



POSTER

MAKING A LONG STORY SHORT (1997-2019): META-ANALYSIS OF VIBRIO PARAHAEMOLYTICUS PREVALENCE IN RAW BIVALVE MUSSELS PRODUCED IN ITALY

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Introduction and Objective. *Vibrio* spp. is part of the natural microbiota of fresh waters and marine environments. Some species, including *V. cholerae*, *V. parahaemolyticus* and *V. vulnificus*, are foodborne pathogens associated with the consumption of raw or undercooked seafood. In 2024, the European Food Safety Authority (EFSA) identified *V. parahaemolyticus* as a major cause of vibriosis in the European Union (EU) and estimated a prevalence of 20.89% (95% CI: 11.65-34.58) of pathogenic strains (tdh+ and/or trh+) in bivalve mollusks (BM). Considering that EFSA did not provide detailed occurrence data for individual Member States, this study aimed to perform a meta-analysis to estimate the pooled prevalence of *V. parahaemolyticus* in raw MB produced in Italy. **Methods:** The meta-analysis was conducted using data from the Pathogens-in-Foods (PIF) database, a systematic repository of EU microbiological occurrence data extracted from peer-reviewed articles. PIF was accessed on 13 March 2026 and the "seafood-borne" section was searched by selecting "Vibrio" as the investigated pathogen. Occurrence data for the pathogenic genes (i.e. tdh+ and/or trh+) were analyzed when available. Records were restricted to the following FoodClass categories: "Clams, cockles, arkshells", "Miscellaneous marine molluscs", "Mussels", "Oysters" and "Scallops, pectens". The dataset was filtered to include only studies on samples collected at primary production, from harvesting to post-depuration, in wild and aquaculture production systems. A random-effects meta-analysis was performed using the metafor R package, with study as random effect and logit-transformed prevalence data. Pooled prevalences and 95% confidence intervals (95% CI) were estimated using restricted maximum likelihood (REML). Heterogeneity was assessed using I^2 (the proportion) and τ^2 (the variance).

Results. Thirteen Italian studies detecting *V. parahaemolyticus* in raw BM at primary production were found in PIF databases, for a total of 4,957 samples analyzed between 1996 and 2019. Most samples originated from Sardinia (74.7%; $n = 3,703/4,957$) followed by the Adriatic Sea (19.1%; $n = 949/4,957$), meanwhile only 1.1% originated from the Ligurian Sea. The overall pooled prevalence of *V. parahaemolyticus* in Italian BM at primary production was 10.07% (95% CI: 4.57 - 20.74), with substantial between-study heterogeneity ($I^2 = 96.0\%$, $\tau^2 = 2.10$). The pooled prevalence of tdh and/or trh + strains was 13.84 (95% CI: 9.16 - 20.38). At FoodClass level, prevalence estimates were similar for mussels (*Mytilus* spp.; 10.40%, 95% CI: 3.94 - 24.76) and clams (*Veneridae*; 11.33%, 95% CI: 3.86 - 28.94), whereas oysters (*Magallana gigas*) showed a lower pooled prevalence (1.44%, 95% CI: 0.47 - 4.34). Stratification by sampling area and MB species highlighted marked geographical differences. In clams, prevalence was higher in Sardinia (17.88%, 95% CI: 2.79-62.32) than in the Adriatic area, including Veneto, Emilia-Romagna and Marche (11.99%, 95% CI: 3.87-31.55). Conversely, mussels showed higher prevalence in the Adriatic Sea (20.74%, 95% CI: 11.12-35.37) than in Sardinia (7.40%, 95% CI: 0.94-40.29).

Conclusions. These region-stratified estimates differed from the national pooled values, suggesting that local epidemiological conditions influence the occurrence of *V. parahaemolyticus* in Italian BM. Overall, these findings indicate that national-level data aggregation may not fully capture local epidemiological patterns, underscoring the need for region-specific surveillance, risk assessment, and management strategies.