A-33: Partial characterization of 6.4 kb repeat from *Wuchereria bancrofti* genome

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Characterization of long repeats in parasite genome helps in the phylogenetic studies and reveals new approaches towards combating the parasitic disease. One such repeat of 6.4 kb of the genome of *Wuchereria bancrofti,* the commonest filarial nematode found in Sri Lanka was partially sequenced. This was done by generating overlapping fragments in pUC 19 with the use of *Sau* 3AI, *Alu* I and *Rsa* I restriction endonucleases.

A discontinuous stretch of sequence of 5282 bp was obtained. The longest continuous stretch of nucleotide sequence of 3655 bp, showed 100% homology to inserts of pWb 2.5, pWb 12 and pWb 6 clones which had been sequenced in a previous study. Thus, 2.5 kb sequence of pWb 2.5 represented as a continuous stretch at one end of 3655 bp sequence. The sequence of pWb 12 and pWb 6 are interspersed within it. The 6.4 kb repeat is arranged in the head-to-tail manner in the parasite genome.

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