

Aquariums as
Reservoirs for
Multidrug-resistant
Salmonella
Paratyphi B

Table. Genetic characteristics of *Salmonella enterica* serovar Paratyphi B dT+ isolates used in this study

Isolate no.*	Source†	Phage type‡	State§	Date of isolation	Age, y/Sex	SGI1¶
Set 1						
SRC229	H	Aus2	ACT	2000	<1/F	+
SRC230	H	Aus2	ACT	2000	1/M	+
SRC231	FT	Aus2	ACT	2000	–	+
Set 2						
SRC232#	H	Aus2	Vic	2000	11/F	+
SRC233#	H	Aus2	Vic	2000	11/F	+
SRC233A	FT	Aus2	Vic	2000	–	ND
Set 3						
SRC145	H	Aus3	Vic	2003	74/F	+
SRC142	FT	Aus3	Vic	2003	–	+
SRC143	FT	Aus3	Vic	2003	–	+
Set 4						
SRC149	H	Aus3	Vic	2003	12/M	+
SRC147	FT	Aus3	Vic	2003	–	+
SRC148	FT	Aus3	Vic	2003	–	+
Control						
SRC50	H	RDNC	Vic	2001	14/M	++

*All isolates were resistant to ampicillin, chloramphenicol, streptomycin, spectinomycin, sulfonamides, and tetracycline.



aquariums of 5 patients with RDNC Aus3-type infections, and identical isolates were recovered from each fish tank. Four matched sets of isolates, 2 from 2000 and 2 from 2003, were further examined (Table). One isolate (SRC50) characterized previously (7) was used as a control (Table).

To determine if the resistance phenotype of these strains was due to SGI1 (4,5,7,8,11), polymerase chain reaction (PCR) with primer pairs shown in Figure 1 was used as previously described (7). The left and right junctions of SGI1 with the chromosome and of In104 with SGI1 were present in all cases. Regions containing the gene cassettes were amplified by using standard primers (L1 and R1) in the 5'- and 3'-conserved segments of class 1 integrons. Fragments of 1.0 and 1.2 kb were amplified from all isolates, and digestion of these amplicons with *RsaI* generated a profile (data not shown) that was indistinguishable from the pattern for the 2 amplicons containing the *aadA2* and *blaP1* cassettes found in In104 and *S. Paratyphi B* dT+ isolates SRC49 and SRC50 from 2001 (7). The *aadA2* gene cassette was linked to SO26 in the SGI1 backbone, which indicates that it is on the left, as in In104, and the expected 1.8-kb PCR fragment was generated by using primers in *groEL* and *blaP1* (Figure 1), which places the *blaP1* cassette on the right. Southern hybridization of *XbaI*-digested whole-cell DNA with a probe for the *floR* gene as described previously (7) identified a band of ≈12 kb, which is consistent with an SGI1 structure identical to that reported previously (7,8,11) and

the *groEL-blaP1* amplicon linked this 12-kb *XbaI* fragment with the adjacent 4.3-kb *XbaI* fragment (Figure 1).

To obtain further evidence for the identity of the matched human and fish tank isolates, macrorestriction analyses of *XbaI*-digested whole-cell DNA by pulsed-field gel electrophoresis (PFGE) were performed as previously described (12). Several studies (3–6,13) suggest that *S. Paratyphi B* dT+ isolates possess considerable genetic heterogeneity. However, the SGI1-containing isolates appear to be homogeneous. The band patterns for all SGI1-containing *S. Paratyphi B* dT+ were identical from humans and fish tanks with phage type RDNC Aus3 (Figure 2A) and Aus2 (data not shown). IS200 profiles were also analyzed by hybridization of an IS200 probe with *Pst* I-digested whole-cell DNA as described elsewhere (6). Again, all strains showed identical profiles (Figure 2B and data not shown) that differed by 1 band from profile IP1 recently described (6). Thus, matched isolates from humans and their fish tanks were indistinguishable from each other.

An unusual observation in this study was that isolates with different phage types showed identical PFGE and IS200 profiles, indicating that they represented a clonal cluster. The control strain SRC50 (RDNC) also displayed the same patterns, demonstrating that it also is a member of the same clone. Thus, variation in phage type (Table) appears to have occurred within a single clone. Variation in phage type has also been reported in other studies of multidrug-resistant *S. Paratyphi B* dT+ strains (4–6), although

Conclusions

This is the first definitive report showing that ornamental fish tanks are a reservoir for multidrug-resistant *S. Paratyphi B* dT+ (ApCmSmSpSuTc phenotype) containing SGI1 that causes severe disease in humans, particularly young children. In addition to containing SGI1, the matched isolates from humans and their fish tanks had the same phage type and the same *Xba*I macrorestriction digest pattern and IS200 profile. These findings identify home aquariums containing tropical fish as the most important, although not necessarily the only, source of multidrug-resistant *S. Paratyphi B* dT+. The fact that 12%–14% of Australian households have ornamental fish (14) and as many as 12 million American and 1 million Canadian families own domestic aquariums (9), together with the young age of most affected patients, indicate that multidrug-resistant *S. Paratyphi B* dT+ in home aquariums is a risk factor for *Salmonella* infection and thus becomes a public health issue.

Acknowledgments

We thank Linda Falconer for skillful technical assistance.

Renee S. Levings is supported by a grant from the New South Wales Department of Primary Industries and a University of Wollongong Postgraduate Research Award.

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a number of related but slightly different *Xba*I PFGE patterns were observed in those studies. This finding suggests that all multidrug-resistant *S. Paratyphi B* dT+ found globally have a single origin, but that variations, possibly because of acquisition of other temperate phages or plasmids, have arisen over time. However, direct comparisons of strains from different countries will be needed to confirm this hypothesis.

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