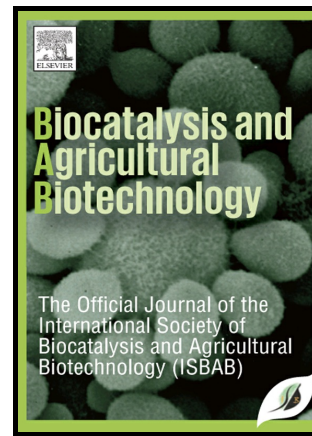


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Microsatellite markers of finger millet (*Eleusine coracana* (L.) Gaertn) and foxtail millet (*Setaria italica* (L.) Beauv) provide resources for cross-genome transferability and genetic diversity analyses in other millets

T. P. Ajeesh Krishna^{a1}, T. Maharajan^{a1}, R. Host Antony David^a, M. Ramakrishnan^a, S. Antony Ceasar^{a, b*}, V. Duraipandiyan^{a*}, G. Victor Roch^a, S. Ignacimuthu^{a*}

¹Division of Plant Biotechnology, Entomology Research Institute, Loyola College, Chennai, India - 600 034

²Laboratory of Functional Genomics and Plant Molecular Imaging, InBioS-PhytoSystems, University of Liège, B4000 Liège, Belgium.

avdpandiyan@yahoo.co.in

antony_sm2003@yahoo.co.in

eriloyola@hotmail.com

***Corresponding authors:** Tel.: +9144-28178348; fax: +9144-28175566

Abstract

The cross-genome transferability of 110 simple sequence repeats (SSR) markers of finger millet and 26 SSR markers of foxtail millet were analyzed in 8 other millets. In total, 33 finger millet and 2 foxtail millet SSR markers showed 100 % cross-genome transferability in other millets. The cross-genome transferability of 101 finger millet and 26 foxtail millet SSR markers ranged from 47.52 % to 61.38 % and from 30.76 % to 69.23 % respectively. Expressed sequence tags SSR (EST-SSR) markers of finger millet showed higher level of cross-genome transferability than genomic SSR (gSSR) markers. The observed polymorphic information content (PIC) values were the same for finger millet and foxtail millet SSR markers which ranged from 0.14 to 1.00. Further, these data were also used for genetic diversity analysis among 8 millets using the software version 2.1 of NTSYSpc tool and PAST version 2. All millet species were grouped in one major cluster based on finger millet SSR markers, through UPGMA analysis. But two major clusters were observed by the analysis using foxtail millet SSR markers. Similarity

¹ **Equal contribution:** T. P. Ajeesh Krishna and T. Maharajan

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