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Massive gene flux in bacterial population fuels adaptation to forest soil ecosystem

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Introduction

As for plant or animal, bacteria are naturally structured in populations, i.e. individuals of the same species that interact together in the same environment.

The strains of a population are not necessarily clones and some can have specific genes that are not shared by all of the individuals of the population1–2. The real extent of this population genome variation in soil bacteria remains poorly described.

We aimed here to decipher by genome comparison the proportion of the specific genes, the mechanisms shaping these variations and their potential roles in a Streptomyces population.

Streptomyces are soil dwelling bacteria. They have a linear chromosome and a prolific specialized metabolism (e.g. enzymes, antibiotics, antifungals...) often of high biotechnological and medical interests. They can play key roles in the plant rhizosphere by contributing to their growth, health and resilience.

Strategy

1. Sampling scheme: To isolate a Streptomyces population we minimized the spatial scale by performing a micro-scale sampling (from grains of soil)

2. Phylogenetic analyses were then performed to select strains belonging to the same species (e.g. identical strains in 16S rRNA)

3. The genomes of 11 strains of the population were sequenced and compared.

The genomes are organized as linear chromosomes, some of them bearing large extrachromosomal elements

They are among the biggest bacterial genomes ever sequenced (ranging from 11.7 to 12.4 Mb)

Phylogenomic analyses confirmed that the strains are closely related at the intra-specific level and derived from a recent common ancestor

Pairwise comparisons of genomes were performed to identify variable gene pools due to insertion or deletion events (indels)

A large number of indels exists between the different strains of the population

- 452 indel events (triangles) ranging from 1 to 241 genes were identified in the population
- Two strains can differ from 2 to 261 indel events revealing a great diversity in the population
- There is a gradient of indel events toward the chromosomal ends
- Some hotspots of diversity have been identified (coloured triangles)
- Many positions have mobile (conjugal) genetic element signatures, indicating that gene transfers can be the motor of the diversity

The population genetic diversity can have ecological impacts

- Genome diversity impacts secondary metabolism among closely related strains.
- Specific metabolites produced by variable genes could serve as public goods in inhibiting competitors but not other population members.

Conclusions

- This study revealed an unexpectedly genetic diversity in term of presence/absence of genes among a Streptomyces population.
- Massive gene fluxes can explain how such diversification can occur within short evolutionary time.
- The diversity observed between individuals can have a functional role and impacts the ecology of the whole population.