

1-19. Phylogenetic Analysis of *Xenorhabdus* spp. Using 16s rDNA and Other Physiological Markers

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A symbiotic bacterium, *Xenorhabdus nematophilus*, was isolated from the entomopathogenic nematode, *Steinernema carpocapsae*, collected in Korea. To understand genetic homology with other *X.nematophilus* strain and other symbiotic bacteria (*X. nematophilus* F1, *X. poinarii* G6, *X. beddingii* Q58, *Photorhabdus luminescens* subsp. *temerata* C1), physiological and molecular characteristics were compared. They were different in pathogenicity to the fifth instar larvae of *Spodoptera exigua* when they were injected into the larval hemoceol. They were different in fatty acid composition and carbon utility analyzed by sherlock and Biolog identification systems, respectively. 16s rDNA of *X. nematophilus* Korean isolate was fully sequenced and compared with other those of *Xenorhabdus* spp. The constructed phylogenetic tree suggests a uniqueness of Korean isolate.