

SPADES

Project title: Functional characterization of a new family of secreted peptides involved in defense and development control in *Arabidopsis*

Acronym: **SPADES** (SCOOP PAthway in DEvelopment and Stress)

Project duration: 36 months - Start date: 01/10/2019 End date: 30/09/2022

Key-words: hormonal peptide, phyto cytokine, ROS detoxification, defense signaling, root development, pathogen resistance

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Summary:

Context:

Plant responses to pests and pathogens are coordinated by regulatory proteins and hormones (Buscaill and Rivas, 2014). Among these actors, small secreted peptides, also named peptide phytohormones or phyto cytokines, may directly interact with pathogens or act in signaling and cell-to-cell communication (Murphy *et al.*, 2012; Gust *et al.*, 2017). However, only a small fraction of the gene space liable to encode such signaling peptides has been described and their structural and functional diversity appears to be largely underestimated (Matsubayashi *et al.*, 2014). Therefore a huge part of the whole array of plant genetic defenses is still unexploited. In this context, by combining meta-analysis of transcriptomes, bioinformatics predictions and experimental assays on mutants and synthetic peptides, we have identified a gene family of 14 paralogs in *Arabidopsis thaliana* encoding precursors of putative secreted peptides, hereinafter referred as SCOOP. We have already shown that among them, SCOOP12 is involved in the control of defense pathway and the root elongation through the regulation of reactive oxygen species (ROS) responses (Gully, Pelletier *et al.*, 2019).

Goals:

The PhD project aims at deciphering the signaling pathway triggered by the SCOOP12 peptide and to enlarge the functional characterization to the 13 other SCOOP12 paralogs identified in the *Arabidopsis* genome. These goals require the identification of functional partners and especially the transmembrane receptor which interact directly with the mature peptide. Our first results provide us the preliminary backbone of a downstream cascade such as the involvement of the *BAK1* as a co-receptor and the induction of the phospholipid pathway (Gully, Pelletier *et al.*, 2019) but numerous gaps remain to fill. Furthermore, the exact processing of SCOOP12 is based on structural comparisons and stay to be experimentally confirmed. Besides its role in plant defenses, we also aim to prove our hypothesis regarding the role of SCOOP12 as a moderator of root elongation, possibly through H₂O₂ level control.

Methodology:

The work, conducted on *A. thaliana* plants and cell suspensions, will include complementary approaches in the fields of functional genomics (genotyping, qPCR, cloning...), cytology (subcellular localization of the peptides), and biochemistry (enzymatic assays, immunoprecipitations, ROS species quantitation). It will allow studying the impact of mutations and peptide application on plant defenses and development, and validate putative players of the SCOOP pathway. Already established collaborations with experts in and outside IRHS will ensure efficient supervisory and formation of the PhD student for the successful achievement of all these goals.