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Different Patterns of Repeat Motifs in SSRs found from Five Different Genomes of Crop Species

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Objectives

This research was conducted to survey the SSR distribution pattern and characteristics of five different crops genome for efficient SSR markers system development.

Materials and Methods

1. Material

Plant Amaranth, Chinese cabbage (*Brassica rapa subsp. pekinensis*), Finger millet(*Eleusine coracana subsp. coracana*), job'tears (*Coix gigantea*), mung-bean(*Vigna radiata var. radiata*)

2. Methods

Genomic DNA of each crop plants was digested with blunt-end restriction enzyme and ligated with adapter. Adapter ligated DNA was hybridized with Biotin SSR oligo and captured by straptavidin-magnetic particles. Bounded DNA was washed and eluted with 3dH₂O. Final elutes was amplified and cloned into pGEM-Teasy vector and sequenced. Randomly selected forty clones from each library were sequenced and sequences were analyzed by mreps program.

Results and discussion

In each library, forty clones were sequenced and analyzed. Enrichment efficiency of SSR was various in each crop and washing conditions. *Brassica rapa* and finger millet had a di- nucleotide(GA) as a predominant SSR unit, but tri-nucleotide predominated in amaranth(GAA), job's tears and mung-bean(TTG). Specially, brassica genome had a sound(not interrupted) and long SSRs units (GA) and this might result in good enrichment rate, this results coincide with other researchers reports that Brassica crop species had a predominant GA repeats.

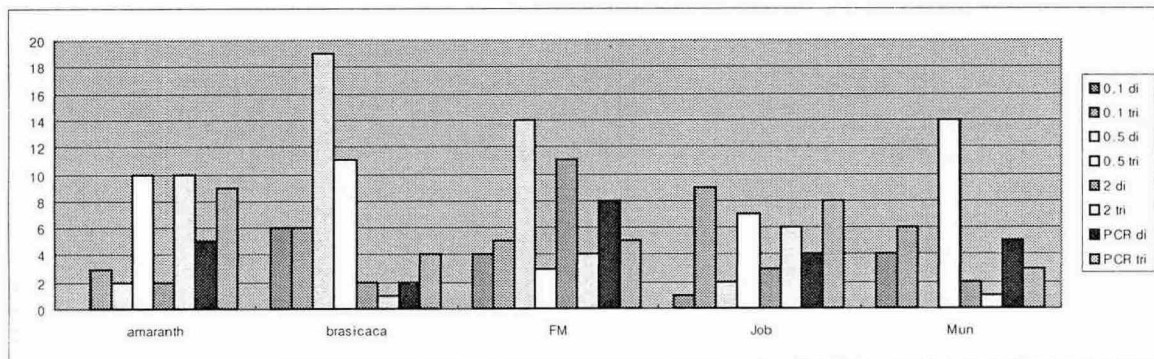


Figure 1. repeating unit length distribution of di and tri unit SSR of five crops.