

Abstract

Background

Genetic diversity of finger millet (*Eleusine coracana*), a nutritious neglected staple cereal in Africa and South Asia is largely uncharacterized. This study analysed 82 published SSR markers for finger millet across 10 diverse accessions to compile an informative set for genetic characterisation. Extensive optimization compared single samples with bulked leaf or bulked DNA samples for capturing within accession genetic diversity. The markers were evaluated to determine (1) how efficiently they amplified target loci during high-throughput genotyping with a generic PCR protocol, (2) ease of scoring PCR products and (3) polymorphism and ability to discern genetic diversity within the tested finger millet germplasm.

Results

Across 88 samples, the 52 markers that worked well amplified 274 alleles, ranging from 2 to 14 per locus with a mean of 4.89. Major allele frequency ranged from 0.18 to 0.93 with a mean of 0.57. Polymorphic Information Content (PIC) ranged from 0.13 to 0.88 with a mean of 0.5 and availability varied between 64 and 100% with a mean of 92.8%. Heterozygosity ranged from 0 to 1.0, with a mean of 0.26.

Discussion

Five individual samples from an accession captured the largest number of alleles per locus compared to the four different bulked sampling strategies but this difference was not significant. The identified set comprised 20 markers: UGEP24, UGEP53, UGEP84, UGEP27, UGEP98, UGEP95, UGEP64, UGEP33, UGEP67, UGEP106, UGEP110, UGEP57, UGEP96, UGEP66, UGEP46, UGEP79, UGEP20, UGEP12, UGEP73 and UGEP5 and was since used to assess East African finger millet genetic diversity in two separate studies.