

Behaviors of Mobile Genetic Elements in Different Environments

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Mobile genetic elements (MGEs) including plasmids and transposons have an important role in the rapid evolution and adaptation of bacteria. A large number of MGEs have been found and studied over the last decades. However, how MGEs behave in natural environments is relatively poorly understood. In this study, we characterized and monitored the behavior of the MGEs under different conditions, in particular, using plasmid pCAR1, a carbazole-degrading plasmid isolated from *Pseudomonas resinovorans* CA10.

pCAR1 belongs to the incompatibility P-7 group and is self-transmissible between different bacteria. *repA* gene and *oriV* region are sufficient for the replication of the pCAR1. *parWAB* region is involved in its partition. We detected conjugative transfer between different *Pseudomonas* bacteria by filter mating assays. Comparison of changes in the transcriptome of different host strains caused by carrying pCAR1 revealed common responses in the hosts (transient Fe deficiency) and host-specific responses (upregulation of efflux pump genes or upregulation of prophage genes) [1]. Three nucleoid associated proteins (NAPs) encoded on pCAR1 are important factors affecting the genetic stability, persistence, and transfer of pCAR1.

Monitoring the survival of the host and transfer of the plasmid in artificial and natural environmental samples revealed several environmental factors, including cations and water content, which changed the behavior of both the host and its plasmid. Based on the composition analysis of model water samples, the conjugative transfer of pCAR1 was affected by the presence of cation(s) such as Mg^{2+} or Ca^{2+} ion(s). From the natural water samples, we detected transconjugants of pCAR1. Notably, we found genus *Stenotrophomonas* bacteria as a host of pCAR1, while most of its transconjugants belonged to genus *Pseudomonas*. Single-cell level analysis to detect the transconjugants of different plasmids including pCAR1 successfully determined the transfer range of the plasmids, which contains previously-unknown host strains [2].

We classified the fully sequenced plasmids (4,602 plasmids) based on their host taxonomy and their features of replication and conjugative transfer [3]. The G+C content of them is likely to be important for determining its host range. Notably, NAP genes are more frequently found on the larger conjugative plasmids than smaller non-conjugative plasmids.

These findings may provide important insights to understand the behaviors of MGEs and to control MGEs spreading in the environment.

References

- [1] Shintani M *et al.*, 2010. Environ. Microbiol., 12:1413-1426.
- [2] Shintani M *et al.*, 2014. Appl. Environ. Microbiol., 80:138-145.
- [3] Shintani M *et al.*, 2015. Front. Microbiol., 6:242.