A COMPUTATIONAL ANALYSIS OF ACHILLEA MILLEFOLIUM SEQUENCE
TO DETERMINE EXPECTATION VALUE COMMONLY USED
IN BIOINFORMATICS DATABASE

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ABSTRACT
Achillea Millefolium economically important crop worldwide, intensively investigated and model system for genetic studies in plant. Achillea L. (Compositae or Asteraceae) distributed widely as a medicinal plant throughout the world and has been used since ancient time as a variability is a measure spread of data set. Genome analysis and annotation using genome from the libraries, automatic annotation using the BLAST (basic local alignment search tools) low complexity sequence has unusual composition that can create a problem in sequence similarity searching of Achillea protein sequence the color bars in the graphic summarize the BLAST. Database such as NCBI, FASTA, BLAST, ClustalW. BLAST has a bioinformatics tool that act as an algorithm to align sequences as if they were found in the database search. When expect value is increases from default value, a larger list with more scoring hits alignment can be reported. The desired subset of the plant Achillea data compiled using BLAST tool can be subsequently used for check the expectation value to analyses and knowledge discovery as the observation.

KEYWORDS: Biological Database, Customized Data Retrieved, Sequence Analysis, Data Compiled, Expectation Value Achillea & Asteraceae

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