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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.

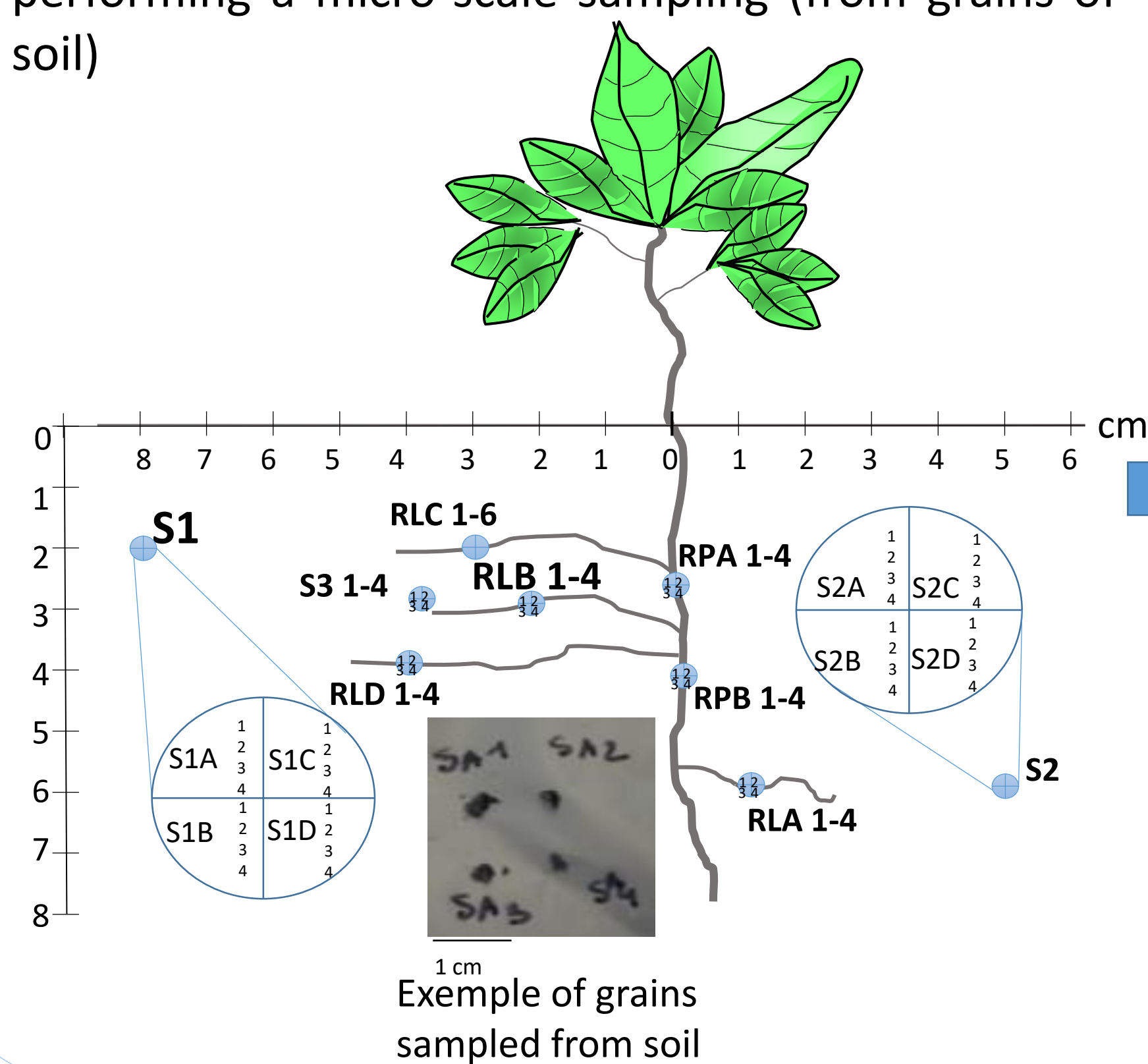
The **strains of a population are not necessarily clones** and some can have specific genes that are not shared by all of the individuals of the population^[1,2]. The real extent of this **population genome variation in soil bacteria remains poorly described**.

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.

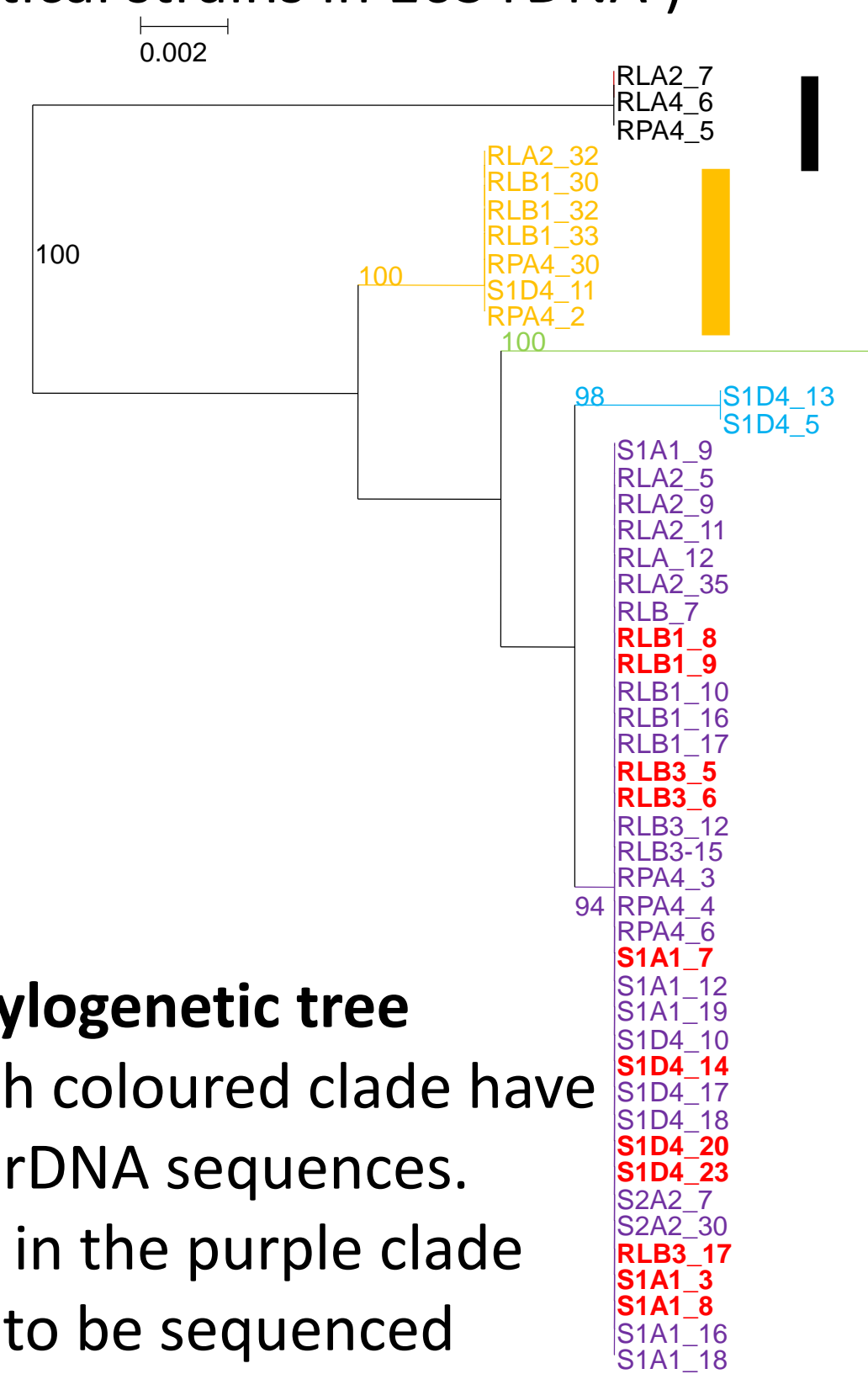
***Streptomyces* are soil dwelling bacteria**. They have a linear chromosome and a prolific specialized metabolism (*e.g.* enzymes, antibiotics, antifungals...) often of high biotechnological and medical interests. They can play key roles in the plant rhizosphere by contributing to their growth, health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



16S rDNA phylogenetic tree
Strains in each coloured clade have identical 16S rDNA sequences. Strains in red in the purple clade were chosen to be sequenced

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

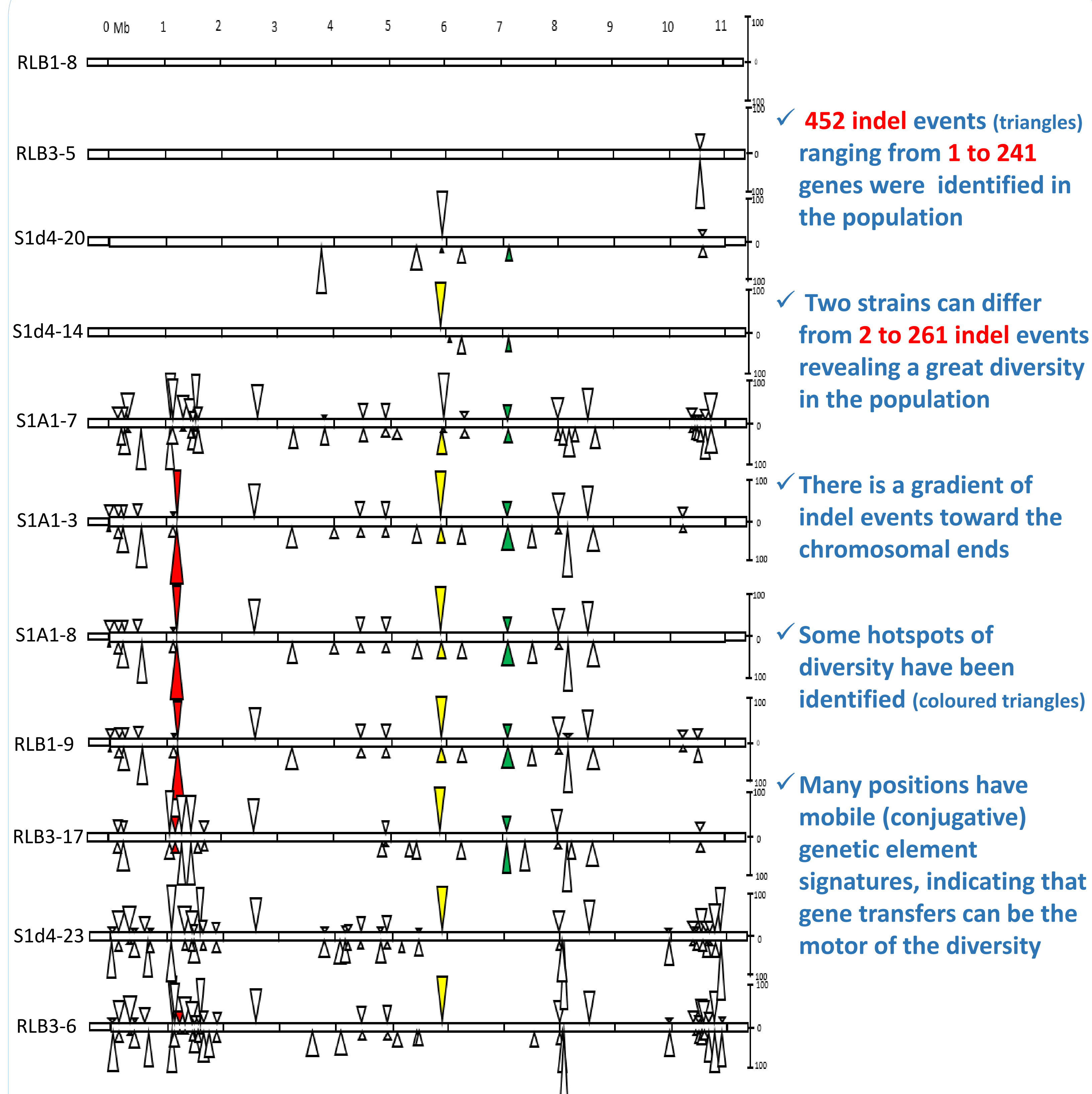
The genomes are organized as linear chromosomes, some of them bearing large extrachromosomal elements

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**

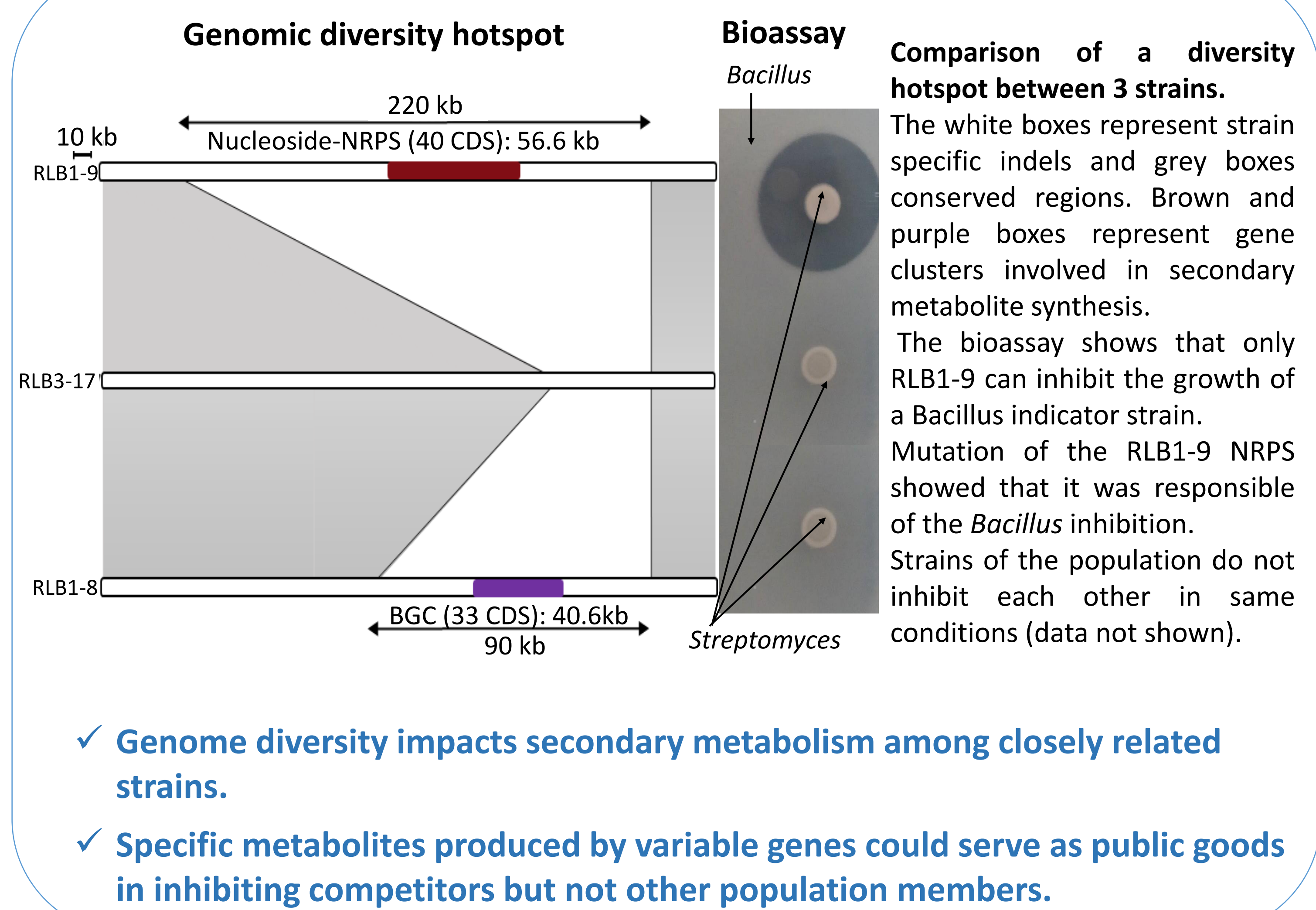
✓ **There is a gradient of indel events toward the chromosomal ends**

✓ **Some hotspots of diversity have been identified (coloured triangles)**

✓ **Many positions have mobile (conjugative) genetic element signatures, indicating that gene transfers can be the motor of the diversity**

The 11 sequenced genomes were compared with one reference chosen among the population (here RLB1_8). Each bar represents a strain chromosome. Triangles above a chromosome represent an insertion of genes in the reference strain and those below, an insertion in the compared strain. The size of the triangle is proportional to the number of genes in the indel. The highlighted triangles show examples of diversity hotspots where different type of indels are present in the population.

The population genetic diversity can have ecological impacts



Comparison of a diversity hotspot between 3 strains.

The white boxes represent strain specific indels and grey boxes conserved regions. Brown and purple boxes represent gene clusters involved in secondary metabolite synthesis.

The bioassay shows that only RLB1-9 can inhibit the growth of a *Bacillus* indicator strain. Mutation of the RLB1-9 NRPS showed that it was responsible of the *Bacillus* inhibition. Strains of the population do not inhibit each other in same conditions (data not shown).

✓ **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.

[1]Hao W., Golding G. B., (2006). The fate of laterally transferred genes: life in the fast lane to adaptation or death. *Genome research*, 16(5), 636-43.

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[3]Vetsigian K., Jajoo R., and Kishony R., (2011). Structure and Evolution of *Streptomyces* Interaction Networks in Soil and In Silico. *PLoS Biol* 9 (10): e1001184. doi:10.1371/journal.pbio.1001184.