Transcriptomic analysis, genic SSR development, and genetic diversity of proso millet (Panicum miliaceum; Poaceae)¹

Siyu Hou²,3,6, Zhaoxia Sun²,6, Yaoshen Li², Yijie Wang², Hubin Ling², Guofang Xing²,3, Yuanchai Han²,4,5, and Hongying Li²,5

²College of Agriculture, Institute of Agricultural Bioengineering, Shanxi Agricultural University, Taigu, Shanxi 030801, People’s Republic of China; ³Shanxi Key Laboratory of Genetic Resources and Genetic Improvement of Minor Crops, Taigu, Shanxi 030801, People’s Republic of China; and ⁴Key Laboratory of Crop Gene Resources and Germplasm Enhancement on the Loess Plateau, Ministry of Agriculture, Institute of Crop Genetic Resources, Shanxi Academy of Agricultural Sciences, Taiyuan, Shanxi 030031, People’s Republic of China

• Premise of the study: Proso millet (Panicum miliaceum; Poaceae) is a minor crop with good nutritional qualities and strong tolerance to drought stress and soil infertility. However, studies on genetic diversity have been limited due to a lack of efficient genetic markers.

• Methods: Illumina sequencing technology was used to generate short read sequences of proso millet, and de novo transcriptome assemblies were used to develop a de novo assembly of proso millet. Genic simple sequence repeat (SSR) markers were identified and used to detect polymorphism among 56 accessions. Population structure and genetic similarity coefficient were estimated.

• Results: In total, 25,341 unique gene sequences and 4724 SSR loci were obtained from the transcriptome, of which 229 pairs of SSR primers were validated, which resulted in 14 polymorphic genic SSR primers exhibiting 43 total alleles. According to the ratio of polymorphic markers (6.1%, 14/229), there are potentially 288 polymorphic genic SSR markers available for genetic assay development in the future. Bayesian population analyses showed that the 56 accessions comprised two distinct groups.

• Discussion: A genetic structure and cluster assay indicated that the accessions from the Loess Plateau of China shared a high genetic similarity coefficient with those from other regions and that there was no correlation between genetic diversity and geographic origin. The transcriptome sequencing data and millet-specific SSR markers developed in this study establish an excellent resource for gene discovery and may improve the development of breeding programs in proso millet in the future.

Key words: de novo transcriptome; genetic diversity; genic SSR; germplasm resources; Panicum miliaceum; Poaceae; proso millet.

Proso millet, also named broomcorn or common millet (Panicum miliaceum L.; Poaceae), was domesticated in Neolithic China ca. 10,000 BP (Lu et al., 2009) and grown across Eurasia as a minor crop. The cultivation area of proso millet is about 30.32 million ha in China, with a total grain production of approximately 0.3 million tons per year (Diao, 2017). Although the grain yield of proso millet is lower than that of major crops such as maize (Zea mays L.), wheat (Triticum aestivum L.), and rice (Oryza sativa L.), it was once cultivated as a large crop in northern China because of its much greater resistance to drought and unfertile soil than these major crops (Diao, 2017). It was introduced to North America in the 18th century and used mainly for animal fodder and birdseed (Bagdi et al., 2011). Across Eurasia, however, proso millet was important in the human diet before the introduction of other crops such as wheat, barley, and potatoes. More attention has been paid to this crop in China, India, Nepal, Pakistan, and Southeast Asian countries, where it is considered a functional food due to its high protein content (11.3–17% of grain dry matter), abundant antioxidant components, and dietary fiber (Kalilnova and Moudry, 2006). A few reports have shown that the phytochemical components of proso millet can prevent certain cancers, heart disease, and relieve liver disease and diabetes (Srivastava et al., 2001; Choi et al., 2005; Shimunoki et al., 2006). The crop has high-water use efficiency, a short growing period (60–90 d), and a high adaptability and tolerance to semiarid climates (Asgad et al., 2001; Graybosch and Ballensperger, 2009). Hence, it is ideally suited to cultivation in areas with hot, dry, and short summer seasons (Saseendran et al., 2009).

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²Authors for correspondence: hongylswgctd@163.com (H.Y.L.), swgctd@163.com (Y.H.H.)

These authors contributed equally to this work.

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