# **Titre d’article**: New insight into genetic variation and haplotype diversity of Fasciola hepatica from Algeria

**Abstract :**

The liver fluke Fasciola hepatica is the main cause of fasciolosis in North Africa leading to significant economic losses and public health problems. In this study, the ribosomal internal transcribed spacer (ITS), cytochrome c oxidase I (COI), the mitochondrial region spanning the COI-trnT-rrnL, and the NADH dehydrogenase subunit I (NADI) markers were used to characterize Fasciola flukes from Algeria. Fasciola appeared widespread from the east to the west of Algeria. Among 1701 sampled cattle from 8 Algerian provinces, 5% were infected. Using morphological and morphometric analysis, one morphotype of Fasciola was observed. Nuclear ITS marker indicated that all collected flukes belong to F. hepatica. Multiple alignments of ITS dataset revealed two haplotypes, one described here for the first time. Analysis of molecular variance (AMOVA) of mitochondrial markers revealed weak population structure in Algeria. Mismatch distributions, neutrality tests, and median-joining network analysis all were compatible with a recent expansion of Algerian F. hepatica population. Fasciolosis appeared common in Algerian cattle, it seems that the absence of control strategy coupled to the favorable Mediterranean climate may lead to a reconstruction and dispersion of its populations. This study provides important results concerning the genetic characterization and variability of F. hepatica in Algeria as well as the significant role of cattle importation in shaping its dispersal route worldwide.tists.