Thesis in plant epitranscriptomics

Title : Development of a new tool to make early diagnostics of plant exposed to climate changes in natural and cultivated environments.

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Epitranscriptomic is a new branch of genetic studying all modifications targeting RNAs and especially messenger RNAs (mRNAs). In the past five years, several studies have shown the importance of plant and animal mRNA chemical modifications to reprogram gene expression in stress situations (1-5). These chemical marks on mRNAs have a tendency to quantitatively vary depending on the nature and intensity of the perceived stresses. For example, in maize, a significant lower level of the mRNA chemical mark "m6A" was observed in drought situations (6). It is important to note dans this drop was observed for a maize variety that is sensible to drought (and present all corresponding phenotypes) but also for a drought resistant line that do not present stress symptom. Therefore, this drop in m6A marks for a drought tolerance variety without symptom, is diagnostic of the stress the plant is experiencing, forcing it to compromised it growth and development functions to invest in the stress response pathways. A precise knowledge of the plant health situation, before phenotype apparition, could allow to set up solution (here irrigation) without compromising future yield. Contrarily to drought, hypoxic stress (often associated to flooded land) led to an increase in mRNA m6A content (7). So for a given chemical mark, an increase or a lowering could be diagnostic of different types of stress. mRNA chemical marks other than m6A can also vary upon stress exposure. For example, Arabidopsis thaliana mRNA pseudouridylation level vary following heat and oxidative stresses (8). Oxidative stress also lead to the increased of N4-AcC (9) et m1G (10) in plant mRNAs while the m5C mark diminished to the profit of the 5hmC (11). At least 18 different chemical marks were detected on plant mRNAs. Therefore, a simultaneous study of all these marks in an individual could be assimilated to a barcode allowing to set up a diagnostic of the plant health situation. This diagnostic, before the apparition of stress-related symptoms, would allow to plan interventions to protect yield in case of cultures or to take preservation actions in case of natural resources.

The objective of this thesis is, by using a mass spectrometry strategy, to develop and calibrate a new generation of monitoring tools to evaluate plant health (in cultured or natural environments) before the apparition of any stress phenotypes. This tool will be develop on Arabidopsis thaliana, as a sentinel species of Occitanie natural areas and on tender wheat and economically important crop for this Region.

We are looking for an highly motivated candidate with a Master degree in biology that included a significant amount of genetic, molecular biology and physiology courses. Practical experiences in most usual molecular biology and RNA extraction and purification protocols would be appreciated.

1. Meyer DD, Jaffrey SR (2014) Nature Reviews Molecular Cell Biology, 15: 313-326
2. Yue Y, Liu J, He C (2015) Genes & Development, 29: 1343-1355
3. Li S, Mason CE (2014) Annual Review of Genomics and Human Genetics, 15:127-150
4. Yue H, Nie X, Yan Z, Weining S (2019) Plant Biotechnology Journal 17:1194-1208
5. Hu J, Manduzio S, Kang H (2019) Frontiers in Plant Science, 10:500.
6. Miao Z, Zhang T, Qi Y, Song J, Han Z, Ma C (2019) Plant Physiology, doi: 10.1104/pp.19.00323. [Epub ahead of print]
7. Fry NJ, Law BA, Ilkayava OR, Holley CL, Mansfield FD (2017) RNA 23:1444-1455.
8. Sun L, Xu Y, Bai S, Bai X, Zhu H, Dong H, Wang W, Zhu X, Hao F, Song CP (2019) Journal of Experimental Botany 70:5089-5600
9. Dominissini D, Rechavi G (2018) Cell, 175 :1725-1727
10. You C, Dai X, Wang Y (2017) Nucleic Acids Research 45:9059-9067
11. David R, Burgess A, Parker B, Li J, Pulsford K, Sibbritt T, Preis T, Searle IR (2017) Plant Cell 29:445-460