e.g., m^6A-seq), complemented by transcriptomic and translatomic analyses.

Cellular localization and developmental phenotypes will be examined using fluorescence and confocal microscopy. Functional consequences will be assessed through pollen viability assays, germination tests, pollen tube growth measurements, and stress-response experiments. The project will integrate genome-wide datasets with cellular and physiological analyses.

Expected background of the student

Applicants are expected to have a basic background in molecular biology, genetics, or RNA biology, with an interest in gene regulation. Motivation for experimental research, critical thinking, and willingness to handle complex datasets are essential. Experience with RNA techniques, sequencing data, or bioinformatics is advantageous but not required.

Research environment, collaboration, and funding

The project will be conducted at the Institute of Experimental Botany of the Czech Academy of Sciences, within the Laboratory of Pollen Biology, in collaboration with Faculty of Science, Charles University, and international partners.

The PhD student will be co-funded by the supervisor through grant and institutional resources guaranteed by the host institution. Funding availability is secured and will not disadvantage the applicant during the admission process.

Suggested reading

- Chaturvedi P, Wiese AJ, Ghatak A, Záveská Drábková L, Weckwerth W, Honys D (2021) Heat stress response mechanisms in pollen development. New Phytol 231: 571-585, DOI: 10.1111/nph.17380
- Hafidh S, Honys D (2021) Reproduction Multitasking – the Male Gametophyte. Annu Rev Plant Biol 72: 581-614, DOI: 10.1146/annurev-arplant-080620-021907
- Klodová B, Potěšil D, Steinbachová L, Michailidis C, Lindner AC, Hackenberg D, Becker JD, Zdráhal Z, Twell D, Honys D (2023) Regulatory dynamics of gene expression in the developing male gametophyte of Arabidopsis. Plant Reprod 36: 213-241
- Shi Y, Yang S, Pei T, Xu Y, Zhao Y, Xue H, Ma X, Ren H, Liu X (2025) The m6A writers, readers, and erasers regulate plant development and respond to biotic/abiotic stresses. Epigenetics Insights 18
- Zaccara S, Ries RJ, Jaffrey SR (2019) Reading, writing and erasing mRNA methylation. Nat Rev Mol Cell Biol 20: 608-624

Application form: https://forms.gle/zxDLQjYW149rYd356

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