

Analysis of Expressed Sequence Tags generated from *Uroctea lesserti* Schenkel (Araneal)

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Objectives

Partial cDNA sequencing to generate expressed sequence tags (ESTs) is being used at present for the fast and efficient obtainment of a detailed profile of genes expressed in various tissues, cell types, or developmental stages. We describe here the construction, DNA sequencing and sequence profiles of cDNA library from *Uroctea lesserti*.

Materials and Methods

Materials - Spider : *Uroctea lesserti* Schenkel (Araneal)

Vector : modified pCNS (GenBank Accession no. AF416744)

Methods - Construction of a full-length enriched cDNA library

- DNA sequencing (ABI 377 sequencer, Applied Biosystems)
- Sequence analysis (DNA star, BLASTx on the BLAST service at NCBI)

Results and Discussion

We constructed the full-length cDNA library from 100 ug of total RNA of *Uroctea lesserti*. The library contained 5×10^6 independent clones with average insert sizes of 1.5 kbp. A total of 2,685 clones were randomly selected, and the 5' ends of the inserts were sequenced. A total 1.8% of the clones were homologous to previously identified *U. lesserti*, while 45.2% had significant matches to genes from other organisms in the database. A total of 53% of the ESTs had no matches in the database. Functional groups of those sequences with matches in the database were constructed according to their putative biological function. The three largest categories were cellular organization (26.8%), metabolism (11.7%) and cell cycle-DNA processing (10.8%). The information reported in this study should be useful for researchers in

the field to analyze genes and proteins of their own interest.

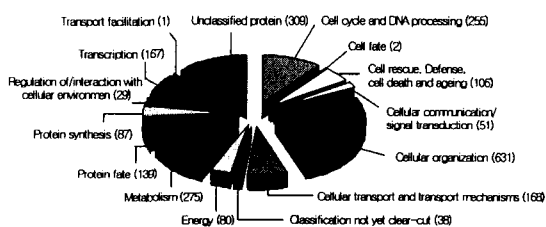


Fig.1. Functional classification of *U. lesserti* ESTs, showing the proportion of predicted genes according to their putative biological functions.

Reference

Verdun, R.E., N.D. Paolo, T.P. Urmenyi, E. Rondielli, A.C.C. Frash and D.O. Sanchez. 1998. Gene Discovery through expressed sequence tag sequencing in *Trypanosoma curi*. *Infection and Immunity*, 66(11): 5393-5398.