

Analysis of Expressed Sequence Tags generated from Korean spider, *Uroctea lesserti* Schenkel

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Partial cDNA sequencing to generate expressed sequence tags (ESTs) is being used at present for the fast and efficient obtainments 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 generated from Korean spider, *Uroctea lesserti* (Araneal). 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 3.0% 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.