Supporting information for:

Dissecting plant-associated bacterial genetic architecture on host development reveals discrepancies among contrasted environments

Rémi Duflos[1], Anaïs Botello[1], Baptiste Mayjonade[1], Sébastien Carrere[1], Céline Lopez-Roques[2], Marine Sallaberry[2], Claudia Bartoli-Kautsky[1], Fabienne Vailleau[1*], and Fabrice Roux[1*]

[1] LIPME, INRAE, CNRS, Université de Toulouse, Castanet-Tolosan, France

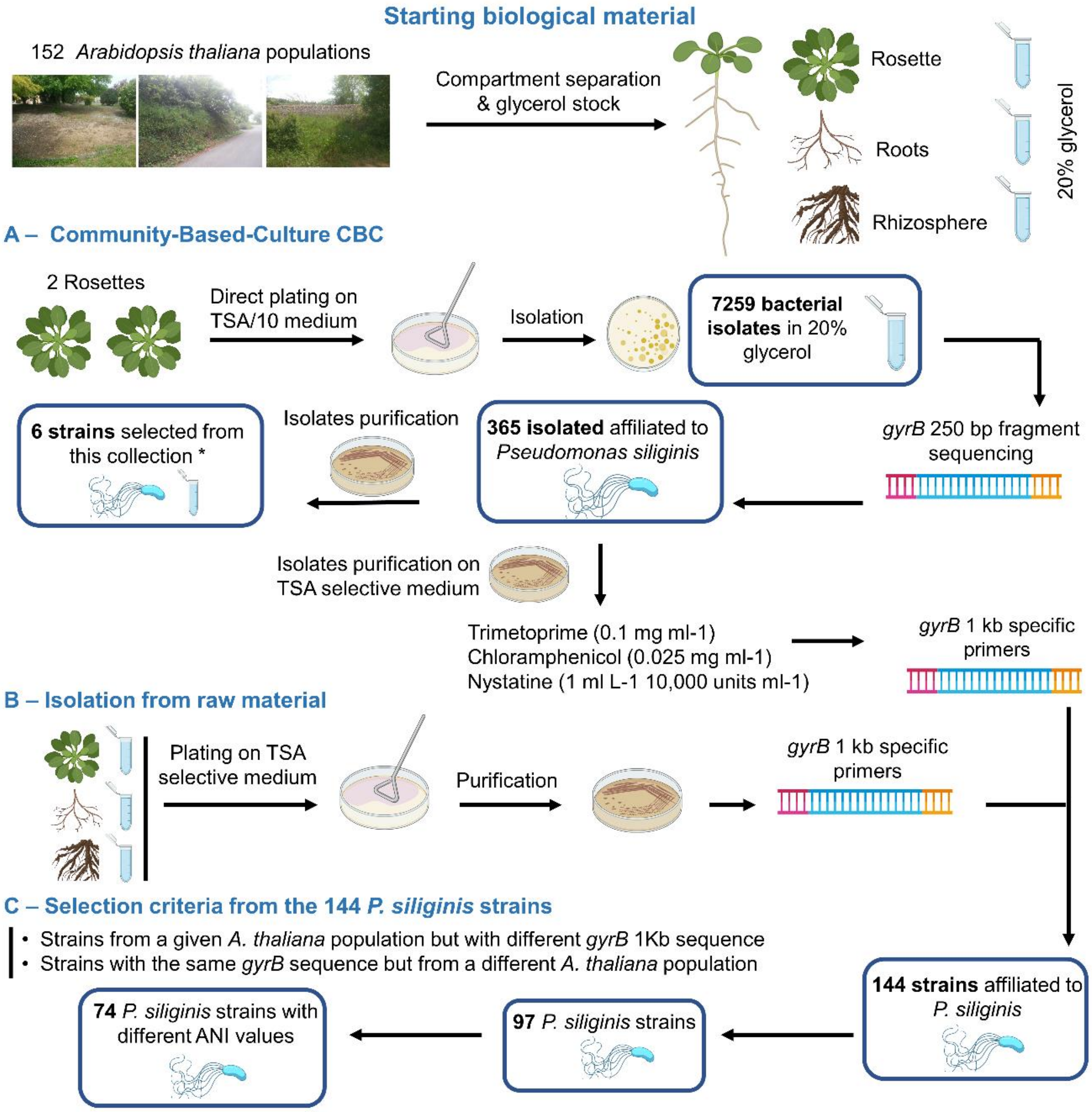
[2] Institut National de la Recherche Agronomique, US 1426, GeT-PlaGe, Genotoul, Castanet-Tolosan, France

[*] To whom correspondence may be addressed: Fabrice Roux and Fabienne Vailleau.

Email: fabrice.roux@inrae.fr, fabienne.vailleau@inrae.fr

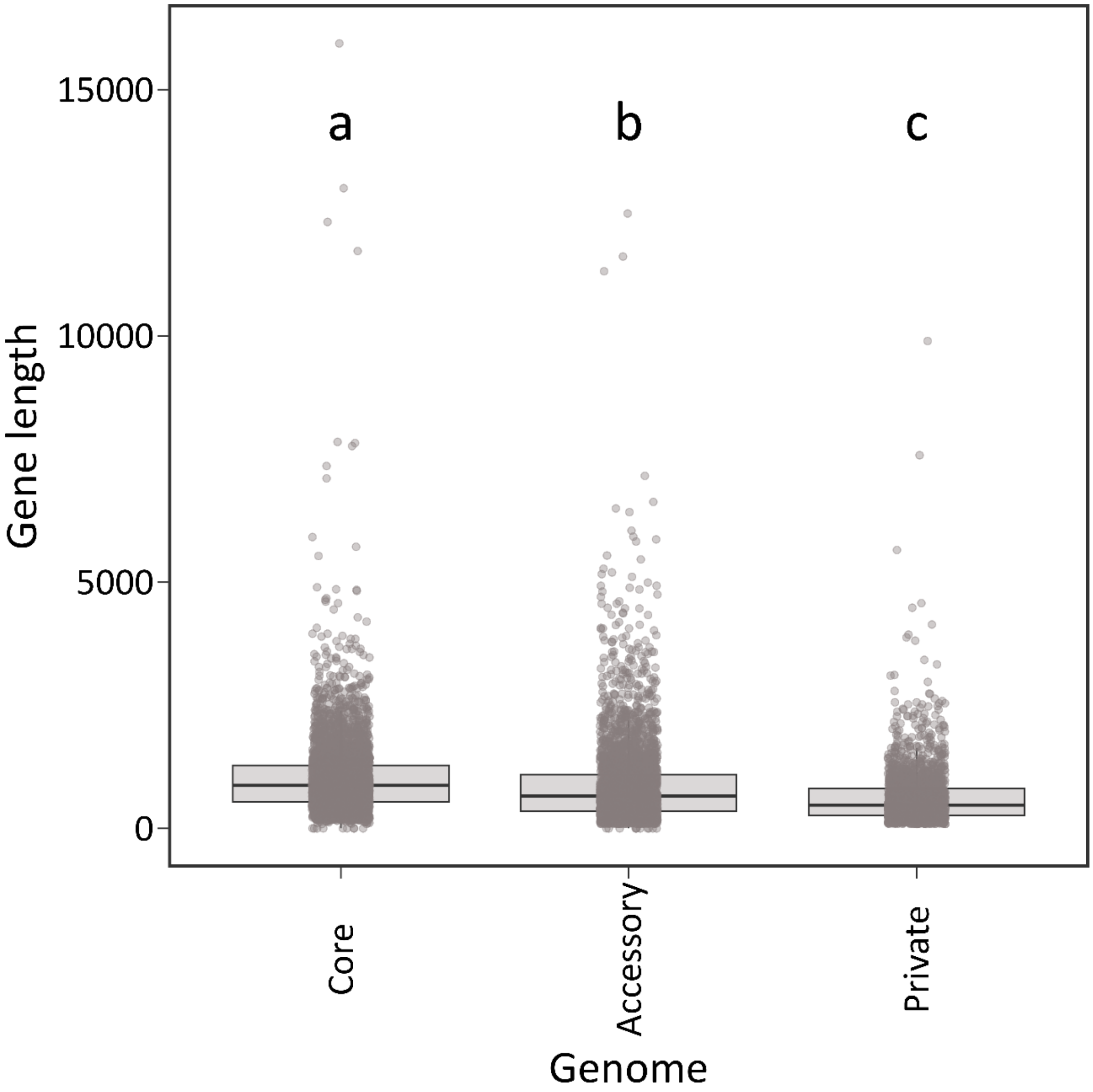
This document includes Supplementary Figures 1 to 3.

Supplementary Figure 1. Experimental framework used to isolate, characterize, and select the 74 *Pseudomonas siliginis* strains used in this study. Strains were isolated from 152 *Arabidopsis thaliana* natural populations located in the southwest of France, using two complementary approaches. **Approach 1** consisted of directly plating homogenized *A. thaliana* rosettes on TSA/10 medium. The resulting isolates were purified and characterized by sequencing a 250 bp fragment of the *gyrB* gene. Six strains were previously purified by this method[1]. In addition, the 365 isolates were purified on TSA selective medium and the resulting strains were sequenced with the 1kb gyrB marker. **Approach 2** involved using a selective TSA medium supplemented with antibiotics specific to the *Pseudomonas* genus. In this second approach, strain identification was performed using a 1 kb *gyrB* sequence. By using both approaches and a combination of selection criteria, we identified 74 *P. siliginis* strains for setting up BGWAS.

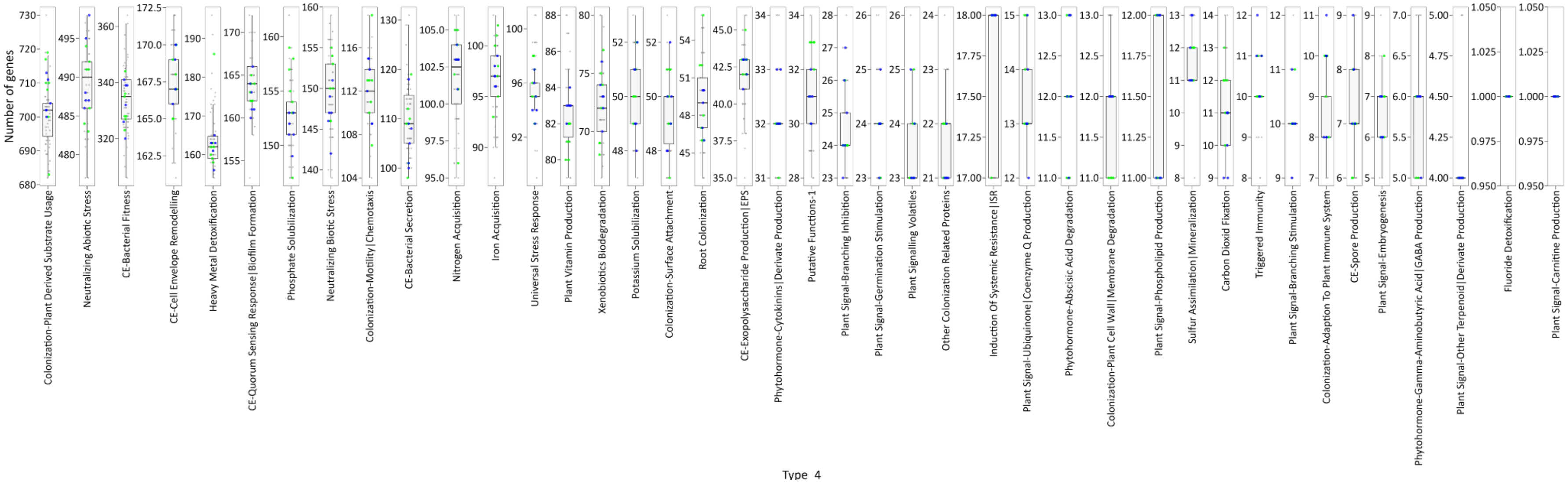


* Ramirez-Sanchez et al., 2022. *Front. Microbiol.*

Supplementary Fig. 2: Length of the core, accessory, and private genes. Gene length is expressed in bp. Core genome: N = 4365 genes, accessory genome: N = 3731 genes, private genome: N = 1974. Different letters indicate different groups after a Tukey correction for multiple pairwise comparisons at *P* = 0.05.



Supplementary Fig. 3: Variation among the 74 *P. siliginis* strains for the number of genes belonging to the 41 functional classes of the Type 4 of Plant Growth-Promoting Traits using the PLaBAse database. Strains isolated from the AMBR-A and ANGE-B *A. thaliana* populations are highlighted by blue and green dots, respectively.



References

1. Ramírez-Sánchez, D. *et al.* Investigating genetic diversity within the most abundant and prevalent non-pathogenic leaf-associated bacteria interacting with Arabidopsis thaliana in natural habitats. *Front. Microbiol.* **13**, 984832 (2022).