

## Tn4401 Carrying $bla_{KPC}$ Is Inserted within Another Insertion in pKpQIL and Related Plasmids

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The  $bla_{\rm KPC-2}$  gene, encoding the KPC-2 carbapenemase, was first identified in the United States in 1996, and  $bla_{\rm KPC}$  variants now appear to be endemic in several countries, including the United States, Israel, Greece, and China, with sporadic reports in other locations (1).  $bla_{\rm KPC}$  genes have generally been found flanked by the insertion sequences IS*Kpn7* and IS*Kpn6* within the Tn3-family transposon Tn4401 (2) or truncated versions of this structure. Tn4401 has been detected in plasmids from several incompatibility groups, including IncFII<sub>K</sub> plasmids related to pKpQIL (3), IncN, ColE (4), IncI2 (5), and IncX3 (6) plasmids.

A recent paper linked an ~11,109-Da peak detected by matrixassisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) with the presence of  $bla_{\rm KPC}$  and used it to track pKpQIL-like plasmids (7). The peak corresponds to the cleavage product of a hypothetical protein designated p019 in the pKpQIL sequence (GenBank accession no. NC\_014016.1). The authors noted that although p019 "appears to be fairly closely linked to the  $bla_{\rm KPC}$  gene," "genetic events in the plasmid may change the association of the pKpQIL\_019 MALDI-TOF MS peak with the presence of functional carbapenemase" (7).

Detailed analysis of the pKpQIL sequence suggests that the p019 gene is part of an insertion into which Tn4401 has then been

inserted. This insertion is flanked by 10-bp direct repeats (DR) and is 2,328 bp in length (excluding one 5-bp DR flanking Tn4401) (Fig. 1A). As noted previously (8), part of this region is related to the insertion sequence ISAs12 (~91% nucleotide identity), which creates 10 bp (ISfinder, https://www-is.biotoul.fr/) (9). The ends of this putative IS, designated ISKpn31 by ISfinder, resemble the terminal inverted repeats (IR) of ISAs12. However, the adjacent region containing the p019 gene and other IS fragments, which has no equivalent in ISAs12, also ends in a similar sequence (Fig. 1C). It is possible that this region had previously become incorporated as an internal part of an ISKpn31-derived mobile element or that it was mobilized in a way similar to that of ISEcp1-mediated capture of regions adjacent to the right IR (IR<sub>R</sub>) (10), except that it lies adjacent to the left end of ISKpn31.

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**FIG 1** Insertion in pKpQIL-like plasmids. (A) Complete insertion (positions 8823 to 21062 in GenBank accession no. NC\_014016.1). (B) Expanded diagram showing details of the inserted region with Tn4401 and one 5-bp DR removed (positions 8823 to 8881 and 18794 to 21062). Inverted repeats (IR) of Tn4401 are shown as tall black triangles, and IR of ISK*pn31* are indicated by black bars. IS are shown by boxes, with the pointed end indicating IR<sub>R</sub>. Labeled arrows indicate the directions and extents of selected genes. The sequences of DR flanking insertions are shown. IS $\Delta$  is a fragment of an IS21-like IS. (C) Comparison of IR sequences. (ISA*s12* IR are from the 16 copies in the *Aeromonas media* chromosome in GenBank accession no. CP007567).

Although BLAST searches indicate that the insertion containing p019 has been found only in plasmids carrying  $bla_{\rm KPC}$  to date, these two genes are part of different mobile elements. Independent movement is already evident for Tn4401, which has been found in different plasmid backbones flanked by 5-bp DR, indicative of direct insertion, e.g., in p15S (GenBank accession no. FJ223606) (4) and pCOL-1 (KC609323) (11). The presence of p019 and  $bla_{\rm KPC}$  on IncFII<sub>K</sub> plasmids less closely related to pKpQIL (e.g., pKPN-101-IT) (12) or those that belong to other Inc groups, e.g., IncI2 (pBK15692) (5) or IncX3 (pKPC-NY79) (6), also means that detecting p019 does not always indicate closely related or even similar plasmids. Thus, caution needs to be used in correlating the presence of p019 with the presence of  $bla_{\rm KPC}$  or a particular plasmid, and understanding the genetic contexts of markers apparently linked to resistance genes is important.

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