INTRODUCTION

- Vibrio parahaemolyticus is a marine bacterium indigenous of coastal areas and 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 these virulence factors.
- Samples of bivalve molluscs collected from harvesting areas of the central Adriatic sea were investigated for levels of total and potentially pathogenic V. parahaemolyticus.

RESULTS AND CONCLUSIONS

- Bivalve molluscs from harvesting areas of the central Adriatic sea were analysed for V. parahaemolyticus by MPN and MPN- toxR Real-Time-PCR (Table 1).
- Highest MPN values were recorded in summer and autumn 2012 and summer 2013.
- None of the samples was positive for V. parahaemolyticus harbouring the tdh gene (MPN-Real-Time-PCR <2 MPN/g), in agreement with previous work performed in Italy on bivalve molluscs (Ottaviani et al., 2013).
- Potentially pathogenic V. parahaemolyticus carrying the trh gene were detected by MPN-PCR in 3 of the 102 samples (Table 2).
- V. parahaemolyticus trh+ colonies were not isolated from the samples. Failure to isolate colonies could be due to over growth of other Vibrio spp. or the trh gene could had been present in other species of Vibrios or other bacteria.
- Sequencing analysis confirmed the presence of the trh gene with 98% (207/212 bp) sequence identity to trh1 (Genbank Sequence n. AB455531) in samples of Autumn 2012.
- It was not possible to sequence the trh PCR product of the sample of Autumn 2013, but a Real-Time-PCR for the trh2 gene confirmed the presence of the trh gene.
- MPN values of potentially pathogenic V. parahaemolyticus indicated a low risks in the studied areas and periods.

MATERIALS AND METHODS

- 102 samples of bivalve molluscs (28 mussels and 74 clams) collected in spring-autumn 2012 and 2013 from bivalve molluscs harvesting areas of the central Adriatic sea.
- V. parahaemolyticus was determined by a 5x3 Most Probable Number (MPN) method and a 5x3 MPN-Real-Time-PCR targeting the toxR gene developed in this study.
- Quantification of potentially pathogenic V. parahaemolyticus was performed by a 5x3 MPN-Real Time PCR for the tdh gene (Nordstrom et al., 2007) and a 5x3 MPN-PCR for the trh gene.

REFERENCES