



## Sex as a driving force for microbial community evolution in forest soil

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Collaboration : Plate-forme de séquençage de l'I2BC Gif-sur-Yvette

**Context** — In contrast to eukaryotes, bacteria are void of meiosis but nevertheless truly have sex! Bacterial sexuality (the more proper term is parasexuality) triggers horizontal gene transfer (HGT) consisting in conjugational exchanges (see the attached picture for the illustration of pock formation in *Streptomyces*); natural transformation or transduction and is the main driving force for genomic diversification and adaptation to the environment. Inferring HGT in bacteria relies on the detection of transfer of selectable functions such as resistance to drugs, heavy metals, catabolism properties...improving the fitness of the receptor cell in the environment. However, HGT was recently shown to lead to the replacement of fraction or full-length genes already present in the receptor strain. This phenomenon, called allelic replacement, involves homologous recombination unlike acquisition/loss of DNA sequences, which mostly implies illegitimate recombination. The development of approaches such as multilocus sequence analysis (MLSA) or the comparative genomics of related bacteria help now to assess this phenomenon.

**Objectives** — Our objective is to address the open question of the contribution of HGT in bacterial adaptation and dynamics of the microbial community. For that purpose we have applied MLSA and NGS sequencing approaches on the bacterial samplings available from a broader project funded in the previous call for project (2013), Inabact (supervised by S. Uroz, IAM, BEF).

**Approaches** — We explored by comparative genomics the genetic relationship between isolates from the same population of soil bacteria (*Streptomyces*). The strains were isolated from soil micro-aggregates ( $\text{mm}^3$ ) and were distant from only few cm. These sympatric strains have a short phylogenetic distance at the intra-specific scale (100% of identity in 16S rDNA coding gene and low MLSA polymorphism).

### Key results —

The genome of 11 strains were fully sequenced using an innovative approach combining the Nanopore (MinION) and illumina sequencing technologies in collaboration with the I2BC sequencing platform (Gif). It enabled to get high quality genomes and to initiate genomic comparative analyses despite their large size (ca. 12Mb, among the largest bacterial genomes ever sequenced).

- Genomic analyses (still in progress) showed that despite a short evolutionary time, the population strains have a large genomic diversity in term of presence/absence of genes, notably scattered in genomic islands.
- We showed a particular geolocalization of these variable genetic events along the chromosome.

- Some of the genomic islands exhibit clear signatures of integrated and conjugative elements, while some other include secondary metabolite biosynthetic genes.
- We showed that some of these genomic islands could be linked with the production of public goods (secondary metabolism) for the population.

**Main conclusions including key points of discussion** — These data suggest that the high level of evolvability of the *Streptomyces* genome affects their structuring and adaptation in their environment. The variable activities between strains of the population can constitute public goods. The mechanisms of rapid evolution can play important roles at short-term times in the functioning and the homeostasis of soil bacteria populations.

**Future perspectives** — Several articles are in preparation regarding these results. New analyses of comparative genomics, in link with the population functioning and genome evolution are still in progress.

**Valorisation** —

#### **Public communication**

<http://presse.inra.fr/Communiqués-de-presse/Une-bacterie-du-sol-championne-de-l-evolution-rapide>, <http://factuel.univ-lorraine.fr/node/12374>.

Journal télévisé FR3 Lorraine du 19/20 : une bactérie du sol, championne de l'évolution rapide  
Pour le voir en direct c'est à la TV ou dans le lien suivant : <https://france3-regions.francetvinfo.fr/grand-est/tv/direct/lorraine>.

Pour le voir en replay à partir de demain ce sera par ici : <https://france3-regions.francetvinfo.fr/grand-est/emissions/jt-1920-lorraine>.

#### **Publications**

Tidjani AR, Lorenzi JN, Toussaint M, van Dijk E, Naquin D, Lespinet O, Bontemps C, Leblond P. Genome Sequences of 11 Conspecific *Streptomyces* sp. Strains. *Microbiol Resour Announc*. 2019 Sep 19;8(38). pii: e00863-19. doi: 10.1128/MRA.00863-19.

Tidjani AR, Lorenzi JN, Toussaint M, van Dijk E, Naquin D, Lespinet O, Bontemps C, Leblond P. Massive Gene Flux Drives Genome Diversity between Sympatric *Streptomyces* Conspecifics. *mBio*. 2019 Sep 3;10(5). pii: e01533-19. doi: 10.1128/mBio.01533-19.

Tidjani AR, Bontemps C, Leblond P. Genome Sequences of Telomeric and sub-telomeric regions undergo rapid turnover within a *Streptomyces* population. *Sc. Rep.* en revision.

#### **Communication at conference**

Micro-time scale genome evolution among natural populations of *Streptomyces*

Maxime Toussaint, Abdoul-Razak Tidjani, Jean-Noël Lorenzi, Laurence Hotel, Olivier Lespinet, Cyril Bontemps, Pierre Leblond

International Symposium of the Biology of Actinomycetes, 2017, may 24-27 may, Jeju, Korea (communication orale).

Evolution génomique au sein d'une population naturelle de *Streptomyces*

Abdoul-Razak Tidjani, Maxime Toussaint, Jean-Noël Lorenzi, Laurence Hotel, Olivier Lespinet, Cyril Bontemps, Pierre Leblond

Actino2017, Lyon 18-20 Octobre 2017 (communication orale).

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



Abdoul-Razak Tidjani, Maxime Toussaint, Jean-Noël Lorenzi, Olivier Lespinet, Cyril Bontemps, Pierre Leblond.

Functional Ecology Conference, Nancy 10-12 décembre 2018 (communication orale)