

Abstract

The gap genes within LSU rRNA of the individual infective larvae of human and pig *T. spiralis* of Thailand isolates were identified. Polymerase chain reaction was performed to increase DNA extracted from each larval parasite. Electrophoretic analysis of the PCR amplicons revealed that the length of the gap gene was less than 500 bp. PCR amplicons were ligated into pGEM[®]-T Easy vector and then transformed into *E. coli* JM 107. Recombinant clones were identified using *Lac* selection and then subjected to automatic DNA sequencing. It was found that the gap region was flanked by the consensus sequence CGAAAG, which have been implicated at both termini of gap processing or recognition site. These flanking sequences were also presented in another organisms such as *D. melanogaster*, *S. coprophila* and *Shistosoma* spp. From sequencing data, the gap genes of the *T. spiralis* larvae of the human isolate could be divided into four different groups and of the pig isolate could be divided into three groups. Comparisons of the gap gene sequences of the parasites from both isolates revealed that they were genetically similar, both in length and base sequences. Nevertheless, the difference of nucleotides at the position 93 could be observed. There were many variables at this position in gap genes of the larvae of the pig isolate such as pig L₂, pig L₄₋₁₀ contained T base, pig L₃ contained G base and pig L₁ showed the deletion at the positions 93-95 whereas those of the human isolate showed consistency at the same position. The designed experimentation in this study may provide a useful means to identify and characterize another parasites.