Methods

Alignments: The sequences used for phylogenetic analysis were aligned using CLUSTALX v. 1.82. The protein alignments were conducted with the Gonnet matrix.

Construction of the phylogenetic trees: Rooted neighbour-joining phylogenetic tree was constructed using the MEGA software package. The nematode *A. ceylanium* was chosen as outgroup. The numbers indicated at each branch node is the bootstrap support value based on 1000 bootstrap repilcations.