

Mining of simple sequence repeats in the Genome of Gentianaceae

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ABSTRACT

Simple sequence repeats (SSRs) or short tandem repeats are short repeat motifs that show high level of length polymorphism due to insertion or deletion mutations of one or more repeat types. Here, we present the detection and abundance of microsatellites or SSRs in nucleotide sequences of Gentianaceae family. A total of 545 SSRs were mined in 4698 nucleotide sequences downloaded from the National Center for Biotechnology Information (NCBI). Among the SSR sequences, the frequency of repeat type was about 429 -mono repeats, 99 -di repeats, 15 -tri repeats, and 2 --hexa repeats. Mononucleotide repeats were found to be abundant repeat types, about 78%, followed by dinucleotide repeats (18.16%) among the SSR sequences. An attempt was made to design primer pairs for 545 identified SSRs but these were found only for 169 sequences.

KEYWORDS

Gentianaceae . nucleotide . simple sequence repeats

REFERENCES

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