Characterization of 6.4 kb repeat from Wucheraria bancrofti
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Colombo : Faculty of medicine, 1997
Degree: M.Sc.

Abstract:

A long repeat of 6.4 kb from the Wuchereria bancrofti genome was partially sequenced, by generating overlapping fragments in pUC 19 with the use of Sau 3A I, Alu I and Rsa I restrication endonucleases. As a result of this, a discontinuous stretch of sequence of 5282 bp was obtained. The longest continuous stretch of nucleotide sequence obtained was 3655 bp. Areas of this long sequence showed 100 percent homology to pWb 2.5, pWb12 and pWb 6 sequences. One end of the pWb 2.5 sequence and one end (5' end) of the 3655 bp sequence showed exact homology. Thus, 2.5 kb fragment of pWb 2.5 is a continuous part of the 6.4 kb repeat and pWb 12 and pWb 6 sequences are interspersed within it. Also, the 6.4 kb repeat is arranged in parasite genome in head-to-tail manner.

Key Words: Wuchereria bancrofti / Wuchereria bancrofti-genetics / Filariasis