Salmonella Agona harboring genomic island 1-A
B. Doublet, P. Butaye, H. Imberechts, J.M. Collard, E. Chaslus-Dancla, A. Clockaert

To cite this version:
B. Doublet, P. Butaye, H. Imberechts, J.M. Collard, E. Chaslus-Dancla, et al.. Salmonella Agona harboring genomic island 1-A. Emerging Infectious Diseases, Centers for Disease Control and Prevention, 2004, 10 (4), pp.756-758. 10.3201/eid1004.030417. hal-02683157

HAL Id: hal-02683157
https://hal.inrae.fr/hal-02683157
Submitted on 1 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Distributed under a Creative Commons Attribution 4.0 International License
isolate more phages in Brazil and neighboring countries.

To date, serotyping is the only identification tool for the characterization of non-O1 strains of *V. cholerae* (8). However, serotyping is only performed at a limited number of laboratories. For this study, all isolates from Brazil were sent to laboratories outside the country for serotyping. This step was expensive and time-consuming and posed risks during transit.

An alternative method is the use of phages for identifying non-O1 strains. This method offers an affordable monitoring system in less-developed countries such as Brazil. Phage O6 and O34 should at least be useful for confirming the diagnosis of *V. cholerae* O6 and O34 infection and for differentiating *V. cholerae* O1 and non-O1 strains.

**Acknowledgment**

The authors are grateful to Eliseu Alves Waldman for providing valuable information.

**B.L. Sarkar***, **Amar N. Ghosh**, **Anindito Sen**, **and D. P. Rodrigues**†

*National Institute of Cholera & Enteric Diseases (ICMR) WHO Collaborating Centre for Research and Training on Diarrheal Diseases, P-33, C.I.T. Road, Scheme–XM, Beleghata, Kolkata 700010, India; fax: +91-33-2350-506; email: bl_sarkar@hotmail.com

---

**Salmonella Agona Harboring Genomic Island 1-A**

To the Editor: Multidrug-resistant *Salmonella enterica* serovar Typhimurium definitive phage type 104 has emerged during the 1980s and 1990s as a world health problem because of its implications in animal and human disease (1–3). Epidemic serovar Typhimurium definitive phage type 104 isolates are commonly resistant to ampicillin (Ap), chlo-
ramphenicol (Cm)/florfenicol (Ff), streptomycin (Sm)/spectinomycin (Sp), sulfonamides (Su), and tetracyclines (Tc) (1,3). This multidrug-resistance phenotype is conferred by an antibiotic resistance gene cluster included in a 43kb genomic island named Salmonella genomic island 1 (4). Salmonella genomic island 1 has been recently characterized and located between the thdF and int2 genes of the chromosome. The int2 gene is part of a retron sequence found only in serovar Typhimurium. Downstream of the retron sequence is the yidY gene, which is also found in the chromosome of other S. enterica serovars. The antibiotic resistance gene cluster of approximately 13 kb is located at the 3' end of Salmonella genomic island 1 (4). All resistance genes are clustered and are bracketed by two integron structures (5,6). The first integron carries the aadA2 gene, which confers resistance to Sm and Sp. The second integron contains the β-lactamase gene pse-1, conferring resistance to Ap. Flanked by these two integron structures are the floR gene, which confers cross-resistance to Cm and Ff, and the tetracycline-resistance genes tetR and tet(G) (5,6). Recently, Salmonella genomic island 1 has also been identified in other serovars of S. enterica namely Agona (4,7), Paratyphi B (8), and Albany (9), indicating the horizontal transfer potential of Salmonella genomic island 1. In these serovars, Salmonella genomic island 1 has the same chromosomal location as in serovar Typhimurium definitive phage type 104, except that they lack the retron sequence found downstream of Salmonella genomic island 1 (4,8,9). Moreover, six variant Salmonella genomic island 1 antibiotic resistance gene clusters (Salmonella genomic island 1-A to -F) have recently been reported for serovars Typhimurium DT104, Agona, and Albany to confer different multidrug resistance phenotypes (9,10). These clusters of genes were probably generated after chromosomal recombinational events or by antibiotic resistance gene cassette replacement in the integron structures. In particular, the dfrA10 gene coding for trimethoprim (Tm) resistance was found downstream of the pse-1 integron in a third unusual integron structure involving orf513 in the variant antibiotic resistance gene cluster called Salmonella genomic island 1-A (ApCmFfSmSpSuTcTm) (10).

Multidrug-resistant serovar Typhimurium definitive phage type 104 was disseminated globally with several outbreaks in humans and animals. At present, in contrast to the world health problem of multidrug-resistant serovar Typhimurium definitive phage type 104, human cases of infections with other S. enterica serovars harboring Salmonella genomic island 1 have not yet been reported. Salmonella genomic island 1-multidrug-resistant serovars Agona, Paratyphi B, and Albany were isolated from different animal species and countries (7–9). In this study, we analysed the first Salmonella genomic island 1 positive serovar Agona strain (02/01177) isolated from a human case in Belgium. A Belgian patient, who had been infected by a multidrug-resistant serovar Agona strain travelling to Turkey; subsequent to the multidrug-resistant serovar Agona strain, gastroenteritis developed. While in Turkey the patient sought medical care and was treated unsuccessfully with antimicrobial agents. Upon his return to Belgium, this serovar Agona strain was isolated from his stools, and he recovered after treatment with ciprofloxacin. The serovar Agona strain 02/01177 displayed the multidrug resistance profile ApCmFfSm SpSuTcTm, which suggested the possible occurrence of Salmonella genomic island 1-A (10). Moreover, the strain showed the same level of resistance to Ff as Salmonella genomic island 1 harboring S. enterica serovars (MIC of 64 µg/mL) (7–9).

To assess the presence of Salmonella genomic island 1 and its location in the chromosome, polymerase chain reactions (PCRs) were performed using primers corresponding to the left and the right (with or without retron) Salmonella genomic island 1 junctions to the chromosome as described previously (4,8–10). PCR results were positive for the left junction between the thdF gene of the chromosome and the int gene of Salmonella genomic island 1 (4). For the right junction, PCR results were positive between open reading frame (ORF) S044 of Salmonella genomic island 1 and yidY gene of the chromosome. Thus, these data indicate that this serovar Agona human isolate contains Salmonella genomic island 1 at the same chromosomal location as in other Salmonella genomic island 1 positive serovars but lacks the retron sequence found to date only in serovar Typhimurium strains (4,8,9).

PCR mapping of the typical antibiotic resistance genes and integrons associated with Salmonella genomic island 1 was realized as described previously (4,8–10). PCR amplifications on genomic DNA extracted from serovar Agona strain 02/01177 yielded all specific fragments of the sizes expected from DNA of serovar Agona control strain 1169SA97 harboring Salmonella genomic island 1-A (data not shown) (10). These PCR mapping results indicated the presence of the typical Salmonella genomic island 1 resistance gene cluster with the insertion of the third unusual orf513 integron structure carrying dfrA10 (8–10). These data are in accordance with the multidrug resistance phenotype of serovar Agona strain 02/01177 and indicate the presence of the variant antibiotic resistance gene cluster Salmonella genomic island 1-A (10).

Macrorestriction analysis by pulsed-field gel electrophoresis of DNA from serovar Agona strain 02/01177 cut by XbaI or BlnI, showed
that this human isolate is indistinguishable by its XbaI or BlnI macrorestriction patterns from the other multidrug-resistant Salmonella genomic island 1-carrying serovar Agona strains isolated from poultry in Belgium (data not shown) (7). Thus, the human serovar Agona isolate appears clonally related to those from poultry.

To our knowledge, this is the first report describing a human infected by a serovar Agona strain harboring Salmonella genomic island 1-A. Moreover, it shows the first case where another S. enterica serovar harboring Salmonella genomic island 1 than the epidemic serovar Typhimurium definitive phage type 104 clone is implicated in human infection. The patient could probably have been infected before his travel to Turkey by a Salmonella genomic island 1-A carrying serovar Agona strain in Belgium where this type of strain is frequently isolated from poultry (Doublet et al., pers. comm.). This hypothesis is also supported by macrorestriction analysis, which showed that the strains from poultry and the human case-patient had identical XbaI and BlnI pulsed-field gel electrophoresis patterns and thus indicate that they are clonally related. Moreover, the patient was not in contact with poultry during his stay in Turkey and, to date, very little is known about the epidemiology of multidrug-resistant serovar Agona strains in this country. Further investigations on the epidemiology of multidrug-resistant serovar Agona strains harboring Salmonella genomic island 1 are warranted to avoid such strains becoming a worldwide epidemic, as was the case for multidrug-resistant serovar Typhimurium definitive phage type 104.

Acknowledgments

We thank C. Mouline for expert technical assistance. We also thank D. Boyd and M.R. Mulvey for their collaboration.

This work was supported by a grant from the French Institut National de la Recherche Agronomique (INRA, Action Transversalité 2001–2003).

Benoit Doublet, * Patrick Butaye, † Hein Imberechts, † Jean-Marc Collard, ‡ Elisabeth Chaslus-Dancla,* and Axel Cloeckaert*

*Institut National de la Recherche Agronomique, Nouzilly, France; †Centre d'Étude et de Recherche Vétérinaires et Agrochimiques, Brussels, Belgium; and ‡Scientific Institute of Public Health, Brussels, Belgium

References

1. Cloeckaert A, Schwarz S. Molecular characterization, spread and evolution of multidrug resistance in Salmonella enterica serotype Typhimurium DT104. Vet Res 2001;32:301–10.
2. Glynn MK, Bopp C, Dewitt W, Dabney P, Mokhtar M, Angulo FJ. Emergence of multidrug-resistant Salmonella enterica serotype Typhimurium DT104 infections in the United States. N Engl J Med 1998;338:1333–8.
3. Ribot EM, Wierzba RK, Angulo FJ, Barrett TJ. Salmonella enterica serotype Typhimurium DT104 isolated from humans, United States, 1985, 1990, and 1995. Emerg Infect Dis 2002;8:387–91.
4. Boyd D, Peters GA, Cloeckaert A, Sidi Boumedine K, Chaslus-Dancla E, Imberechts H, et al. Complete nucleotide sequence of a 43-kilobase genomic island associated with the multidrug resistance region of Salmonella enterica serovar Typhimurium DT104 and its identification in phage type DT120 and serovar Agona. J Bacteriol 2001;183:5725–32.
5. Arcangiol MA, Leroy-Sétrin S, Martel JL, Chaslus-Dancla E. A new chloramphenicol and florfenicol resistance gene flanked by two integron structures in Salmonella typhimurium DT104. FEMS Microbiol Lett 1999;174:327–32.
6. Briggs CE, Fratamico PM. Molecular characterization of an antibiotic resistance gene cluster of Salmonella typhimurium DT104. Antimicrob Agents Chemother 1999;43:846–9.
7. Cloeckaert A, Sidi Boumedine K, Flaujac G, Imberechts H, D’Hooghe I, Chaslus-Dancla E. Occurrence of a Salmonella enterica serovar Typhimurium DT104-like antibiotic resistance gene cluster including the floR gene in S. enterica serovar Agona. Antimicrob Agents Chemother 2000;44:1359–61.
8. Meunier D, Boyd D, Mulvey MR, Baucheron S, Mammina C, Nastasi A, et al. Salmonella enterica serotype Typhimurium DT104 antibiotic resistance genomic island 1 in serotype Paratyphi B. Emerg Infect Dis 2002;8:430–3.
9. Doublet B, Lailier R, Meunier D, Brasibois A, Boyd D, Mulvey MR, et al. Variant Salmonella genomic island 1 antibiotic resistance gene cluster in Salmonella enterica serovar Albany. Emerg Infect Dis 2003;9:585–91.
10. Boyd D, Cloeckaert A, Chaslus-Dancla E, Mulvey MR. Characterization of variant Salmonella genomic island 1 multidrug resistance regions from serovars Typhimurium DT104 and Agona. Antimicrob Agents Chemother 2002;46:1714–22.

Address for correspondence: Axel Cloeckaert, Unité 086, Bio-Agrisseurs, Santé, Environnement Institut National de la Recherche Agronomique, 37380 Nouzilly, France, email: cloeckae@tours.inra.fr