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GENOME ANNOUNCEMENT

Genome Sequences of *Pseudomonas luteola* XLDN4-9 and *Pseudomonas stutzeri* XLDN-R, Two Efficient Carbazole-Degrading Strains

Xiaorui Liu, Zhonghui Gai, Fei Tao, Hao Yu, Hongzhi Tang, and Ping Xu

State Key Laboratory of Microbial Metabolism and School of Life Sciences & Biotechnology, Shanghai Jiao Tong University, Shanghai, People's Republic of China

***Pseudomonas luteola* XLDN4-9 and *Pseudomonas stutzeri* XLDN-R are two efficient carbazole-degrading pseudomonad strains. Here we present 4.63- and 4.70-Mb assemblies of their genomes. Their annotated key genes for carbazole catabolism are similar, which may provide further insights into the molecular mechanism of carbazole degradation in *Pseudomonas*.**

Carbazole and its derivatives in *N*-heterocyclic compounds have a dioxin-like structure, and some of them are toxic and mutagenic (5). They are most common in creosote, crude oil, and shale oil and are environmental pollutants and recalcitrant molecules, as well as raw materials for dyes, reagents, explosives, insecticides, lubricants, etc. (11). Microbial degradation is an effective way to remove such pollutants from the environment (1, 13). The genus *Pseudomonas* is a diverse group and has the ability to degrade various aromatic compounds, including carbazole (2, 12). Moreover, some strains of this genus have drawn much attention because of their denitrification and nitrogen fixation abilities (6).

We have previously isolated *Pseudomonas luteola* XLDN4-9 (CCTCC M 205094) and *Pseudomonas stutzeri* XLDN-R (CCTCC AB 2012149) from soil samples on the basis of their abilities to utilize carbazole as their sole source of carbon and nitrogen. They can degrade 99 and 97% of the carbazole present (500 mg/liter) in 16 and 13 h, respectively. It was reported that the carbazole degradation ability of strain XLDN4-9 could be enhanced in the presence of a nonaqueous-phase liquid (8). The derivatives of carbazole were also biodegradable by this strain (7).

The genomes of strains XLDN4-9 and XLDN-R were sequenced using the Illumina HiSeq 2000 system. The reads were assembled into 232 and 167 contigs, respectively, using Velvet 1.2.03. The largest contigs of strains XLDN4-9 and XLDN-R are 265,571 and 235,018 bp. The draft genome sequence of strain XLDN4-9 consists of 4,627,073 bases with a G+C content of 54.2%, while the draft genome sequence of strain XLDN-R contains 4,695,416 bases with a G+C content of 63.9%, which is in accordance with other *P. stutzeri* strains (6, 14, 15). There were 45 and 58 predicted tRNAs, 4,454 and 4,247 coding sequences, and 444 and 496 subsystems in strains XLDN4-9 and XLDN-R, respectively.

As expected, the genomes of strains XLDN4-9 and XLDN-R encode a diverse array of related proteins with predicted roles in the metabolism of aromatic compounds, such as biphenyl, benzoate, and chloroaromatic compounds. With respect to carbazole degradation, the *car* genes in strains XLDN4-9 and XLDN-R were found to be clustered in an arrangement similar to that of the *car* cluster in *Pseudomonas* sp. strain CA10 (10), which is different from that of *Sphingobium yanoikuyae* XLDN2-5 (3, 4).

The genomes of strains XLDN4-9 and XLDN-R contain 59 and 69 contigs involved in the degradation of aromatic compounds and multiple predicted pathways of protection against environmental stress. In our previous study, we found that carotenoids produced by strain XLDN2-5 might play a positive role in the degradation of heterocycles (9); however, the carotenoid biosynthetic pathway genes have not been found in these two strains. The above information may be helpful in elucidating the evolution and horizontal transfer of genes for carbazole degradation in *Pseudomonas*.

Nucleotide sequence accession numbers. These whole-genome shotgun projects have been deposited at DDBJ/EMBL/GenBank under accession numbers ALAT00000000 and AKYE00000000 for strains XLDN4-9 and XLDN-R, respectively. The versions described in this paper are the first versions, ALAT01000000 and AKYE01000000.

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Address correspondence to Ping Xu, pingxu@sjtu.edu.cn.

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