

Genotype specific responses of *Musa* spp. baseline phytomicrobiome to *Fusarium oxysporum* f. sp. *cubense* infection

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Banana (*Musa* spp.), a major crop providing food security to millions of people, is highly threatened by ***Fusarium oxysporum* f. sp. *cubense*** (Foc), a destructive **soil-borne pathogen** responsible of the Fusarium wilt. In **Benin**, banana production is heavily damaged by the Fusarium wilt (Figures 1-2).



Figure 1: Typical wilting and rotting symptoms caused by Foc in Benin. Microconidia and macroconidia can be observed under microscopy.

The importance of **plant associated microorganisms** in supporting plant health is increasingly recognized. In particular, banana **root endophytes** could play a key role to limit Foc infection.

Resistant Aloga and **susceptible Sotoumon** banana are grown in **association** to **reduce disease** incidence (Figure 2). **Plantains** such as Aloga have been less studied but present very interesting resistance against Foc.

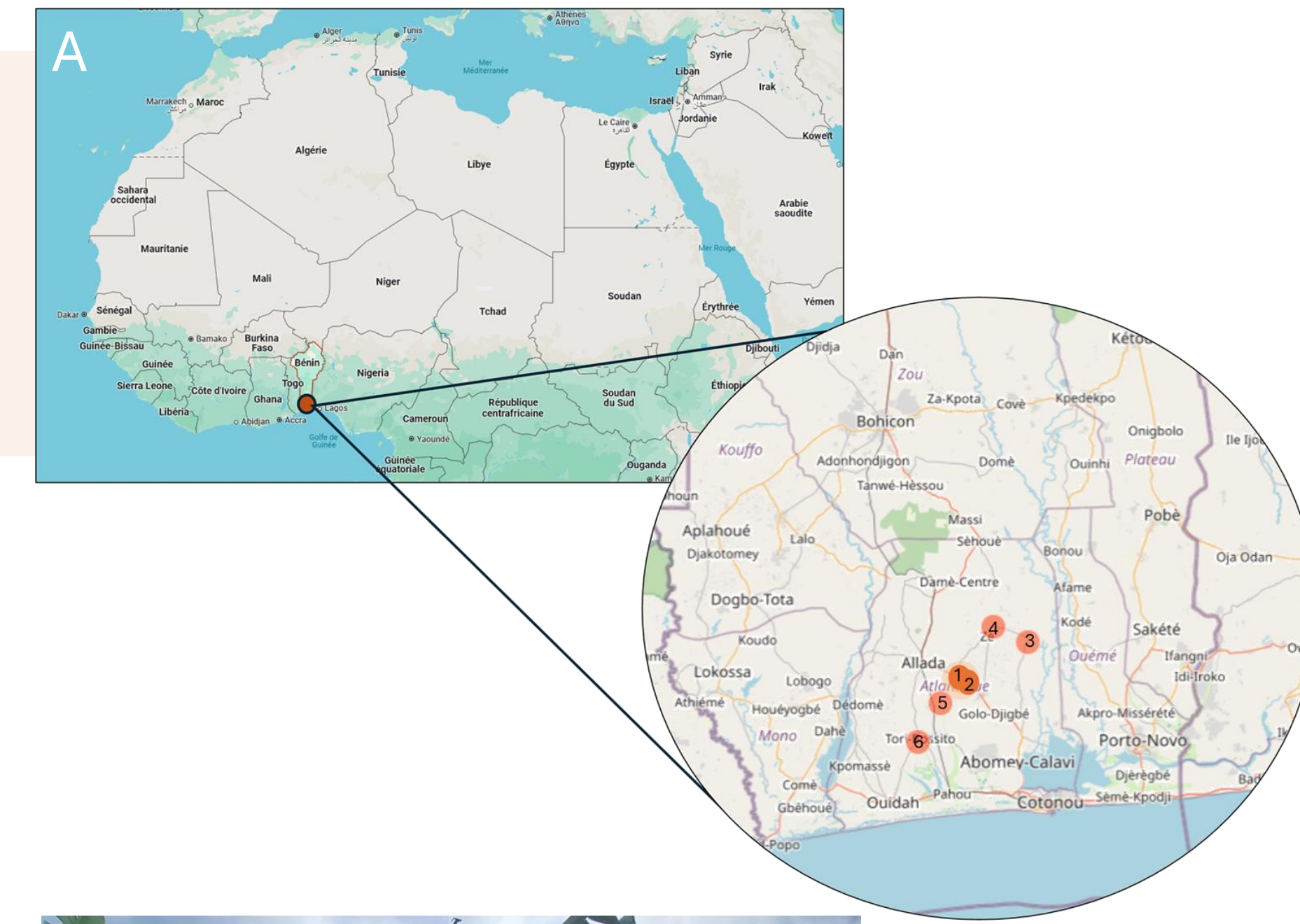


Figure 2: A: Map of the six studied banana plantations in South Benin; B: Aloga plantain (*Musa* AAB x *paradisiaca*) and Sotoumon dessert banana (*Musa* AAB, Silk group), Benin.

What is the core phytomicrobiome of *Musa* spp. roots ?

BANANA ROOT ENDOPHYTES IN RESISTANT AND SUSCEPTIBLE CULTIVARS

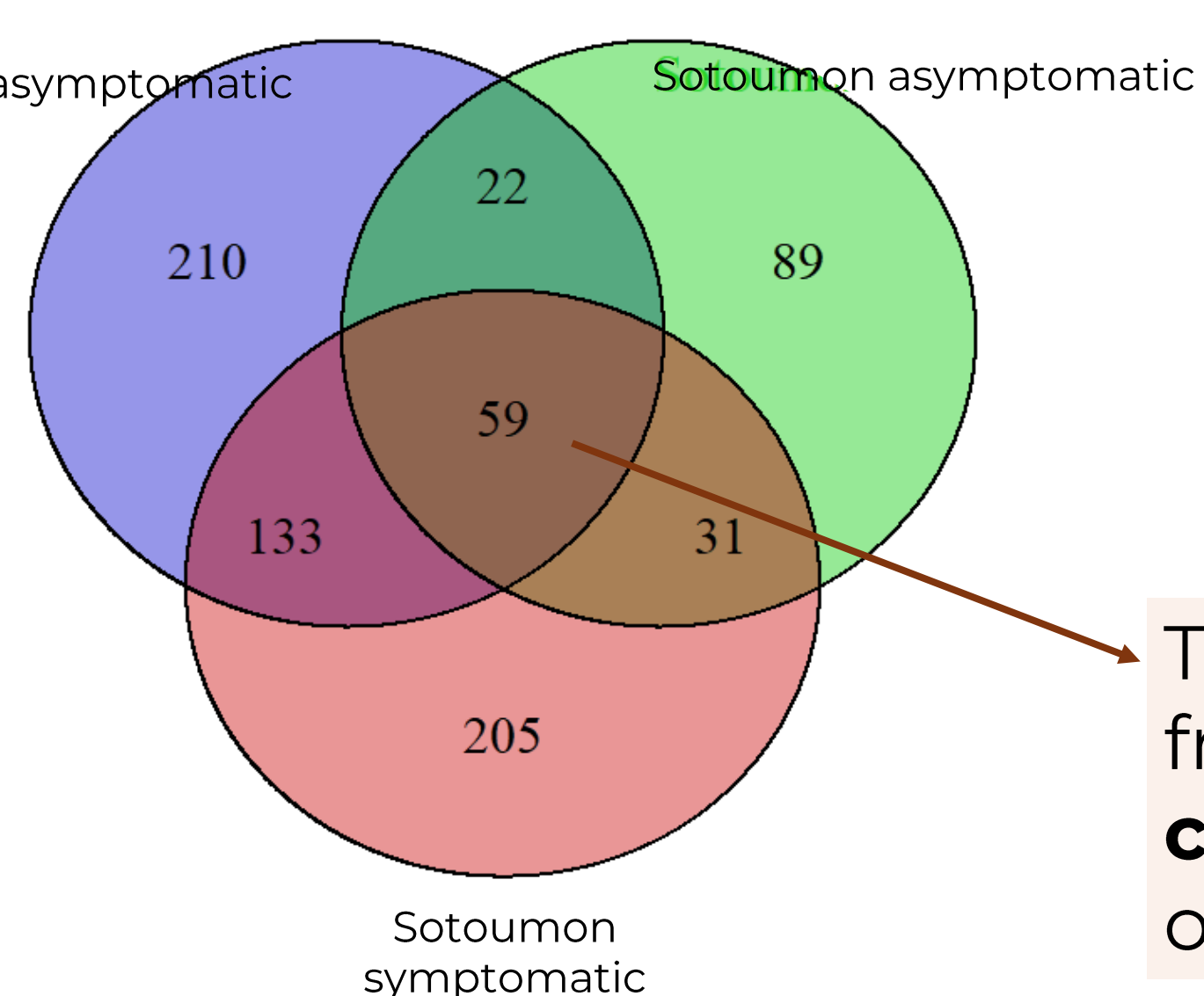


Figure 3: Venn diagram of the phytomicrobiomes associated to asymptomatic Aloga and (a)symptomatic Sotoumon. Results from a limited number of samples.

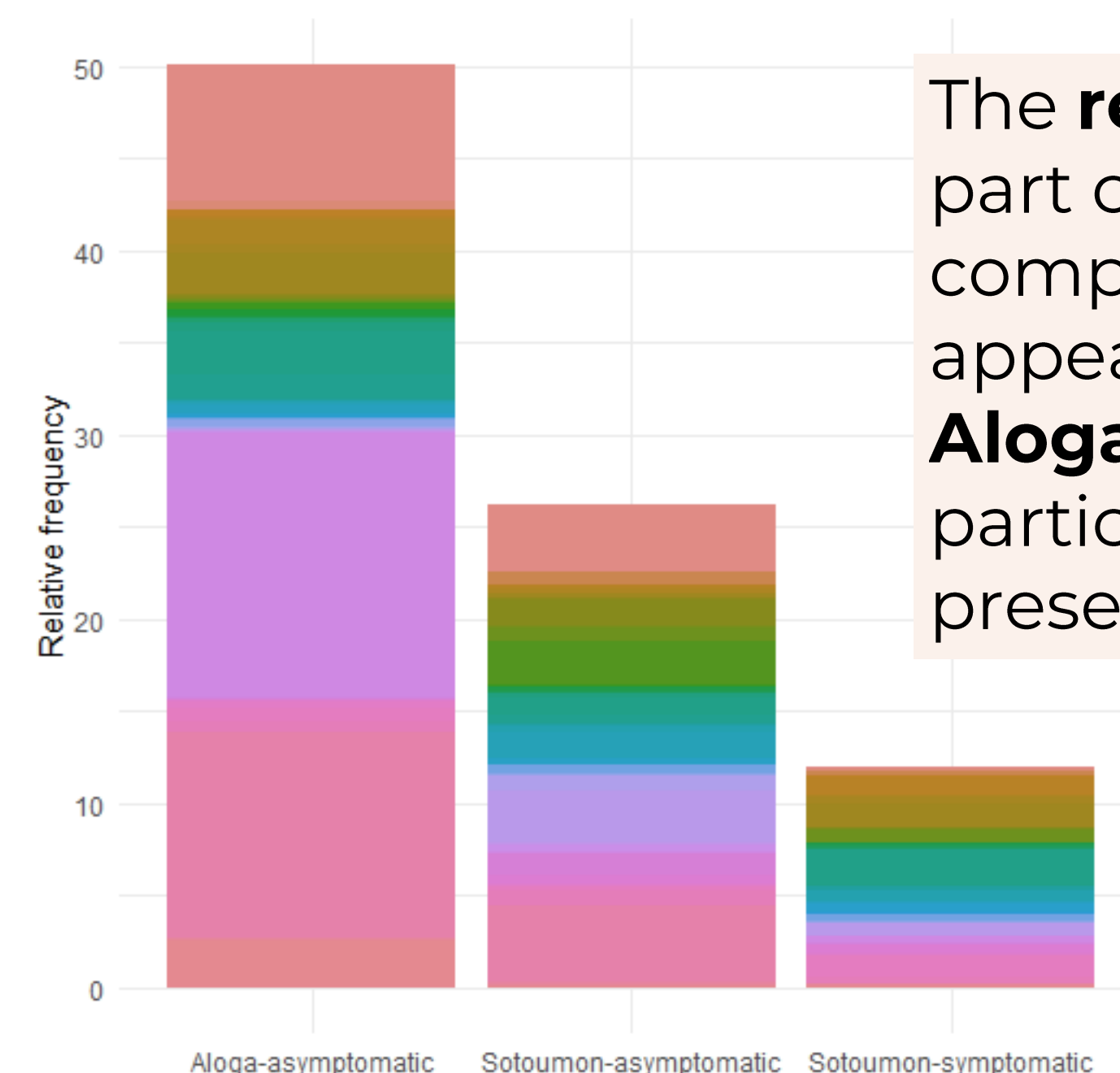
The **bacterial 16S-ITS-23S** region was sequenced, using MinION technology, for **metabarcoding**.



The study of the phytomicrobiomes from two **cultivars** allows to define a **core microbiome** systematically observed (Figure 3).

How is the phytomicrobiome impacted by disease development? Is it cultivar-dependent?

DYSBIOSIS ASSOCIATED WITH FOC DEVELOPMENT



The **relative frequency** of the species part of the « **core microbiome** » compared to the whole microbiome appears to be **higher** in **resistant Aloga** than in susceptible Sotoumon, particularly when the pathogen is present (Figure 4).

Taxa associated with disease absence or presence are being analyzed.

Figure 4: Relative frequency of the species associated to the core microbiome compared to the whole microbiome of asymptomatic Aloga and (a)symptomatic Sotoumon. The colors refer to the 59 species identified in the core microbiome. Results from a limited number of samples.

Could the phytomicrobiome play a role for plant resistance ?

DIVERSITY OF FOC POPULATIONS IN BENIN AND SCREENING OF ISOLATED ENDOPHYTIC BACTERIA

The **pathogen** has been isolated and **phylogeny trees** were inferred from the Elongation factor 1- α (**TEF1 α**) and the RNA polymerase II (**RPB2**) genes (Figure 5).

Endophytic bacteria were **isolated** from Aloga and Sotoumon roots. Their interactions with the pathogen are screened to identify **in vitro** **antagonism** or **synergism** (Figure 6).

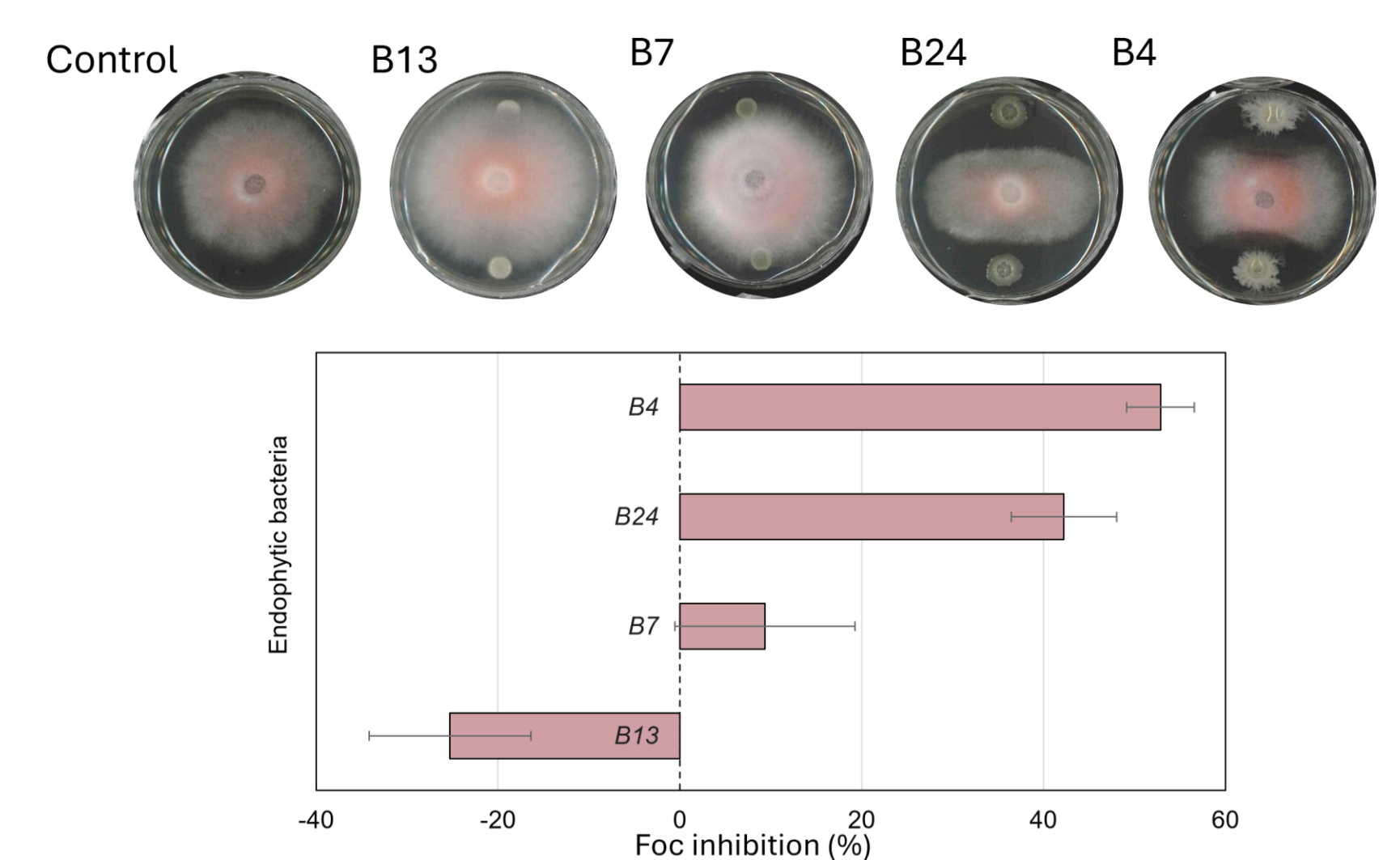


Figure 6: Impact of four endophytic bacteria (B13, B7, B24 and B4) on Foc growth on PDA medium. Positive and negative interactions are observed.

Figure 5: Maximum likelihood tree inferred from the *TEF1 α* gene of Maryani et al. (2019) reference sequences and three strains isolated in Benin (F7, F8 and F9).

References :
Maryani N., Lombard L., Poerba Y.S., Subandiyah S., Crous P.W., Kema G.H.J. (2019). Phylogeny and genetic diversity of the banana Fusarium wilt pathogen *Fusarium oxysporum* f. sp. *cubense* in the Indonesian centre of origin. Studies in Mycology, 92, 155-194.
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