

## IDENTIFICATION OF NOVEL LTR-RETROTRANSPOSONS IN THE GENOME OF *CULEX QUINQUEFASCIATUS*

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Transposable elements are ubiquitous component of eukaryotic genomes and, besides their mutagenic role, they are considered as the major source of variability that can change genomes and their expression, either considering short term or large evolutionary scale time. The post-genomic era offers a great opportunity to shed light on the evolution of mobile genetic elements with respect to eukaryotic genome. In the last years a special interest in the field of mosquitoes' genomics is highlighted by the completion of three genomic sequences (i.e. *Anopheles gambiae*, *Aedes aegypti* and *Culex quinquefasciatus*); this interest come from their role to function as vectors of virus-borne diseases. Few transposon families have been described in the *Culex* genus before the sequencing of *C. quinquefasciatus* genome. The genomic sequence analysis recently performed by Arensburger et al. (1) has revealed that nearly 30% of this genome is composed of TEs. The TE-related sequences described in Arensburger et al. were deposited in the *TEfam* database.

The genome of *C. quinquefasciatus* has been analyzed using the LTR\_STRUC program. Thirty novel families of LTR retrotransposons have been identified. Furthermore a group of non-autonomous elements has been identified, featured by tandem repeated sequences between the LTRs and apparently unrelated to any known *Culex* retrotransposon family.

The potential role of the LTR-retrotransposon insertions on the host gene structure has been studied, and several insertions that may potentially contribute to the mature transcripts of endogenous genes have been identified.

These results integrate the existing data on the genomics of an important disease vector.

### REFERENCE

Arensburger P, Megy K, Waterhouse RM, Abrudan J, Amedeo P, et al. Sequencing of *Culex quinquefasciatus* establishes a platform for mosquito comparative genomics. *Science* 330: 86-88.