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

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**Abstract**

Purpose The present study aimed to estimate the prevalence and molecular characterization of *Cryptosporidium* spp. in six different fish 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 fish belonged to six different species, two of which are cultured marine and four are wild freshwater fish. 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 different risk factors.

Results Nested PCR analysis of SSU gene revealed 173 *Cryptosporidium* positive fish, giving an overall prevalence of

20.11% (17.5–23.0). *Cryptosporidium* spp. was detected in 8.93% (42/470) of cultured marine fish and 33.58% (131/390) of wild freshwater fish. Overall, the prevalence was affected 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 fish species *Sparus aurata***.**

Conclusion The present study provides the first epidemiological data on the prevalence and associated risk factors of *Cryptosporidium* spp. in farmed marine and wild freshwater fish and the first molecular data on the occurrence of zoonotic

*C. parvum* in fish from North Africa (Algeria).

Keywords Fish ・ *Cryptosporidium* spp. ・ Prevalence ・ Molecular characterization ・ Algeria

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