

Opinion

Genomics of Entomopathogenic Nematodes and Implications for Pest Control

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Entomopathogenic nematodes (EPNs) have been used in biological control but improvement is needed to realize their full potential for broader application in agriculture. Some improvements have been gained through selective breeding and the isolation of additional species and populations. Having genomic sequences for at least six EPNs opens the possibility of genetic improvement, either by facilitating the selection of candidate genes for hypothesis-driven studies of gene–trait relations or by genomics-assisted breeding for desirable traits. However, the genomic data will be of limited use without a more mechanistic understanding of the genes underlying traits that are important for biological control. Additionally, molecular tools are required to fully translate the genomic resources into further functional studies and better biological control.

Entomopathogenic Nematodes in Biological Control

Global annual crop loss due to herbivory by pests is 32.1% [1]. Farmers and researchers have applied many methods to reduce this crop loss, one of which is the application of specialized insect-parasitic nematodes called EPNs. EPNs differ from other insect-parasitic nematodes in two meaningful ways: (i) EPNs associate with symbiotic bacteria to facilitate pathogenesis; and (ii) they rapidly kill their hosts, usually within 72 h after infection [2–4] (Figure 1). Entomopathogenic species within the genera *Heterorhabditis* and *Steinernema* are the most extensively studied and most often used in biological control [4–7]. EPNs are highly pathogenic and are used as biological control agents of numerous insect pests. They have been commercialized on several continents and are used in large-scale agriculture and in individual home gardens.

Despite their promise as biological control agents, the lack of consistent efficacy in the field has prevented these nematodes from being more widely used. Researchers have worked on improving their efficacy against arthropod pests under field conditions for decades, using two main strategies: (i) artificial selection; and (ii) genetic improvement via mutagenesis or other molecular methods (Figure 2). Artificial selection is enhanced by the continued collection of new EPN species and/or populations that are adapted to certain environmental conditions and pests (Figure 2). Occasionally, locally adapted EPNs provide superior control when compared with non-native species or populations [8–10]. Many new EPN isolates have been identified, which may lead to increased genetic variation and the development of new nematode strains [11]. Isolation and/or breeding of EPNs for improved insect pest suppression relies on the identification and manipulation of certain traits [12–14]. These traits include, but are not limited to, increased tolerance to temperature, desiccation, and ultraviolet (UV) light, as well as increased or modified host-seeking ability, virulence, and resistance to nematicides (Figure 3). Improving

Trends

EPNs have been used in biological control but improvement is needed to realize their full potential as an alternative to chemical pesticides.

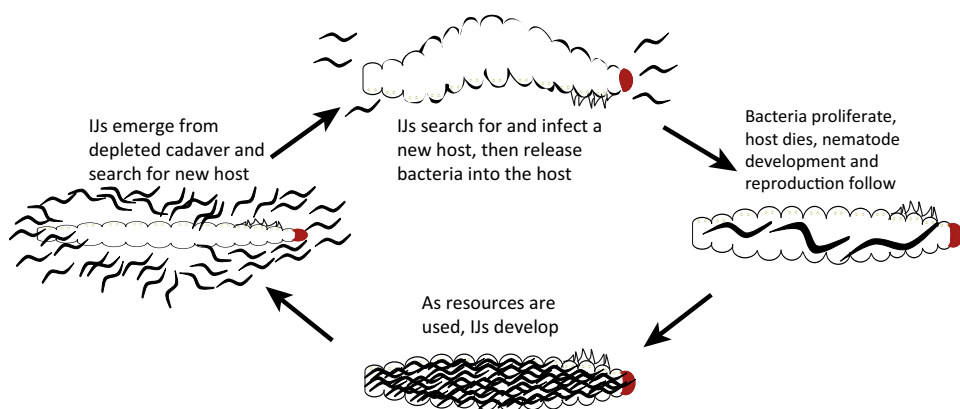
The genome sequences of six species of EPNs are now available and more are being sequenced.

As we increase our knowledge of the genes underlying traits that are important for the field efficacy of EPNs, these genomic data will become more useful in improving EPNs as biocontrol agents.

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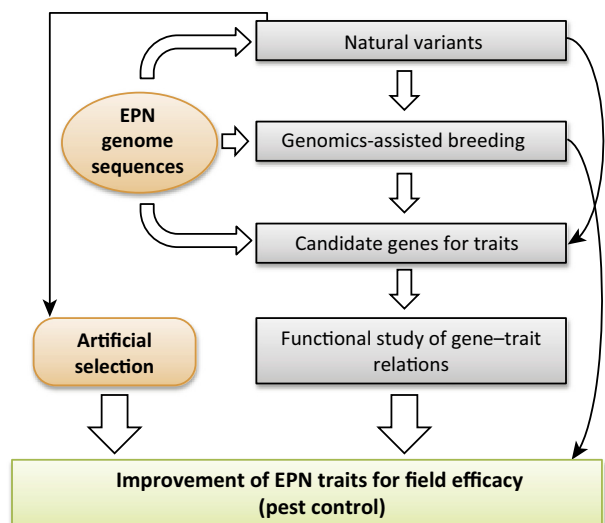
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Figure 1. The Life Cycle of Entomopathogenic Nematodes (EPN). The infective juvenile (IJ) stage is a developmentally arrested third larval stage and is the only free-living stage of EPN; all other stages exist exclusively within the host. EPN IJs carry symbiotic bacteria and search for potential insect hosts. They enter a host, gain access to the hemolymph, and release their bacterial symbiont. The symbiont helps overcome host immunity and facilitates nutrient liberation from insect tissues. The nematodes develop and reproduce in the resulting nutrient-rich environment until their population density is high and resources begin to deplete, at which point new IJs develop and disperse, carrying the symbiotic bacteria to new hosts. Adapted from [2].

these traits in EPNs has been done primarily by classical genetic techniques, such as breeding and selection. However, traits improved this way are not always stable and individual trait gains can sometime be lost once the selective pressure is removed [13]. Moreover, selection of some traits can lead to the inadvertent reduction of others or of overall fitness [12,15,16]. Inbreeding depression or other means of fitness loss during EPN mass production or as a result of continuous laboratory culture are also concerns [17,18]. The second major strategy to improve EPN field efficacy is to use modern genetic and molecular tools. These tools have not yet been fully used to improve EPN field efficacy in biological control [12–14]. Progress has been made toward tool development and technology transfer from the *Caenorhabditis elegans* research community, but the application of modern techniques to improve EPN efficacy is still in its infancy. EPNs are model nematode parasites for studies of ecology [19,20], behavior [21–23],



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Figure 2. Schematic Illustration of how to Improve Entomopathogenic Nematode (EPN) Traits for Enhancing Field Efficacy. The recently sequenced genomes of EPN can be used for selecting candidate genes that influence desirable traits and for identifying the diversity of natural gene variants for artificial selection and genomics-assisted breeding. Genome-wide association analysis of natural variants and strains obtained by genomics-assisted breeding could result in finding the candidate genes underlying certain traits that, when further validated by functional study of gene–trait relations, may facilitate the improvement of EPN traits for enhanced field efficacy. Genomics-assisted breeding can be used to improve EPN traits without knowing specific gene–trait relations. Artificial selection can be used to improve EPNs without previous knowledge of genomes or gene functions.

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