



## Proposition d'un sujet de stage au M2 ADAM (2019)

Titre	<b>SWEET genes as candidates plant susceptibility genes to develop broad-spectrum pathogen resistances in cauliflower and Arabidopsis</b>
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Equipe(s)	SIX, Stratégies infectieuses des <i>Xanthomonas</i>  Acceptez-vous que ce sujet soit également proposé à l'itinéraire PRO ? OUI <input checked="" type="checkbox"/> NON <input type="checkbox"/>
Résumé	<p>Xanthomonas bacteria are the causal agent of numerous diseases on crop plants including black rot disease on cauliflower and Arabidopsis. Most Xanthomonas species translocate Transcription Activator-Like (TALEs) effectors into plant cells. TALEs are a unique type of bacterial effector proteins that help the pathogen to exploit and modify the plant environment by directly and specifically modifying the expression of plant genes. TALE-mediated induction of those plant genes, referred to as susceptibility genes (S genes), can promote host colonization and disease. Interestingly, the SIX team has demonstrated the capacity of Brassica-infecting Xanthomonas to induce SWEET genes expression by several TALEs correlates with a higher Xanthomonas aggressiveness. The objective of the proposal is to investigate the importance of SWEET genes to microbial pathogenicity and plant susceptibility in cauliflower and Arabidopsis. Modulation of the expression of the SWEET genes will be analyzed by qRT-PCR in plant after bacterial inoculation using Xanthomonas TALE mutants. In order to determine the biological significance of candidate SWEET genes to disease development, we will engineer artificial TALEs designed to specifically induce the expression of SWEET genes. In parallel, we will initiate a functional analysis of SWEET genes in Arabidopsis mutants.</p>
Photo	<p>Zoe Dubrow, Cornell U.</p>