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Poster presentation

Techniques for the analysis of trichome *Pelagonium xhortorum* expressed sequence tags

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Background

An important aspect of bioinformatics is the infrastructure for storage and display of high throughput sequence data generated by biologists. The construction of databases and applications to display the results in a meaningful and useful way is not a trivial task. A well-designed and executed system can vastly improve the results obtained from an experiment. We present a system for storing and viewing EST sequences based on a set generated for a geranium genome.

Results

A series of over 4,000 expressed-sequence tags (ESTs) originating from the trichome of the geranium, *Pelagonium xhortorum*, were generated in a wet lab. EST sequences were organized into clusters of overlapping sequences using CAP3. The resulting clusters, including single EST clusters, were analyzed and annotated by hand in order to classify the sequences into families and subfamilies of genes. Further refinement using Blast2GO classifies these sequences into annotated groups based on biological process, cellular component, and molecular function. Presentation of the results were accomplished through a MySQL database and java servlet web pages used to analyze, group, and display the resulting data. Queries into the data can be performed by using blast or by searching by known gene families.

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