



CHARACTERISATION OF *VIBRIO PARAHAEMOLYTICUS* ISOLATED IN ITALY FROM BIVALVE MOLLUSCS AND ENVIRONMENTAL SAMPLES BY MULTILOCUS SEQUENCE TYPING (MLST)

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INTRODUCTION

- ✓ *Vibrio parahaemolyticus* is a gastrointestinal human pathogen. Bivalve molluscs are the most common food associated with *V. parahaemolyticus* infection.
- ✓ The Thermostable direct haemolysin (TDH) and the TDH-related haemolysin (TRH) are recognized virulence factors.
- ✓ Only a small proportion of environmental strains harbours virulence factors.
- ✓ The aim of this study was to further characterize by MLST analysis potentially pathogenic *V. parahaemolyticus* strains carrying the *trh* gene isolated from indigenous bivalve molluscs, environmental and clinical samples in Italy between 2006 and 2009.



MATERIALS AND METHODS

- ✓ Clinical isolate: a *V. parahaemolyticus* isolate of O1:KUT serotype harbouring the *trh* gene isolated in 2008. Epidemiological information suggested local shellfish as the most probable source of infection (Ottaviani *et al.*, 2010).
- ✓ Food and environmental isolates: 9 *trh*-positive *V. parahaemolyticus* strains isolated between 2006 and 2009 from bivalve molluscs and environmental samples in Italy, belonging to the Laboratory Culture Collection.
- ✓ PCR methods: *toxR*, *tdh* and *trh* genes were performed according to Tada *et al.*, 1992; Kim *et al.*, 1999.
- ✓ MLST analysis: performed on seven housekeeping genes as previously described (González-Escalona *et al.*, 2008).

RESULTS AND DISCUSSION

- ✓ MLST analysis of *V. parahaemolyticus* carrying the *trh* gene and isolated from bivalve molluscs and environmental samples is shown in Table 1. Overall, 3 different Sequence Types (STs) were identified.
- ✓ MLST analysis also revealed that 6 of the 9 strains isolated in different years from environmental and food samples originating from areas of the Northern Adriatic Sea (Table 2) belonged to the same ST, which was not registered in the MLST database.
- ✓ Other 2 of the 9 analysed strains shared a same ST, which was not registered in the MLST database. The last of the 9 strains had ST 104.
- ✓ The O1:KUT *trh*-positive clinical isolate of 2008 had an allelic combination (Table 1), which was not registered in the MLST database.

Table 2. *V. parahaemolyticus* harbouring the *trh* gene isolated between 2006 and 2009 from bivalve molluscs and environmental samples originating from areas of the Northern Adriatic Sea.

O:K Serotype	Year of isolation	N° of isolates	Matrix
O6:KUT	2006	1	Clams
O7:KUT	2007	1	Plankton
O6:KUT	2007	1	Plankton
O2:KUT	2008	1	Sediment
O3:KUT	2009	1	Clams
OUT:KUT	2009	1	Bivalve molluscs

Table 1. MLST allelic profile and sequence type (ST) of *V. parahaemolyticus* harbouring the *trh* gene isolated from bivalve molluscs and environmental samples.

MLST allele n°							ST	n° of isolates	Type of Sample
<i>dnaE</i>	<i>gyrB</i>	<i>recA</i>	<i>dtdS</i>	<i>pntA</i>	<i>pyrC</i>	<i>tnaA</i>			
162	New	80	150	11	158	51	Not Registered	6	Bivalve molluscs and Environmental
47	52	19	New	24	43	37	Not Registered	2	Bivalve molluscs
60	67	4	53	43	63	23	104	1	Bivalve molluscs
102	4	91	69	23	3	23	Not Registered	1	Clinical

CONCLUSIONS

- ✓ The clinical *Vibrio parahaemolyticus* *trh*-positive O1:KUT isolate had a different ST from all the food and environmental *trh*-positive isolates analysed in this study.
- ✓ *trh*-positive strains sharing the same MLST Sequence Type were isolated from different samples collected in different years in areas of the Northern Adriatic Sea.

REFERENCES

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