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# INTERACTION BETWEEN DEGRADATIVE PLASMID AND HOST CHROMOSOME DIFFER BETWEEN THREE PSEUDOMONAS HOSTS

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**Abstract**

Carbazole degradative plasmid pCAR1 was originally isolated from *Pseudomonas resinovorans*, and was proven to be IncP-7 plasmid transferable to other *Pseudomonas* and *Stenotrophomonas* bacteria. Its 200,231-bp entire nucleotide sequence has already been determined.
To understand the mode of function of pCAR1 as an agent making its host to be carbazole degrader, it is necessary to understand the mechanisms of pCAR1 behaviour and to determine how much its behaviour is changeable in diverse types of host strains. On the other hand, pCAR1 carriage also alters its host strains in their growth, phenotype or cell physiology. While this phenomenon has been empirically known as "plasmid cost" or "metabolic burden," it has not been well-characterized how much these phenomena are affected by host cell type. Therefore, behavior of pCAR1-harboring strain should be determined by both host's effects on pCAR1 function and impacts of its carriage on host cell. In this study, such interaction between pCAR1 and chromosome were comprehensively evaluated using three *Pseudomonas* hosts, *P. putida* KT2440, *P. aeruginosa* PAO1, and *P. fluorescens* Pf0-1.
Growth phase-dependent transcriptome analyses of three host chromosomes showed that pCAR1 carriage affected more greatly at the transition and stationary phases in all hosts. Comprehensive phenotype comparisons showed that pCAR1 carriage reduced host fitness, swimming motility, and stress resistance and suggested the reduction of primary metabolic capacities in the TCA cycle and branching metabolisms. Interestingly, the extent of the impacts was different host by host, which was the largest in KT2440 and the lowest in Pf0-1. The impacts were more similar between KT2440 and PAO1 than between other combinations.
Comparison of pCAR1 transcriptome in the three hosts showed that the transcriptional pattern from early log to stationary phase of some genes (e.g. transposase gene and transcriptional activator gene) were different, while the genes related to degradation and plasmid maintenance were transcribed similarly in three hosts. The numbers of genes transcribed was the largest in KT2440, which may be the reason of above-mentioned different host cell response.
These results reported here suggested the importance of host choice in bioaugmentation using degradative plasmid.