IDENTIFICATION OF *ENTAMOEBA HISTOLYTICA* AND *ENTAMOEBA DISPAR* BY PCR ASSAY OF FECAL SPECIMENS OBTAINED FROM THAI/MYANMAR BORDER REGION

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Abstract. Due to the indistinguishable morphology between *Entamoeba histolytica* (pathogenic) and *Entamoeba dispar* (non pathogenic), PCR-based assays were conducted. Based on microscopy, suspected *Entamoeba* cells were detected in 30 out of 455 fecal samples obtained from individuals residing at Thai/Myanmar border region. The target genes for PCR amplification included genes encoding small subunit rRNA (SSU-rRNA), chitinase and serine rich *Entamoeba* protein. PCR primers derived from SSU-rRNA gene amplified both *E. histolytica* and *E. dispar* genes producing an amplicon of 1,080 bp, and detected 3 out of 30 samples. PCR primers derived from chitinase gene of *E. histolytica* generating amplicons of 500 and 1,260 bp, samples were positive in 12 out of 30 samples. Due the large difference of gene encoding serine rich protein between *E. histolytica* and *E. dispar*, two specific sets of primers were designed. SREH-primer set, specific for *E. histolytica,* generated amplicons of 550 and 700 bp and detected 22 out of 30 samples. SED-primer set, specific to *E. dispar,* produced an amplicon of 550 bp, and together with a nested primer pair generating an amplicon of 477 bp, detected 16 out of 30 samples. Thus, detection of single and mixed infections of the two *Entamoeba* species could be effectively achieved directly from DNA extracted from feces without the need to culture the parasites.

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