

ABSTRACTS BOOK

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P0146 EGMIDB: THE EGGPLANT MICROSATELLITE DATABASE

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1 Full text

Microsatellites or simple sequence repeats (SSRs) represent one of the most informative, versatile and practical DNA-based markers used in plant breeding programs, since they are easy to score and have wide genomic distribution, codominant inheritance and a multi-allelic nature. Pseudomolecules as well as unmapped scaffolds, of the recently developed high quality reference eggplant genome, were used for the bulk mining of SSR markers and for the construction of the first microsatellite marker database *EgMiDB* (Eggplant Microsatellite Database - <http://www.eggplantmicrosatellite.org>). From the ~1.1 Gb of the ungapped eggplant genomic sequence, we identified 132,831 perfect SSR motifs (density of about 120 SSR/Mb), which included 20,670 (15.6%) compound SSRs while the imperfect SSR motifs were over 178,400. Dinucleotides were the most common, representing 42.8% of all microsatellites, followed by tri- (37.0%), mono (8.4%) and tetranucleotides (7.1%). Penta- and hexanucleotide repeats were the least frequent, together representing less than 5% of the set of perfect SSRs. *EgMiDB* is an user-friendly and freely accessible tool, which offers chromosome wise as well as location wise search of primers by implementing Primer3, and represents a one-stop resource for the global community of scientists and breeders. The database has been projected to gain benefit of the genome sequence linked to pseudomolecules/scaffold and, having user need-based primer designing facilities with mobile-friendly features, will facilitate rapid selection of suitable custom markers for a wide range of genetic analyses.