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The multiple antibiotic resistance IncP-1 plasmid pKJK5 isolated from a soil environment is phylogenetically divergent from members of the previously established alpha, beta and delta sub-groups. The 54,383 by plasmid pKJK5 was recovered from a soil environment by exogenous plasmid isolation and conveys resistance towards tetracycline and trimethoprim. Sequencing and annotation revealed a high level of structural similarity of the backbone genes to other IncP-1 plasmids containing a Tra1 and Tra2 region, a central control module and a replication initiation module. A considerable degree of divergence was associated with the backbone genes of pKJK5 as compared to homologous genes in the α, β and δ subgroups, which indicates that pKJK5 may belong to a novel subgroup of IncP-1 plasmids, which may also accommodate the partially sequenced non-subgroup classified plasmid pEMT3. Individual backbone genes in pKJK5 have a GC-content, which is consistently lower (average 6.3%) than the homologous genes from the archetype IncP-1 (3 plasmid 8751 indicating homogenous amelioration of IncP-1 plasmid backbone genes. Two discrete accessory elements of 2145 by (load 1) and 11678 by (load 2) respectively are situated between the Tra1 and Tra2 regions of pKJK5, both bounded by inverted repeats and direct flanking repeats indicative of transposon-mediated insertion. Load 1 consists of an insertion sequence ISPa17 and load 2 is a Tn402-derivative containing a class 1 integron, IS1326 and a fragment identical to a region of plasmid pTB11 harboring a tetracycline resistance determinant and part of an IncP-1 alpha oriV region. (c) 2006 Elsevier Inc. All rights reserved.
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