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SEP.
2015

de 11h à 12h

SÉMINAIRE

Characterisation of the bacterial replicons

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The genome of bacteria is classically separated into essential, stable and slow evolving replicons (chromosomes) and accessory, mobile and rapidly evolving replicons (plasmids). This paradigm is being questioned since the discovery of genomic elements that possess both chromosomal and plasmidic features. These Extra-Chromosomal Essential Replicons (ECERs), be they called "megaplasmids", "secondary chromosomes" or "chromids", are found in diverse lineages across the bacterial phylogeny and are generally believed to be modified plasmids. However, their true nature and the mechanisms permitting their integration within the sable genome are yet to be formally determined. The relationships between replicons, with reference to their Genetic Information Inheritance Systems (GIIS), were explored under the assumption that the inheritance of ECERs is integrated to the cell cycle and highly constrained in contrast to that of standard plasmids. A global comparative genomics analysis including all available complete bacterial genome sequences, was performed using GIIS functional homologues as parameters and applying several analytical procedures. GIIS proved appropriate in characterizing the level of integration within the stable genome, as well as the origins, of the replicons. The study of ECERs thus provides clues to the genetic mechanisms and evolutionary processes involved in the replicon stabilization into the essential genome and to the continuity of the genomic material.