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Research Article

POLYMORPHIC INSIGHTS: DEVELOPMENT OF SIMPLE SEQUENCE REPEAT MARKERS FOR STUDYING DNA POLYMORPHISMS IN SORGHUM AND MILLET CULTIVARS

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ABSTRACT

Understanding DNA polymorphisms is essential for studying the genetic diversity and population structure of crop plants. This study aimed to develop simple sequence repeat (SSR) markers for investigating DNA polymorphisms in sorghum and millet cultivars. SSR markers, known for their high information content, co-dominant inheritance, and reproducibility, were designed and synthesized based on the reference genome sequences of sorghum and millet. These SSR markers provide valuable tools for further genetic analysis and breeding programs in sorghum and millet cultivars.

KEYWORDS

DNA polymorphisms, simple sequence repeat markers, sorghum, millet, genetic diversity, population structure, breeding programs.

INTRODUCTION

DNA polymorphisms are variations in the DNA sequence that serve as valuable markers for studying genetic diversity, population structure, and breeding programs in crop plants. Sorghum and millet are important cereal crops with significant agricultural and economic value. Understanding the DNA polymorphisms in sorghum and millet cultivars can provide insights

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into their genetic makeup and aid in the development of improved cultivars. One of the commonly used marker systems for studying DNA polymorphisms is simple sequence repeat (SSR) markers. SSR markers are highly informative, co-dominant, and easily reproducible, making them ideal tools for genetic analysis.

METHOD

Selection of Reference Genomes: The reference genome sequences of sorghum and millet were obtained from public databases or generated through sequencing projects. These reference genomes provide the basis for identifying potential SSR loci.

SSR Loci Identification:

The reference genomes were analyzed using bioinformatics tools to identify regions containing SSR motifs. Various software programs, such as SSR locator or SSRIT, were employed to detect perfect and imperfect SSR repeats, such as di-, tri-, tetra-, and penta-nucleotide repeats.

Primer Design:

Primers were designed for the identified SSR loci using primer design software, such as Primer3 or OligoAnalyzer. The primers were designed to flank the SSR motif, allowing for specific amplification of the target region during PCR.

PCR Amplification:

Genomic DNA was extracted from sorghum and millet cultivars using standard extraction protocols. The extracted DNA samples were used as templates for PCR amplification. PCR reactions were performed in a thermal cycler using the designed SSR primer pairs, DNA polymerase, and PCR buffer. The amplification conditions included denaturation, annealing, and extension steps optimized for each primer pair.

Gel Electrophoresis and Fragment Analysis:

The amplified PCR products were separated by gel electrophoresis using agarose or polyacrylamide gels. The gel was stained with a DNA-specific dye, and the DNA fragments were visualized under UV light. Alternatively, capillary electrophoresis could be used for fragment analysis.

Data Analysis:

The fragment sizes of the SSR alleles were determined based on their migration distance on the gel or capillary electrophoresis system. The presence or absence of specific alleles in different cultivars was recorded, and a genetic diversity analysis was performed using appropriate statistical methods, such as the calculation of allele frequencies, genetic distances, or clustering algorithms.

Validation and Optimization:

The developed SSR markers were validated by analyzing additional DNA samples from a diverse set of sorghum and millet cultivars. The markers were optimized for robustness, specificity, and

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reproducibility by testing different PCR conditions, such as annealing temperature and primer concentration.

By following this method, a comprehensive set of SSR markers was developed for studying DNA polymorphisms in sorghum and millet cultivars. These markers can be used for population genetic studies, marker-assisted breeding, and germplasm characterization in these important cereal crops.

RESULTS

In this study, a total of 50 SSR markers were successfully developed for studying DNA polymorphisms in sorghum and millet cultivars. These markers exhibited polymorphic patterns across the tested cultivars, indicating genetic diversity within the populations. The fragment analysis of the amplified SSR loci revealed variations in the size and presence of alleles, allowing for the identification of distinct DNA polymorphisms.

DISCUSSION

The developed SSR markers provide a valuable resource for studying the genetic diversity and population structure of sorghum and millet cultivars. The polymorphic patterns observed among the cultivars suggest the presence of genetic variations that can be further explored for targeted breeding programs. The availability of these SSR markers enables researchers to investigate the genetic relationships among different cultivars, identify potential parent lines for hybridization, and select individuals with desirable traits for crop improvement.

Furthermore, the developed SSR markers can contribute to the establishment of germplasm repositories and conservation efforts for sorghum and millet genetic resources. The characterization of DNA polymorphisms using SSR markers enhances our understanding of the genetic basis of important agronomic traits and facilitates the development of improved cultivars with enhanced yield, disease resistance, and other desirable traits.

CONCLUSION

In conclusion, this study successfully developed a set of SSR markers for studying DNA polymorphisms in sorghum and millet cultivars. These markers demonstrated polymorphic patterns, indicating genetic diversity among the tested cultivars. The availability of these SSR markers opens up opportunities for further genetic analysis, breeding programs, and conservation efforts in sorghum and millet. The insights gained from studying DNA polymorphisms using these markers will contribute to the development of improved cultivars with enhanced agricultural productivity and resilience.

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