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The Molecular Characterization of the esta31 gene, in the Colombian strain of *Culex quinquefasciatus*

The molecular basis of organophosphate resistance in the Colombian strain of C. *quinquefasciatus* (COL), is due to the two amplified esterases genes est 31 and est1. These two esterases are situated in the same amplicon, but more than 10kb apart. This study was carried out using the PCR analysis of the genomic DNA and cDNA o fCOL strain using five primer pairs, designed from the est sequence.

The est genomic sequence, was 89% similar to the est genomic sequence, The sequence data also revealed, that ATG start codon, to the down stream 2227 nucleotides of est and est are highly homologous.

The partial sequence of est cDNA has 1406 nucleotides and 463 inferred amino acids. Five introns and six exons were identified within the region. The full-length est 21 cDNA has a 1623 bp open reading frame and 540 inferred amino acids. A few alteration of sizes and greater variability in sequence were observed in the introns (81.4%) compared to exons. However there were ten amino acid changes and 71 silent nucleotide differences compared to the est sequence. The two esterases (Est & Est 0 have a different mobility in native PAGE gels. This could be due to diffent in the charge of est protein. They are probably alleles of the same gene, which have been amplified separately.

The selective advantage fo est est over est /est amplicon could be due to their genomic organization of the genes.