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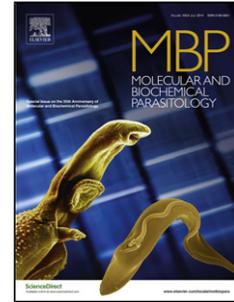
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Lessons from the genomes and transcriptomes of filarial nematodes

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Abstract:

Human filarial infections are a leading cause of morbidity in the developing world. While a small arsenal of drugs exists to treat these infections, there remains a tremendous need for the development of additional interventions. Recent genome sequences and transcriptome analyses of filarial nematodes have provided novel biological insight and allowed for the prediction of novel drug targets as well as potential vaccine candidates. In this review, we discuss the currently available data, insights gained into the metabolism of these organisms, and how the filaria field can move forward by leveraging these data.

Keywords: filaria, parasitic nematodes, genomics, transcriptomics

Introduction:

Nematodes cause the most common parasitic infections in humans, and the tissue-dwelling filarial worms produce the most severe pathology associated with these infections. Current control programs, universally based upon the mass distribution of a small arsenal of drugs

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