Reply to “Mobilization of *bla*_{BKC-1} by ISKpn23?”

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We read with great interest the letter by Partridge (1) in response to the article reporting the new class A carbapenemase BKC-1 (2). Partridge has found the probable DR sequences of ISKpn23, which are located upstream of ISKpn23 and downstream of the *bla*_{BKC-1} gene. The author suggests that this element was responsible for *bla*_{BKC-1} and *aph*(3)-VI expression.

In our previous study, we showed that the BL21 clone harboring only *bla*_{BKC-1} exhibited very low carbapenem MICs (0.12 to 0.5 µg/ml) compared to those of the T3 transformant strain (MICs, 8 to 64 µg/ml), which carries the entire plasmid (p60136). We agree with Partridge that the presence of ISKpn23 may have driven the expression of *bla*_{BKC-1}. The level of variation in carbapenem MICs was too high to be justified only by the distinct machineries of the recipient strains. To confirm this hypothesis, we are currently working on the construction of laboratory derivative strains carrying the identical genetic background of *bla*_{BKC-1}, except for the deletion of ISKpn23.

Partridge has also demonstrated curiosity about the mobilization of *bla*_{BKC-1}, since ISKpn23 belongs to the IS1380 family, as does ISEcp1. ISEcp1 has been shown to mobilize the *bla*_{CTX-M-19} gene. It was also responsible for transferring the *bla*_{CTX-M-2} gene from the *Kluyvera ascorbata* chromosome to plasmids (3). We also agree with Partridge that it will be interesting to see how successful *bla*_{BKC-1} will become, in comparison with *bla*_{CTX-M} genes associated with ISEcp1. So far, the frequency of *bla*_{BKC-1} seems to be very low. Recently, we found only two *K. pneumoniae* strains harboring

*bla*_{BKC-1} among the 635 investigated *Klebsiella* species clinical isolates (4). The spread of an epidemic clone rather than the spread or mobilization of *bla*_{BKC-1} by ISKpn23 was detected among the studied *K. pneumoniae* isolates.

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