# IS*200* is not a member of the IS*600* family of insertion sequences

Isidre Gibert, Karen Carroll[1], David R.Hillyard[1], Jordi Barbé and Josep Casadesus[2]*
Departament de Genètica i Microbiologia, Universitat Autònoma de Barcelona, 08193 Bellaterra, Barcelona, Spain, [1]Department of Pathology, University of Utah, Salt Lake City, UT 84112, USA and [2]Departamento de Genética, Universidad de Sevilla, Apartado 1095, 41080 Seville, Spain

Submitted January 2, 1991 EMBL accession no. X56834

IS*200* is an insertion sequence present in all *Salmonella* species except *S. agona* (1, 2). The element is absent from all other Enterobacteriaceae, with the exception of some strains of *Shigella flexneri* and *Shigella sonnei* (2). It had been hypothesized that the first mutation characterized as an IS*200* insertion, *hisD984*::IS*200* (1, 3) might actually be a deletion mutant of the *Shigella* insertion element IS*630* (4). However, sequencing of the ends of a second mutation caused by IS*200* insertion later suggested that IS*200* was a distinct insertion element (5).

We recently obtained the complete nucleotide sequence of the insertion element IS*200* inserted in the histidine operon of *S. typhimurium* (causing the mutation *hisD984*::*IS*200). The element is 708 bp long; if this size corresponds to a wild-type element, IS*200* can be considered the smallest insertion sequence known (6). A diagram of the hypothetical structure of IS*200* is presented in Figure 1. Unlike many insertion elements, IS*200* lacks terminal inverted repeats, as previously reported (3, 5). The element contains three potential open reading frames (ORF 1, ORF 2 and ORF 3), whose coding capabilities are 69, 71 and 58 amino acids, respectively. ORF2 and ORF3 are overlapping; the existence of overlapping ORFs is not surprising, since it seems to be extremely common among bacterial insertion sequences (6). Other interesting features of IS*200* are the following:

(i) Three potential hairpin loops are located near the 'right' end of the element (Figure 1). One of the loops, centered on base 688, strongly reminds of a Rho-independent transcription terminator, as previously suggested (3). Two smaller hairpins are centered on bases 608 and 665.

(ii) Two nearly perfect inverted repeats of 20 bp exist within the sequence. Both repeats are located near the 'right' end, extending between nucleotides 565–584 and 629–648 (Figure 1). The repeats differ by only 4 mismatches and their potential biological significance is unknown.

A search in the EMBL data bank has confirmed that IS*200* is not a deletion mutant of IS*630*, although two discrete regions of homology (8 and 10 bp long) appear to exist between IS*200* and IS*630*. Likewise, two short regions of homology (7 and 8 bp long) are found between IS*200* and the *Shigella sonnei* insertion sequence IS*640*. Two DNA stretches, 10 and 11 bp long, homologous to the *S. sonnei* element IS*600* have also been found. Probes lacking homology with the *Shigella* elements IS*600*, IS*630* and IS*640* can now be obtained by cloning specific, internal fragments of IS*200*. These probes are expected to be useful to find out whether the hybridization found between IS*200* probes and certain *Shigella* DNAs (2) was caused or not by cross-hybridization between IS*200* and *Shigella* insertion elements.

## ACKNOWLEDGMENTS

The *S. typhimurium* strain carrying the mutation *hisD984*::IS*200* was kindly provided by John R.Roth. We are grateful to Andrés Garzón for interesting discussions and to Maren Marsh for helpful assistance.

## REFERENCES

1. Lam,S. and Roth,J.R. (1983) *Cell* **34**, 951–960.
2. Gibert,I., Barbé,J. and Casadesús,J. (1990) *J. Gen. Microbiol.* **136**, 2555–2560.
3. Lam,S. and Roth,J.R. (1986) *J. Mol. Biol.* **187**, 157–167.
4. Matsutani,S., Othsubo,H., Maeda,Y. and Othsubo,E. (1987). *J. Mol. Biol.* **196**, 445–455.
5. O'Reilly,C., Black,G.W., Laffey,R. and McConnell,D.J. (1990). *J. Bacteriol.* **172**, 6599–6601.
6. Galas,D.J. and Chandler,M. (1989). In Berg,D.M. and Howe,M.M. (eds) *Mobile DNA*. American Society for Microbiology, pp. 109–162.

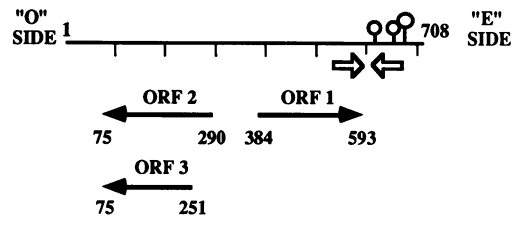


**Figure 1.** A diagram of the insertion *hisD984*::IS*200*. The orientation of the insertion element in the *hisD* gene is indicated by the 'O' and 'E' sides. Potential ORFs, hairpin loops and internal inverted repeats are also shown. The relative sizes of the hairpins is indicated (but not drawn to scale).

* To whom correspondence should be addressed