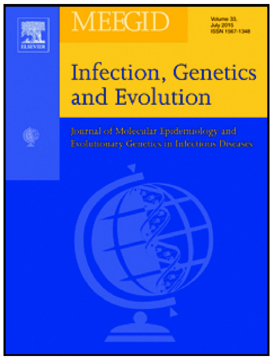

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Mitochondrial genomic comparison of *Clonorchis sinensis* from South Korea with other isolates of this species

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ABSTRACT

Clonorchiasis is a neglected tropical disease that affects more than 35 million people mainly in China, Vietnam, South Korea and some parts of Russia. The disease-causing agent, *Clonorchis sinensis*, is a liver fluke of humans and other piscivorous animals, and has a complex aquatic life cycle involving snails and fish intermediate hosts. Chronic infection in humans causes liver disease and associated complications including malignant bile duct cancer. Central to control and to understanding the epidemiology of this disease is knowledge of the specific identity of the causative agent as well as genetic variation within and among populations of this parasite. Although most published molecular studies seem to suggest that *C. sinensis* represents a single species and that genetic variation within the species is limited, karyotypic variation within *C. sinensis* among China, Korea ($2n = 56$) and Russian Far East ($2n = 14$) suggests that this taxon might contain sibling species. Here, we assessed and applied a deep sequencing-bioinformatic approach to sequence and define a reference mitochondrial (mt) genome for a particular isolate of *C. sinensis* from Korea (*Cs*-k2), to confirm its specific identity, and compared this mt genome with homologous data sets available for this species. Comparative analyses revealed consistency in the number and structure of genes as well as in the lengths of protein-coding genes, and limited genetic variation among isolates of *C. sinensis*. Phylogenetic analyses of amino acid sequences predicted from mt genes showed that representatives of *C. sinensis* clustered together, with absolute nodal support, to the exclusion of other liver fluke representatives, but sub-structuring within *C. sinensis* was not well supported. The plan now is to proceed with the sequencing, assembly and annotation of a high quality draft nuclear genome of this defined isolate (*Cs*-k2) as a basis for a detailed investigation of molecular variation within *C. sinensis* from disparate geographical locations in parts of Asia and to prospect for cryptic species.

Keywords:
Mitochondrial genome
Clonorchis sinensis
Genetic variation

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Note: The nucleotide sequence of the mitochondrial genome reported in this article is publicly available in the GenBank database under accession no. KY564177.