Species Identification of Entomopathogeneic Nematode (Steinernema spp.) by Sequencing of ITS Region in Ribosomal DNA

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Two isolates of Stinernema species were collected from different locations in Korea. Steinernema 55 was originated from Pocheon, Gyeonggi and Steinernema 223 was from Sangju, Gyeongbuk. Both isolates represented high pathogenicity to Plutella xylostella, Spodoptera litura, and Spodoptera exgua in laboratory experiment. The mortality of juvenile(2-3rd stage) Plutella xylostella reached 96.7% and 93.3% by the 25 nematodes inoculation of Steinernema 55 and Steinernemema 223, respectively. Under the same inoculation level Spodoptera litura showed 90.0% and 73.3%, and Spodoptera exgua showed 86.7% and 90.0% mortality by Steinernema 55 and Steinernemema 223, respectively. The mortality of Plutella xylostella increased almost to 100% when they became 4th stage juvenile. Currently the species identification work was approached by PCR amplification of ribosomal DNA. The amplified sizes of target gene including ITS-1 and ITS-2 were approximately 1 kb in both isolates, and now the PCR product is in the process of sequencing. The result of sequencing data will be informative to identify unknown Steinernema. species which have high potential to be a biocontrol agent in agriculture.