

学 位 論 文 要 旨	
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題 目	Genetic analysis of virulence in the entomopathogenic bacterium <i>Photorhabdus luminescens</i> using model nematode <i>Caenorhabditis elegans</i> (モデル線虫 <i>Caenorhabditis elegans</i> を用いた昆虫病原性細菌 <i>Photorhabdus luminescens</i> が発揮する病原性の遺伝学的解析)
<p>The Gram-negative bacterium <i>Photorhabdus luminescens</i> symbiotically associates with entomopathogenic nematode <i>Heterorhabditis bacteriophora</i>. Although <i>P. luminescens</i> is highly virulent to many insects and nonsymbiotic nematodes, the complete picture of its virulence still remains unclear. The combination of genetically tractable free-living nematode <i>Caenorhabditis elegans</i> and pathogens has contributed to our understanding of virulence mechanisms and innate immune systems. The purpose of this study is to demonstrate the virulence mechanisms of <i>P. luminescens</i> using model nematode <i>C. elegans</i>.</p> <p>Firstly, the pathogenicity of <i>P. luminescens</i> against <i>C. elegans</i> has been described in detail. Because of a transparent body, the collapse of the intestinal cells of <i>C. elegans</i> was observed when fed on <i>P. luminescens</i>. Observation of <i>gfp</i>-tagged cells revealed that <i>P. luminescens</i> killed <i>C. elegans</i> without colonization of the intestinal lumen. Secondly, I examined the activities of conserved signaling pathways involved in innate immunity, including the p38 mitogen-activated protein kinase (MAPK) and insulin/IGF-1 signaling pathways of <i>C. elegans</i>, during the ingestion of <i>P. luminescens</i>. Using reverse genetic approaches, the p38 MAPK pathway was activated and required for the host defense against <i>P. luminescens</i>. In contrast, the innate immune responses via insulin/IGF-1 signaling pathway were rather inactivated by <i>P. luminescens</i> through the overexpression of an insulin-like gene. In addition, I obtained virulence-attenuated <i>P. luminescens</i> mutants against <i>C. elegans</i> through the screening of a transposon-mutagenized library. One of the mutants had a mutation in <i>pdxB</i> that encodes erythronate-4-phosphate dehydrogenase, which is required in <i>de novo</i> vitamin B₆ biosynthesis pathway. <i>pdxB</i> mutants were growth deficient in nutrient-poor medium and less virulent against <i>C. elegans</i>. However, when <i>pdxB</i> mutants were supplemented with vitamin B₆, their growth in minimal medium and virulence against <i>C. elegans</i> were restored. Lastly, I confirmed that the mutation in <i>pdxB</i> caused a reduction in insecticidal activity against <i>Zophobas morio</i>. These results suggest that production of appropriate amounts of vitamin B₆ is critical for the pathogenicity of <i>P. luminescens</i>.</p> <p>The present study demonstrated the suitability of <i>C. elegans</i> as a model host to analyze the pathogenicity of <i>P. luminescens</i>, and it is hoped that this model system will contribute to the complete elucidation of the virulence mechanisms of <i>P. luminescens</i>.</p>	