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# P0380 Assessing molecular PCR-ribotypes of *Clostridium difficile* in marine bivalve shellfish

Fabrizio Agnoletti*[1,2], Ilena Drigo[3], Patrizia Spigaglia[4], Giuseppe Arcangeli[2], Lisa Barco[2], Gabriella Conedera[5], Monia Cocchi[6], Laura D'este[2], Patrizia Gambarin[2], Arianna Peruzzo[2], Silvia Deotto[6], Elena Tonon[3], Chiara Targhetta[5], Fabrizio Barbanti[7], Elena Mazzolini[2,8]

[1] Treviso's Diagnostic Department, Istituto Zooprofilattico Sperimentale delle Venezie, Legnaro (PD), Italy, [2] Istituto Zooprofilattico Sperimentale delle Venezie - Sede Centrale, Legnaro, Italy, [3] Istituto Zooprofilattico Sperimentale delle Venezie - Sezione di Treviso, Villorba, Italy, [4] Infectious Diseases, Istituto Superiore di Sanità, Rome, Italy, [5] Istituto Zooprofilattico Sperimentale delle Venezie - Sezione di Pordenone, Italy, [6] Istituto Zooprofilattico Sperimentale delle Venezie - Sezione di Udine, Basaldella, Italy, [7] Department of Infectious, Parasitic and Immune-mediated Diseases,, Istituto Superiore di Sanità, Roma, Italy, [8] Osservatorio epidemiologico veterinario e sicurezza alimentare della Regione Autonoma Friuli Venezia Giulia, Direzione Centrale Salute, Regione Autonoma Friuli Venezia Giulia, Udine , Italy

**Background:** *Clostridium difficile* (CD) is a primary cause of hospital and community acquired infections (CDI). Patient-to-patient CD transmission is common but other contamination sources should be evaluated. Detection and assessing the contribution of CD animal reservoirs is of importance to evaluate new hazards of human food-borne infections. Aim of our study was to describe presence and genotypic heterogeneity of CD in shellfish in order to estimate their overlapping with CD genotypes isolated from hospitalized patients.

**Materials/methods:** A cross-sectional study was carried in Dec-2015 and Aug-2017 by sampling 385 mussel (*M. galloprovincialis*) and 313 clam samples (*R. philippinarum* and *C. gallina*) collected in Italian Adriatic Sea. Samples were cultured using selective enrichment procedures and CD isolates were confirmed by MALDI-TOF MS and *tpi* detection by PCR.

PCR-ribotyping, PCR-toxinotyping, detection of the *tcdA*, *tcdB*, *cdtA* and *cdtB* genes and of the *tcdC* regulatory gene deletions were performed to compare shellfish CD isolates with European clinical isolates.

**Results:** 122 CD strains were genotyped: 43 from *M. galloprovincialis*, 61 from *R. philippinarum* and 18 from *C. gallina*. 79 CD (64.7%) were toxigenic and overall 53 PCR-ribotypes were identified. The most common toxigenic PCR-ribotypes were 014 (8 isolates), 078 and 070 (7 isolates each), 002 and 020 (6 isolates each), 106 and 651 (4 isolates each) and 449 (3 isolates).

**Conclusions:** The role of animals and foods in transmission of CD to humans needs to be assessed. In this study, a high genotypic diversity among Italian isolates from shellfish was observed. Almost 40% (47/122) of these isolates belong to the most common PCR-ribotypes identified as cause of CDI in European hospitals. Some ribotypes are considered hypervirulent, such as 126 toxinotype V and 078 toxinotype V, usually detected in pigs and cattle and both displaying the *tcdC* regulatory gene deletion that is associated with increased production of toxins. Our results indicate an overlap between the CD genotypes identified in shellfish and those cause of CDI in humans. Although shellfish samples analysed were from primary production and not yet food our results suggest CD transmission to humans via contaminated food shellfish requires a thorough risk assessment.