

## Transferability of EST SSR-Markers from Foxtail Millet to Barnyard Millet (*Echinochloa esculenta*)

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A large number of expressed sequence tags (ESTs) in public databases have provided an opportunity for the systematic development of simple sequence repeat (SSR) markers. EST-SSRs derived from conserved coding sequences show considerable cross-species transferability in related species. In the present study, we assessed the utility of foxtail millet EST-SSRs in barnyard millet. A total of 312 EST-SSRs of foxtail millet were tested using 84 *Echinochloa crus-galli* germplasm accessions; a high rate of transferability (62%) and 46 primer sets (13%) were shown the polymorphism in barnyard millet. The 13% of functional EST-SSRs) was demonstrated between cereals and barnyard millet. SSR marker profile data were scored for the computation of pairwise distances as well as a Neighbor Joining (NJ) tree of all the genotypes. The averaged values of gene diversity ( $H_E$ ) and polymorphism information content (PIC) were 0.213 and 0.179 within populations, respectively. The 84 barnyard millet germplasm accessions were divided into five different groups, which agreed well with their geographical origins. The exotic 12 accessions of India type barnyard millet (*E. frumentacea*) were all separated from Korean local collection genotype. The present results provide evidence of divergence between cultured and wild type barnyard, as a millet and grass. The polymorphic SSR markers indicated in this study were of great value in analysis of genetic diversity that can be further used for crop improvement through breeding.

**Key words:** Barnyard millet, EST-SSR markers, Transferability

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