Valuing GEMs! When does the soil microbiota matters in explaining plant phenotypes?

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Résumé

Introduction - Traditionally, quantitative genetics considers that the phenotype of a plant (P) is determined by its genotype (G), the environmental conditions where it grows (E), and the GxE interaction (P = G + E+ GxE; Via & Lande 1985). This formalism guided plant breeding for decades, yielding our artificially selected crops. Soil microbiota, often considered as a part of E, have also a renowned importance in defining the plant phenotype. Yet, it remains unclear when we should care for the effect of the soil microbiota on plant phenotypes, relatively to G and E. Our objective was to assess this relative importance of the soil microbiota (M). We tested the inclusion of M as a distinct factor in this formalism, in order to quantify its relative importance next to G and E (P = G + E + M + GxE + GxM + MxE + GxExM; Oyserman et al., 2021). Such a formalism would help identifying cases where the soil microbiota could be a significant action lever for improving plant phenotype, or not.

M&M - In a full factorial design experiment, we grew three different genotypic accessions *Arabidospis thaliana* (G: Can-0, Col-0, Cvi-0) in three different autoclaved soils with contrasting textures (E: sandy, loamy, clayey), inoculated with the three different soil microbial communities originating from these soils (M: sandy, loamy, clayey microbiota). Using variance partition analysis, we quantified how G, E and M affected two important plant traits: growth, and tolerance to the necrotrophic fungi *Botrytis cinerea*, the causal agent of the grey mold disease. The three genotypic accessions were selected based on their different susceptibility over *B. cinerea* (Can-0: highly susceptible > Col-0: mid-susceptible > Cvi-0: more tolerant; Denby et al. 2004).

*Intervenant

Results - We showed that M ranked as the third significant source of variance in plant growth (6%, $p < 0.001$), behind G (10%, $p < 0.001$) and E (57.5%, $p < 0.001$). The GxExM interaction (3.1% $p = 0.03$) showed that part of the plasticity in plant growth can be attributed to M. This overall effect of M on plant growth resulted in a difference of 29% between the most extreme microbiota modalities. We found that the GxExM interaction (14.7%, $p < 0.001$) and GxM (5.6%, $p < 0.01$) together ranked second in explaining the tolerance to fungal infection, behind G (29.3%, $p < 0.001$). In the most extreme cases, the soil microbiota would explain a reduction of foliar necrosis size up to 2-folds.
Conclusions - Our results clearly indicate that the soil microbiota is a non-neglectable source of variance in explaining plant phenotypes. This effect, often referred to as ”microbiability” could represent a promising alternative to the traditional genetic selection for improving plant phenotype under the current context of global changes.

Mots-Clés: plant phenotype, soil microbiota, rhizosphere, environment, genetic, plant growth, phytopathogen, phenotypic plasticity