**PREVALENCE AND MOLECULAR STUDIES OF TAENIA SOLIUM AND ASSESSMENT OF SANITARY CONDITIONS OF SOME PIG SLAUGHTER SLABS IN KADUNA METROPOLIS, NIGERIA**

**ASUKE U.A.E.**

**ABSTRACT**

A community-based cross-sectional survey was undertaken to investigate the prevalence and risk factors of Taenia solium infections along with genotyping T. solium and assessment of sanitary conditions of some home-based pig slaughter slabs in Kaduna metropolis, Nigeria. The study was conducted in pig raising areas of Kaduna South and Chikun Local Government Areas in Kaduna metropolis. Three hundred (300) human blood and four hundred and fifty (450) human stool samples were obtained and analysed for cysticercosis and T. solium taeniasis from individuals who gave their consent to participate in the survey. Structured, self-administered questionnaires were used to obtain relevant information on sociodemography and risk factors that might be associated with cysticercosis and taeniasis in the study area. The blood samples were analysed for cysticercal antibodies by use of IgG antibody ELISA, while stool samples were analysed using microscopic examination for taeniid ova, in-house coproantigen ELISA for detection of coproantigens and by molecular assays for confirmation of T. solium present. Taenia solium DNA was extracted from corpoantigen positive stool samples by Qiagen stool mini kit and then amplified by polymerase chain reactions using species-specific primers. Genetic markers targeted were, nuclear internal transcribed spacer regions (ITS I) and mitochondrial cytochrome oxidase C subunit 1 (mt cox 1) genes. The amplified PCR products were partially sequenced, edited and aligned for phylogenetic analysis using BioEdit and CLUSTAL W computer programs. Evolutionary distances were computed by Kimura’s two parameter method, and neighbor joining, bayesian and maximum likelihood trees were constructed using the PAUP vers-5.0 packages. The trees were evaluated using the bootstrap test based on 1000 resamplings. Phylogenetic trees were out group-rooted using nucleotide sequences from Echinococcus