# **Titre d’article**: First Epidemiological Report on the Prevalence and Associated Risk Factors of Cryptosporidium spp. in Farmed Marine and Wild Freshwater Fish in Central and Eastern of Algeria

**Abstract :**

Purpose The present study aimed to estimate the prevalence and molecular characterization of Cryptosporidium spp. in six diferent fsh species both from marine and freshwater environments. Methods During a period of 2 years (2018–2020), a total of 415 fecal samples and 565 intestinal scrapings were collected in seven provinces from the central and eastern Algeria. From those, 860 fsh belonged to six diferent species, two of which are cultured marine and four are wild freshwater fsh. All samples were screened for Cryptosporidium spp. presence using molecular techniques. Nested PCR approach was performed to amplify partial sequences of the small subunit ribosomal RNA (SSU rRNA) and 60-kDa glycoprotein (GP60) genes for Cryptosporidium genotyping and subtyping. Detailed statistical analysis was performed to assess the prevalence variation of Cryptosporidium infection according to diferent risk factors. Results Nested PCR analysis of SSU gene revealed 173 Cryptosporidium positive fsh, giving an overall prevalence of 20.11% (17.5–23.0). Cryptosporidium spp. was detected in 8.93% (42/470) of cultured marine fsh and 33.58% (131/390) of wild freshwater fsh. Overall, the prevalence was afected by all studied risk factors, except the gender. Molecular characterization and subtyping of Cryptosporidium isolates showed occurrence of IIaA16G2R1 and IIaA17G2R1 subtypes of C. parvum in the fsh species Sparus aurata. Conclusion The present study provides the frst epidemiological data on the prevalence and associated risk factors of Cryptosporidium spp. in farmed marine and wild freshwater fsh and the frst molecular data on the occurrence of zoonotic C. parvum in fsh from North Africa (Algeria).