Retrovirology



Poster presentation



# LTRs; Universal structure, detection and phylogeny

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## Background

Retroviral LTRs, paired or single, are plastic structures which contribute profoundly to genomic and transcriptional diversity. Some genomes are studded with LTRs. However, detection and alignment of single LTRs is a bioinformatic challenge.

## Materials and methods

LTRs found by RetroTector [1,2], and from RepBase, from vertebrate, insect and plant genomes. Profile Hidden Markov models (HMMs) [3].

## Results

Representatives of all known LTR containing genetic elements and viruses were analyzed using HMMs. Nine more or less specialized HMMs (Vertebrate, Human MMTV-like, Gamma-retroviruslike, Betaretroviruslike, Lentivirus, Spumaretroviruslike, *gypsy*, *copia* and BEL) yielded Viterbi alignments, allowing detection of common consensus structures (match states). The match states of the nine HMMs could be arranged into modules with small internal and longer intermodule insert states stretches, revealing a common conserved LTR structure. An LTR-based phylogenetic tree covering all known LTR retrotransposons came out with a similar branch pattern as a reverse transcriptase-based tree. All LTRs started with TG and ended with CA. R-U5 was most conserved, AATAAA being the most conserved motif. The high degree of LTR structural conservation in LTR retrotransposons indicates that they all have a common origin, and a common mode of function, which thus should have originated billions of years ago. The HMMs could also be used for detection of single LTRs, with 10-90% sensitivity, in human, fungal and insect genomes. The specificity ranged from 30 to 90%, depending on how a "true" positive was defined. It is likely that a substantial part of host genomes consists of remnants of LTR retrotransposons which are hard to detect, but which are partially recognized by the HMMs.

## Conclusion

Besides providing a better understanding of LTR retrotransposons and their phylogeny, the more precise knowledge of LTR structure now at hand should be useful for optimization of gene therapeutic vectors, and for design of LTR-targeted drugs.

## References

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