



PhD program 2020 call for proposals: LabEx fellowships

MitoTALENs for the manipulation of the maintenance, segregation and editing of the mitochondrial genome

LabEx Mitocross

Research Unit

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Research team and team leader

Team: Maintenance and segregation of the mitochondrial genome

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Rebecca Therby-Vale (Master M2)

3 relevant publications:

Gualberto J.M. and Newton K.J. (2017). Plant mitochondrial genomes: dynamics and mechanisms of mutation. Annu. Rev. Plant Biol., 68: 225-252

Le Ret M., Belcher S., Graindorge S., Wallet C., Koechler S., Erhardt M., Williams-Carrier R., Barkan A., Gualberto J.M. (2018). An Organellar thymidine kinase is required for the efficient replication of the maize plastidial genome. Plant Physiology, 178:1643-1656



Chevigny, N.; Nadiras, C.; Raynaud, C.; Le Ret, M.; Bichara, M.; Erhardt, M.; Dietrich, A.; Gualberto, J.M. (2019). RADA is the main branch migration factor in plant mitochondrial recombination and its defect leads to mtDNA instability and cell cycle arrest. bioRxiv, doi:10.1101/856716.

Number of PhDs in progress: 2 (starting date) Arnaud Fertet (Janvier 2017). Défense prevue Avril 2020 Déborah Schatz (Octobre 2018). Défense prévue 2021

PhD supervisors

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PhD subject

Title: MitoTALENs for the manipulation of the maintenance, segregation and editing of the mitochondrial genome

Description: about 200 word

The mitochondrial genomes of (mtDNA) of higher plants are very large, and constituted by a complex array of subgenomes that are interconvertible by recombination. However, the recombination activities and their roles in the repair and segregation of the plant mtDNA are still not well understood, mainly because of the lack of tools to manipulate this genome. Such tools could be used to generate cytoplasmic genetic variability for the development of new plant varieties of agronomic interest, because of the maternal segregation of the interesting traits.

Recently it has been shown that it is possible to introduce specific breaks in the plant mtDNA, using TALEN endonucleases carrying a mitochondrial targeting sequence. In collaboration with the japanese group expert in the approach we want to study in the Arabidopsis model plant how specific double-strand breaks induced by these "MitoTALEN" are repaired, in wild plants and in mutant lines deficient in recombination factors. We also want to exploit MitoTALENs as tools for the selective inhibition of the replication of specific mtDNA subgenomes, and thus direct the preferential segregation of specific mitotypes. Other approaches combining mitoTALEN fused to editing factors (cytidine deaminases) will be also exploited as tools for the direct mutagenesis of mitochondrial genes.



Key words:

Mitochondrial genome, Arabidopsis, TALEN, recombination