Difference of PmTDC1 expression levels results the formation of brown and yellow seed color in broomcorn millet (Panicum miliaceum)

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Abstract: (Objective) Broomcorn millet is a cereal crop with abundant genetic variation in morphology, agronomy and yield-related traits. Diversity of seed color is one of the most distinctive morphological characteristic. To identify genes regulating seed color will provide a basis for precise identification of germplasms at molecular level, molecular assisted selection breeding and application of gene editing technology in broomcorn millet. [Method] Phenotype identification and statistical analysis were used to dissect inheritance law. And bulked segregant analysis sequencing (BSA-seq), substitution mapping and transcriptome sequencing were performed to identify the casual gene of brown yellow grain color in broomcorn millet. **[Result]** Here, F_2 and F_3 populations from a cross between Longmi12 and Zhang778 were constructed. The statistical analysis of the seed color in F_1 , F_2 and F_3 progenies confirmed that the brown seed color was controlled by a dominant single gene in broomcorn millet. The genetic control locus, SC9.1, was preliminarily located in the interval between 32175878 to 44281406 bp on chromosome 9 through the bulked segregant analysis sequencing (BSA-seq). Further, SC9.1 was narrowed down to a 101kb interval harboring 11 genes by substitution mapping based on 258 recessive individual genotypes. Of 11 genes, PmTDC1 had a single A to G transition in CDS region and a significantly different expression in seed color formation stage, indicating that *PmTDC1* was the causal gene resulting brown and yellow seed color formation in broomcorn millet. **Conclusion** Difference of *PmTDC1* expression levels results the formation of brown and yellow seed color in broomcorn millet.

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