Ecological genomics of adaptation of native interactions between Arabidopsis thaliana and its bacterial microbiota

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Résumé

There is growing interest in the potential of harnessing the microbiota towards the improvement of plant health to achieve agricultural goals. To do so through plant and microbe breeding requires a better description of the extent of natural genetic variation of plant-microbiota interactions and the underlying genetic architecture of both host plants and the main members of the microbiota. To dissect the genetic architecture driving adaptive plant-microbiota interactions, I will first present results on the host side using two complementary approaches in association genetics applied to *Arabidopsis thaliana*: (i) a Genome-Environment Association (GEA) analysis on 141 whole-genome sequenced natural populations of *A. thaliana* characterized *in situ* for their leaf and root bacterial communities and a large set of non-microbial ecological factors (i.e., climate, soil, and plant communities), and (ii) a Genome-Wide Association study conducted in field conditions on 162 whole-genome sequenced accessions of *A. thaliana* inoculated with 13 native Plant Growth-Promoting Bacteria (PGPB) isolated from these populations. By combining these two approaches, we established a genomic map of local adaptation in *A. thaliana* to its native bacterial microbiota. Plant immunity appears as a major source of adaptive genetic variation structuring beneficial interactions between *A. thaliana* and the main members of its microbiota. I will then present results on the microbe side. In particular, I will present the results of a GWAS based on the pangenomes of 74 whole-genome sequenced strains of the PGPB *Pseudomonas siliginis* inoculated on nine accessions of *A. thaliana* in *in vitro* and field conditions. The benefits conferred by *P. siliginis* onto A. thaliana are driven by a polygenic architecture that was highly dependent on both growth conditions and plant genotype. Finally, I will present a free-phenotyping GWA mapping approach to describe the genomic landscape of interactions between *A. thaliana* and the main members of its microbiota and pathobiota.

Mots-Clés: microbiota, Arabidopsis thaliana, Plant Growth, Promoting Bacteria, GWAS, native interactions, pathobiota, co, evolution

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