ics, and antifungal and nematicidal compositions are also secreted (Boemare & Akhurst, J. Gen. Microbiol. 134: 751-761 (1988); Li et al., Can. J. Microbiol. 43(8):770-773 (1997); McInerney et al., J. Nat. Prod. 54(3):774-84 (1991); McInerney et al., J. Nat. Prod. 54(3):785-95 (1991); Sundar and Chang, J. Gen. Microbiol. 139 (Pt 12):3139-48 (1993)). It has been discovered that some compounds secreted by *Xenorhabdus* exhibit anti-neoplastic (U.S. Pat. No. 5,827,872), acaricidal, anti-inflammatory and anti-ulcerogenic properties (U.S. Pat. No. 4,837,222). U.S. Pat. No. 6,048,838 describes insect inhibitory proteins which exhibit a molecular weight of greater than 100 kDa produced by *Xenorhabdus* sp. which are orally active against a variety of insect species including the orders Lepidoptera, Coleoptera, Diptera, and Acarina.

[0006] The nomenclature and taxonomic characterization of *Xenorhabdus* has recently been subject to innovations in the state of the art. The genus *Photorhabdus* was separated from the genus *Xenorhabdus* in 1993 because of significant differences in biochemical and molecular characterization (Boemare et al., Int. J. Syst. Bacteriol. 43: 249-255 (1993)). *Xenorhabdus* exists of at least 4 known species: *X. nematophilus, X. beddingii, X. poinarii* and *X. bovienii*. (Brunel et al., Appl. & Environm. Microbiol. 63: 574-580 (1997)). Species of *Xenorhabdus* as well as *Photorhabdus* species can be distinguished from each other by restriction analysis of thermally amplified 16S rRNA genes (Brunel et al., Appl. Environm. Microbiol. 63: 574-580 (1997)).

[0007] The genetic diversity of symbiotic *Xenorhabdus* and *Photorhabdus* bacteria associated with entomopathogenic nematodes appears to be quite large. The genus *Xenorhabdus* appears more diverse than the genus *Photorhabdus*, and for both genera, the bacterial genotype diversity is in congruence with the host-nematode taxonomy. It has been found that the occurrence of symbiotic bacterial genotypes was related to the ecological distribution of host nematodes (Fisher-Le Saux et al., Appl. Environ. Microbiol. 64(11):4246-54 (1998)). *Xenorhabdus* bacteria isolated from the same geographical location seem to be more similar to each other, regardless of nematode species than bacteria from one nematode species found in very diverse geographical locations (Liu et al., Intl. J. Syst. Bacteriol. 47:948-951; 1997).

[0008] Therefore, there is a great deal of interest in identifying the genes that encode new insect inhibiting proteins, and proteins involved in the biosynthetic pathways of novel antibiotics produced by *Xenorhabdus* and *Photorhabdus* bacteria, as well as other useful proteins. Sequencing of the entire genome of *Xenorhabdus* would facilitate such an endeavor, because it would allow dissection and analysis of the genome into discrete genes encoding proteins having beneficial properties as described herein.

SUMMARY OF THE INVENTION

[0009] The present invention provides an isolated and purified nucleic acid molecule having a nucleotide sequence, wherein: (1) the nucleotide sequence hybridizes under stringent conditions to a second isolated and purified nucleic acid molecule selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 4384 or complement thereof; (2) the nucleotide sequence is a portion of any sequence selected from the group consisting of SEQ ID NO:1 through SEQ ID NO: 4384; or (3) the nucleotide sequence is the complement of (1) or (2).

[0010] The present invention also provides an isolated and purified nucleic acid molecule comprising a nucleotide sequence, wherein: (1) the nucleotide sequence hybridizes under stringent conditions to a second isolated and purified nucleic acid molecule, wherein the hybridizing portion of the nucleotide sequence of the second nucleic acid molecule encodes a polypeptide or protein having an amino acid sequence selected from the group consisting of SEQ ID NO: 4385 to SEQ ID NO: 8409; (2) the nucleotide sequence encodes a polypeptide or protein, wherein the amino acid sequence of the polypeptide or protein is substantially identical to any one set forth in SEQ ID NO: 4385 to SEQ ID NO: 8409; or (3) the nucleotide sequence is the complement of (1) or (2). In alternative embodiments, the amino acid sequence of the above described polypeptide or protein is at least 70% identical, at least 80% identical, at least 85% identical, at least 90% identical, or at least 95% identical to an amino acid sequence selected from the group consisting of SEQ ID NO: 4385 to SEQ ID NO: 8409. In a preferred embodiment, the amino acid sequence of the above described polypeptide or protein is one of the sequences set forth in SEQ ID NO: 4385 to SEQ ID NO: 8409, or one of the sequences set forth in SEQ ID NO: 4385 to SEQ ID NO: 8409 with conservative amino acid substitutions.

[0011] The present invention further provides a method for obtaining a nucleic acid molecule comprising a nucleotide sequence encoding a polypeptide or protein the amino acid sequence of which is at least 70% identical to a member selected from the group consisting of SEQ ID NO: 4385 to SEQ ID NO: 8409.

[0012] The present invention, in another aspect, provides a substantially purified polypeptide or protein comprising an amino acid sequence, wherein the amino acid sequence is defined as follows: (1) the amino acid sequence is encoded by a first nucleotide sequence which specifically hybridizes to the complement of a second nucleotide sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 4150; (2) the amino acid sequence is encoded by a third nucleotide sequence that is at least 50% identical to a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 4150; or (3) the amino acid sequence is at least 70% identical to a member selected from the group consisting of SEQ ID NO: 4385 to SEQ ID NO: 8409. In alternative embodiments, the above described third nucleotide sequence is at least 55% identical, at least 60% identical, at least 65% identical, at least 70% identical, at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, or at least 95% identical to a sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 4150; and, the above described third nucleotide sequence can have one of the sequences set forth in SEQ ID NO: 1 through SEQ ID NO: 4150. In a preferred embodiment, the above described amino acid sequence is at least 70% identical, at least 80% identical, at least 90% identical, or at least 95% identical to a member selected from the group consisting of SEQ ID NO: 4385 to SEQ ID NO: 8409.

[0013] The present invention also provides a recombinant construct comprising: (A) a promoter region which functions in a host cell to cause the production of a mRNA molecule; which is operably linked to (B) a structural nucleotide sequence, wherein the structural nucleotide sequence is substantially identical to a member selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 125; which is