Acta Tropica 148 (2015) 51–57

Contents lists available at ScienceDirect

Acta Tropica

journal homepage: www.elsevier.com/locate/actatropica

Draft genome of neurotropic nematode parasite *Angiostrongylus cantonensis*, causative agent of human eosinophilic meningitis

Hoi-Sen Yong[a], Praphathip Eamsobhana[b,*], Phaik-Eem Lim[a,c], Rozaimi Razali[d], Farhanah Abdul Aziz[d], Nurul Shielawati Mohamed Rosli[d], Johan Poole-Johnson[d], Arif Anwar[d]

[a] *Institute of Biological Sciences, University of Malaya, 50603 Kuala Lumpur, Malaysia*
[b] *Department of Parasitology, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok 10700, Thailand*
[c] *Institute of Ocean and Earth Sciences, University of Malaya, 50603 Kuala Lumpur, Malaysia*
[d] *Sengenics HIR, University of Malaya, 50603 Kuala Lumpur, Malaysia*

ARTICLE INFO

Article history:
Received 24 November 2014
Received in revised form 9 April 2015
Accepted 14 April 2015
Available online 21 April 2015

Keywords:
Angiostrongylus cantonensis
Genome
Kinases
Transferases
Excretory–secretory proteins
Metalloproteases
Homeobox genes
Neurotransmitters

ABSTRACT

Angiostrongylus cantonensis is a bursate nematode parasite that causes eosinophilic meningitis (or meningoencephalitis) in humans in many parts of the world. The genomic data from *A. cantonensis* will form a useful resource for comparative genomic and chemogenomic studies to aid the development of diagnostics and therapeutics. We have sequenced, assembled and annotated the genome of *A. cantonensis*. The genome size is estimated to be ~260 Mb, with 17,280 genomic scaffolds, 91X coverage, 81.45% for complete and 93.95% for partial score based on CEGMA analysis of genome completeness. The number of predicted genes of ≥300 bp was 17,482. A total of 7737 predicted protein-coding genes of ≥50 amino acids were identified in the assembled genome. Among the proteins of known function, kinases are the most abundant followed by transferases. The draft genome contains 34 excretory–secretory proteins (ES), a minimum of 44 Nematode Astacin (NAS) metalloproteases, 12 Homeobox (HOX) genes, and 30 neurotransmitters. The assembled genome size (260 Mb) is larger than those of *Pristionchus pacificus*, *Caenorhabditis elegans*, *Necator americanus*, *Caenorhabditis briggsae*, *Trichinella spiralis*, *Brugia malayi* and *Loa loa*, but smaller than *Haemonchus contortus* and *Ascaris suum*. The repeat content (25%) is similar to *H. contortus*. The GC content (41.17%) is lower compared to *P. pacificus* (42.7%) and *H. contortus* (43.1%) but higher compared to *C. briggsae* (37.69%), *A. suum* (37.9%) and *N. americanus* (40.2%) while the scaffold N50 is 42,191. This draft genome will facilitate the understanding of many unresolved issues on the parasite and the disorder it causes.

1. Introduction

Angiostrongylus cantonensis is an important emerging pathogen causing human eosinophilic meningitis (or meningoencephalitis) with thousands of cases in many parts of the world (Kliks and Palumbo, 1992; Wang et al., 2012). Presently, it has spread from its typical endemic regions of Asia and the Pacific to many other regions of the world, including the Americas, Australia, Caribbean islands and Africa (Eamsobhana, 2014). Its natural life cycle involves a definitive rodent host and a mollusk intermediate host. The adult worms live in the pulmonary arteries of rats. Humans are accidentally or incidentally infected with this parasite by ingestion of the third-stage larvae in intermediate hosts, paratenic hosts or contaminated raw or undercooked vegetables. The migration of larvae through the brain results in cerebral hemorrhage and eosinophilic meningitis, which can be fatal. Treatment for eosinophilic meningitis due to *A. cantonensis* is generally symptomatic and supportive in nature. Because of its importance in public health, *A. cantonensis* has received great attention in laboratory and clinical studies (Graeff-Teixeira et al., 2009). In particular, immunodiagnosis of human angiostrongyliasis has been explored extensively (Eamsobhana and Yong, 2009). Recently a number of studies have been reported on *A. cantonensis* high throughput sequencing (Morassutti et al., 2013a), microRNAs (Chang et al., 2013) and transcriptome profiling (Chang et al., 2013; Wang et al., 2013).

The DNA random high throughput sequencing based on 454 (Roche) platform by Morassutti et al. (2013a) consisted of 141 351

* Corresponding author. Tel.: +66 0 24196468.
E-mail address: praphathip.eam@mahidol.ac.th (P. Eamsobhana).

http://dx.doi.org/10.1016/j.actatropica.2015.04.012
0001-706X/