

عنوان مقاله:

.Identification of novel short tandem repeats based markers in the expressed sequence of Malus domestica Borkh

محل انتشار:

سومین کنگره بین المللی و پانزدهمین کنگره ملی ژنتیک ایران (سال: 1397)

تعداد صفحات اصل مقاله: 6

نویسنده:

Abdolkarim Zarei - Department of Biotechnology, Agriculture College, Jahrom University, Jahrom, Iran

خلاصه مقاله:

Apple (*Malus domestica* Borkh.) is an economically important fruit crop worldwide. There are huge amount of transcriptomics derived sequences of this fruit tree in the public databases that provide a good source for development of expressed sequence tags (ESTs) based markers including EST-SSRs. In the present study, EST sequences of apple available in NCBI were exploited to estimate, analysis and characterize simple sequence repeats and to develop SSR molecular markers. Data mining in 326941 sequences revealed that 10340 sequences contained at least one SSR (on average 3.16 % of deposited sequences). In total 10693 EST-SSRs were identified that 4295 ones (40.16%) were suitable for primer development. Motif frequencies were highly variable and dinucleotide repeats with 86% of identified SSRs were the most abundant followed by trinucleotide (12%), and tetranucleotide (2%) repeats. The same trend was observed for SSRs with primers. AG/GA/CT/TC motif were the most abundant repeat unit in apple ESTs and included 76% of identified SSRs. Validation of some of the identified SSRs are underway by .evaluation their polymorphism on different apple cultivars

کلمات کلیدی:

Repeat unit, data mining, apple, EST-SSR

لینک ثابت مقاله در پایگاه سیویلیکا:

<https://civilica.com/doc/983769>

