NANYANG TECHNOLOGICAL UNIVERSITY

School of Biological Sciences

Reg. No. 200604393R

Research Theme: **Transcriptional regulation of plant oil biosynthesis**

Research Project Title: **Functional characterization of transcriptional regulator(s) in plant oil biosynthesis and plant development**

Principal Investigator/Supervisor: **Asst/Prof Wei Ma**

Co-supervisor/ Collaborator(s) (if any): **NA**

Project Description

a) Background:

Plant cells accumulate oil in the form of triacylglycerol (TAG) in their seeds as a main resource of carbon and energy for seedling development. Plant oils are not only essential for the human diet but also provide renewable feedstocks for many industrial uses. The transcription factor WRINKLED1 (WRI1) is a key regulator of plant oil biosynthesis. We show that post-translational modifications (PTMs), interacting partners, and regulatory domains (or motifs) of WRI1 are critical for its functions. For example, a C-terminal IDR (intrinsically disordered region) domain 3 (containing a PEST motif) affects the stability of AtWRI1. Removal of the IDR3-PEST motif or mutation of putative phosphorylation-sites in the IDR3-PEST motif increases the stability of AtWRI1, resulting in increased oil production. In addition, we have demonstrated that AtWRI1 interacts with 14-3-3s, a family of phosphopeptide-binding proteins. Co-expression of 14-3-3s with AtWRI1 increases AtWRI1-mediated oil biosynthesis as a consequence of increased transcriptional activity of AtWRI1.

Research in the lab focuses on mechanistic understanding of gene regulation of plant oil biosynthesis and translation of knowledge gained from our research into benefits for the agro-economy.

b) Proposed work:

Currently, various research projects are available in the lab. We aim to further elucidate the effects of PTMs on WRI1-mediated plant oil biosynthesis and seedling development based on our previous work. We seek to establish an interactome of WRI1 through identification of the WRI1 interacting protein partners. We will continue to uncover the functions of the IDRs that we identified recently. We are interested in globally mapping binding targets for WRI1 via whole-genome chromatin immunoprecipitation sequencing (ChIP-Seq) and DNA affinity purification sequencing (DAP-seq). Our lab will also investigate combinatorial transcriptional regulation of fatty acid biosynthesis in oil crops, with a goal of identifying novel regulators that can be used to improve oil crops.

Supervisor contact:

If you have questions regarding this project, please email the Principal Investigator:
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SBS contact and how to apply:

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Please apply at the following: http://admissions.ntu.edu.sg/graduate/R-Programs/RWhenYouApply/