Molecular characterisation of the actin gene of the filarial parasite Wuchereria bancrofti

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Abstract

Wuchereria bancrofti is the major cause of lymphatic filariasis in humans. Although it is responsible for this immensely morbid and debilitating disease, very little is known of the basic molecular biology of this parasite, and there is a vast lack of knowledge on its gene organisation. In this study, the actin gene of W. bancrofti has been characterised by sequencing a clone isolated from a genomic DNA library of this parasite. The 5' flanking region had a potential TATA box and a putative mRNA initiation site. The gene had five exons encoding 376 amino acids, and four introns ranging in size from 109 to 190bp. The 3' flanking region had a potential polyadenylation signal with the sequence ATTAAA which is a common natural variant of the conventional sequence AATAAA. The gene was AT-rich, with a GC content of 37.2%. Southern blot analysis of W. bancrofti genomic DNA indicated that the gene is possibly found as a single copy. The actin amino acid sequence of W. bancrofti showed a high degree of homology to the actin of many organisms of different taxonomic groups, but the highest homology was observed with the free-living nematode Plectus acuminatus. This suggests that P. acuminatus may bear a close evolutionary relationship to W. bancrofti.

Keywords: Actin; Filariasis; Wuchereria bancrofti