Name and surname:	**Magdalena Wołoszyńska**
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UPWr Base of Knowledge - link:	https://bazawiedzy.upwr.edu.pl/info/author/UPWr4ecca1af86b34c1bbdb073f9c33fcf2c?r=author&tab=&title=Profil%2Bosoby%2B%25E2%2580%2593%2BMagdalena%2BWo%25C5%2582oszy%25C5%2584ska%2B%25E2%2580%2593%2BUniwersytet%2BPrzyrodniczy%2Bwe%2BWroc%25C5%2582awiu&lang=pl
Researchgate:	
Personal website / Working group website:	
Participation in projects in last 5 years (chronological; with distinction into PI (kierownik) and RF (wykonawca)):	1. The Elongator protein complex integrates regulation of transcription and translation during photomorphogenesis in Arabidopsis thaliana, PI, OPUS-22 NCN, Nr 2021/43/B/NZ1/02236
Do you plan to engage support of second supervisor or auxiliary supervisor?	YES
	Auxiliary supervisor
Name and surname:	Małgorzata Kwaśniak-Owczarek
Academic Degree:	dr (Dr.)
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UPWr Base of Knowledge - link or most important publications from last 3 year (JCR) / patents from last 3 years (maximum 5):	Pani dr Małgorzata Kwaśniak-Owczarek w 2021 i 2022 roku przebywała na zwolnieniu lekarskim i urlopie macierzyńskim, dlatego podaję jej wcześniejsze publikacje: 1. Kwasniak-Owczarek M#, Tomal A, Janska H. Assessment of Protein Synthesis in Mitochondria Isolated from Rosette Leaves and Liquid Culture Seedlings of Arabidopsis. Methods Mol Biol, 2022, 2363:183-197. doi: 10.1007/978-1-0716-1653-6_14. 2. Adamowicz-Skrzypkowska A*, Kwasniak-Owczarek M*#, Van Aken O, Kazmierczak U, Janska H. Joint inhibition of mitochondrial complex IV and AOX by genetic or chemical means represses chloroplast transcription in Arabidopsis. Philos Trans R Soc Lond B Biol Sci, 2020, doi.10.1098/rstb.2019.0409. IF= 6.139. 3. Tomal A*, Kwasniak-Owczarek M*, Janska H. An update on mitochondrial ribosome biology:the plant mitoribosome in the spotlight. Cells 8(12), 2019, pii: E1562,. doi: 10.3390/cells8121562. IF= 5.656. 4. Kwasniak-Owczarek M*, Kazmierczak U*, Tomal A, Mackiewicz P, Janska H. Deficiency of mitoribosomal S10 protein affects translation and splicing in Arabidopsis mitochondria. Nucleic Acids Res 47(22):11790-11806, 2019, doi: 10.1093/nar/gkz1069. IF=11.147. 5. Kazmierczak U, Kwasniak-Owczarek M#. Profilowanie rybosomów jako innowacyjne narzędzie do badania procesu syntezy białek. Postępy Biochemii 65 (1): 41-51, 2019, doi: 10.18388/pb.2019_255. IF=0.55
Researchgate:	
Personal website / Working group website:	
Projects in last 5 years (chronological; with distinction into PI (kierownik) and RF (wykonawca)):	• Research grant 2021/41/B/NZ3/00571, RF, „A link between deficiency of ribosomal S10 protein and RNA metabolism in Arabidopsis mitochondria" (2022-2024), main performer of the project, 2 280 040 PLN. • Research grant 2014/15/B/NZ2/01065, RF, „Make a jump into understanding of selective ribosome-dependent translation in plan mitochondria" (2015-2020), main performer of the project, 1 134 730 PLN.
PhD topic:	The Elongator complex in Arabidopsis thaliana - regulator of gene expression during photomorphogenesis.
Research discipline in Doctoral School:	Biological Sciences
Short description of the research problem to be solved in the PhD (minimum 1000 characters):	The six subunit protein complex of Elongator was discovered in yeast and functionally characterized as the interactor of RNA polymerase II facilitating the elongation phase of transcription via its epigenetic activity of histone acetylation. However, methylation of the wobble uridine in some tRNA molecules was later proven as the main activity of the yeast Elongator complex while its role in transcription has been questioned. In the meantime the complex was identified in animals and plants and appeared highly conserved across the life kingdoms in terms of its structure while understanding of the true Elongator function remains still challenging. Although in animals, as in yeast, the complex was shown to be mainly involved in tRNA modification and therefore protein translation, in plants the situation is more complex. Majority of the published reports indicate that Elongator is a histone acetyltransferase accompanying RNAPolII during transcription and consequently epigenetically regulating gene expression. However, less numerous but convincing data point to other roles of Elongator including fine tuning of translation according to the mechanism described for yeast and animals. Independent experiments performed by several research groups to identify localization of the complex in plants, always position Elongator both in nucleus and in cytoplasm supporting the possibility that it regulates gene expression at different stages and in different cell compartments. Our research has been focused on the role played by Elongator during transcriptional regulation of early Arabidopsis thaliana seedling development in darkness and light during skoto- and photomorphogenesis respectively. Applying diverse techniques like RNASeq, qPCR, ChIP-qPCR and mutant analysis we were able to prove alterations of transcriptome and histone acetylation occurring in mutants with compromised function of Elongator (elo) which correlate with phenotypes of mutated plants. However, as reported also by other researchers, transcriptome changes cannot explain all aspects of phenotypes observed in the elo mutants which could be potentially linked to tRNA modification and protein translation related roles of Elongator. In this proposal we present the preliminary data showing that development disturbances observed during photomorphogenesis of the elo seedlings result from disturbed functioning of Elongator in both transcription and translation regulation. The main goal of this project is to define, characterize and evaluate the impact and correlation of the two roles played by Elongator during photomorphogenesis: regulation of transcription elongation and tRNA modification required for optimal rate of protein translation.
Professional skills for PhD candidate (e.g. master program, specializations, softwares, language, analytical techniques, minimum 500 characters):	The candidate should have completed a Master's course in Plant Molecular Biology. They should be familiar with plant in vitro and in vivo cultures, techniques of isolation and analysis of nucleic acids and proteins from plant material, including, qPCR, ddPCR, RNASeq, ChIP, proteomics. They should know the software tools for PCR primer design, nucleotide sequences analysis, RNASeq results analysis (GO enrichment identification), literature databases search. The candidate should be fluent in English both in speaking and in reading the state-of-the-art literature.
a) Project title:	The Elongator protein complex integrates regulation of transcription and translation during photomorphogenesis in Arabidopsis thaliana.
b) Agreement number:	UMO-2021/43/B/NZ1/02236
c) Number of months in the project to support PhD student (in months; starting from 1st of October 2024):	11
Project website:	