New variant Salmonella genomic island 1–U in Proteus mirabilis clinical and food isolates from South China

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Keywords: multidrug resistance, integrons, genotyping

Sir,

Salmonella genomic island 1 (SGI1) is a 43 kb genomic island containing a 13 kb multidrug resistance (MDR) region antibiotic resistance gene cluster initially identified in Salmonella enterica serovar Typhimurium definitive phase type (DT) 104 strains. Classically, the MDR region contains five antibiotic resistance genes, all of which are located within the boundaries of a complex class 1 integron, designated In104.1 Over the past few years, SGI1 with variant antibiotic resistance gene clusters (termed variable SGI1) named SGI1-A to SGI1-T have been identified in several other Salmonella serotypes and also in Proteus mirabilis,2–4 suggesting possible horizontal gene transmission of the genetic element among microbes. However, it is worth noting that the direct association of the int2 gene, which is part of a retron sequence, with SGI1 has been reported only in S. enterica Typhimurium, while SGI1 is located between the thdF and yidC genes in other S. enterica serovars.5 The integration of SGI1 into the P. mirabilis chromosome takes place between the thdF and hipB genes, according to the report by Boyd et al.1 However, our overall understanding of the evolution of SGI1 and the potential risk of its dissemination among microbes remains very limited.

To reveal the genetic difference between SGI1 variants and the potential molecular events involved in the evolution and transmission of the MDR-encoding unit, based on an identical MDR profile to sulfamethoxazole, trimethoprim, tetracycline and erythromycin, a total of 23 P. mirabilis strains isolated in Guangzhou, China, were examined in this study. Seventeen of them originated from stools of 17 patients with diarrhoea in the First Affiliated Hospital of Jinan University from 2006 to 2008. The remaining six isolates were from 35 raw chicken meat samples purchased from two markets in 2009. PCR primers used in the screening for SGI1 are listed in Table S1 (available as Supplementary data at JAC Online). Eight P. mirabilis strains including three from chicken samples from the same seller in one of the markets and the other five from patients from 2006 to 2008 were found to harbour the dfrA5 cassette of class 1 integrons. To confirm the presence of SGI1, primer pairs corresponding to the left junction region (PmlLj/Lj-R1) and right junction region (104–RJ/PmRJ1) of SGI1 in the P. mirabilis chromosome were used. PCR results were positive for the left junction of SGI1 with the thdF gene, but negative for the right junction with the hipB gene. The right junction region of SGI1 was then analysed by PCR with primers hipA-R1 (hipA specific) and MP-R1 (specific for the membrane protein PM3124-encoding gene) targeting the two genes downstream of hipB of P. mirabilis HA4320. Positive results were found in all eight strains using primer pair 104–RJ and MP-R1. The PCR products were sequenced and the sequences flanking SGI1 were, with the exception of a few base changes, identical to part of the S044- and PM3124-encoding genes. Thus, the eight P. mirabilis strains appeared to have SGI1 or variants integrated between thdF and the gene encoding PM3124. Besides, the same integration site has been reported in a P. mirabilis isolate from France containing the SGI1-O variant.6 Interestingly, the hipB and hipA genes were further screened using specific primers hipB-F1 and hipA-R1, and the results were negative. The results indicated that the eight P. mirabilis strains lacked the sequences of hipB and hipA genes (Figure 1).

PCR mapping of the antibiotic resistance gene cluster was performed using primers described in Table S1. PCR cloning and DNA sequencing revealed that all eight strains harboured a new variant designated SGI1-U. It contained the dfrA5 gene cassette within the integron structure. It is noteworthy that the dfrA5 cassette coding for trimethoprim resistance had not been reported in P. mirabilis before. Thus, the strains probably obtained the dfrA5 gene cassette from other microorganisms.

The three strains from food and the five strains from patients had 100% identical SfiI and NotI PFGE patterns, suggesting that they might be clonally related.

In conclusion, for the first time, the new variant SGI1-U was identified in eight P. mirabilis clinical and food isolates from South China. It is also interesting that this is the first time the dfrA5 gene has been identified in P. mirabilis. In particular, the deletions of hipB and hipA genes found at the right junction region of SGI1-U showed that SGI1-U was located between the thdF gene and a gene encoding a membrane protein on the P. mirabilis chromosome.

Nucleotide sequence accession numbers

The right junction region of SGI1-U and the nucleotide sequence of the dfrA5 cassette have been deposited in the GenBank database under accession numbers HM747960 and HM747961, respectively.
Funding
This work was supported by the National Natural Science Foundation of China (20877028) and the Guangdong Nature Science Foundation of China (10451064101005159).

Transparency declarations
None to declare.

Supplementary data
Table S1 is available as Supplementary data at JAC Online (http://jac.oxfordjournals.org/).

References

Report of an outbreak of CO2-dependent methicillin-resistant Staphylococcus aureus on a regional liver transplant unit

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Keywords: MRSA, Staphylococcus sp., healthcare-associated infections