Cystic echinococcosis in water buffaloes *(Bubalus bubalis)*

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ABSTRACT: An epidemiological and molecular survey of cystic echinococcosis (CE) caused by *Echinococcus granulosus* in the water buffalo (*Bubalus bubalis*) of the Italian Mediterranean breed was carried out in the Campania region of southern Italy. Out of a total of 799 water buffaloes examined at slaughterhouses, 80 (10.0%) were found infected. The molecular study was performed on 58 hydatid cysts in order to determine the *E. granulosus* strain(s) present in this host. A region of cytocrome c oxydase 1 gene (CO1) was amplified by polymerase chain reaction and the PCR products were then purified and sequenced. DNA amplification of the partial CO1 gene gave a 446 bp fragment for all isolates examined. After sequencing, a region of 419 bp was identified for each sample. Thirty-two isolates were identified as the common sheep strain G1, 15 as the buffalo strain G3, 3 as the Tasmanian sheep strain G2, and 3 as the G1 c genotype (GenBank AF458873). In addition, 5 isolates presented 99% identity with the G2 genotype (Tasmanian sheep strain).

Key words: Parasites, *Echinococcus granulosus*, Cystic Echinococcosis.

INTRODUCTION - Cystic echinococcosis (CE) caused by *Echinococcus granulosus* is known to be one of the most important parasitic infection in livestock worldwide with severe zoonotic implications. *E. granulosus* has a high degree of genetic divergence. Various strains also exhibit differences in morphology, development rate, host range, pathogenicity, and geographical distribution (Thompson *et al*., 1995; Thompson and McManus, 2001). In total 10 distinct strains (genotypes) of *E. granulosus* have been described using DNA sequence data: G1 (common sheep strain), G2 (Tasmania sheep strain), G3 (buffalo strain), G4 (horse strain), G5 (cattle strain), G6 (camel strain), G7 (pig strain), G8 (cervid strain), G9 (human strain) and G10 (Fennoscandian cervid strain) (McManus, 2002; Lavikainen *et al*., 2003; Maravilla *et al*., 2004), although the validity of the G9 genotype has been questioned (Snábel *et al*., 2000) and it might correspond to the G7 genotype. The water buffalo (*Bubalus bubalis*) is an intermediate host of *E. granulosus.* Nevertheless epidemiological surveys aimed to evaluate the presence and distribution of CE in this ruminant species have not been performed in Italy and in the Mediterranean area. In addition, comprehensive molecular studies have not been performed on *E. granulosus* isolates from water buffaloes worldwide as well as the buffalo

strain G3 is considered a poorly characterized form, transmitted by water buffaloes in South Asia (Jenkins *et al*., 2005). In order to address this lack of information on bubaline CE, the present study is aimed to evaluate the presence and distribution of CE in the water buffaloes of the Italian Mediterranean breed and the molecular characterization of the strain(s) present in this intermediate host. The survey was carried out in Campania, a region of Southern Italy where most of Italian water buffaloes are bred.

MATERIAL AND METHODS - Water buffaloes (n = 799) were examined for CE at 3 slaughterhouses located in Caserta and Salerno provinces (Campania region, southern Italy), with a twice weekly frequency. At each slaughtering day, each animal carcass was inspected in order to detect and collect hydatid cysts from the parasitized organs (liver and lungs). The molecular study was performed on 58 hydatid cysts coming from 58 water buffaloes in order to determine the *E. granulosus* strain(s) present in this host. A region of cytocrome c oxydase 1 gene (CO1) was amplified by polymerase chain reaction and the PCR products were then purified and sequenced.

RESULTS AND CONCLUSIONS - Out of a total of 799 water buffaloes examined at slaughterhouses, 80 (10.0%; 95% Confidence Interval = 8.1-12.4%) were found infected. DNA amplification of the partial CO1 gene gave a 446 bp fragment for all the isolates. After sequencing, a region of 419 bp was identified for each sample. Thirty-two isolates were identified as the common sheep strain G1, 15 as the buffalo strain G3, 3 as the Tasmanian sheep strain G2, and 3 as the G1 c genotype (GenBank AF458873). In addition, 5 isolates showed 99% identity with the G2 genotype (Tasmanian sheep strain). In conclusion, our findings demonstrated that CE is present in water buffaloes reared in the considered Mediterranean area. This survey is the first epidemiological and molecular study on bubaline CE in this endemic area for *E. granulosus*. Furthermore, the water buffalo should be included within the efficient hosts for the maintenance of *E. granulosus* in the area of concern and where this ruminant is present.

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