

Ticks are medically important arthropods because they carry numerous pathogens of humans and domesticated animals. Recent studies showed that besides pathogenic microorganisms, ticks carry numerous endosymbionts which significantly affect different aspects of tick biology. For example, endosymbiotic microorganisms can reduce tick's ability to carry pathogens. So far, studies have mostly focused on molecular identification of bacterial endosymbionts of ticks targeting prokaryotic 16S ribosomal RNA. In our study we attempted to identify fungal species that are associated with ticks. We used a molecular approach to detect fungal spp. in a *D. variabilis* tick. Using fungi specific primers, we amplified a sequence of fungal ITS region by PCR in which as a template we used DNA extracted from tick. To identify origins of fungal DNA in sample we purified amplified sequences and performed cloning in pGEM-T vector plasmid followed by sequencing around 30 clones per samples. After bioinformatic analysis of obtained sequences, which consists of using BLAST tool in Genbank, we identified 20 fungal species associated with used tick species, with at least 10 of them being possible tick endosymbionts. Future studies, focused on tick dissection and determination of which part of tick body contains fungal endosymbionts, are required to determine role of fungal endosymbionts in tick biology.