
The two ruminant parasites, Paramphistomum cervi and Carmyerius gregarius, were collected from fresh-slaughtered native cattle at local abattoirs in Sadat district, Menoufia province and identified morphologically, then molecularly by sequencing the nucleotides of 18S ribosomal RNA gene (18S rRNA). The nucleotide sequences of the two isolates were 456 (P. cervi) and 401 bases for (C. gregarius). The data were used along with those of several other helminth species from the GenBank to identify these two species genetically. The nucleotide sequences were aligned using multiple sequence alignments of nucleotides by Clustal W 12.1 V and construct their relationship. Neighbor-joining analytical method was used showing sister relationship between C. gregarius from Sadat district and Gastrodiscoides hominis (EF027096) with relative identity of (98%) due to the presence of single nucleotides polymorphisms (SNPs) in the form of indels as nine nucleotides positions. But when clustering of P. cervi Sadat isolate with Paramphistomoidea sp. S4 isolate P5 (GU735643), this relationship shows complete identity (99%) between them. The homology and diversity was done using Bayesian analyses in MrBayes v3.1. This work will give a useful guide for other researchers for the molecular taxonomic position of Paramphistomatidae spp. in Sadat district among the different species around the world.