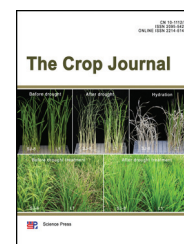
Available online at www.sciencedirect.com

ScienceDirect



Waxy allelic diversity in common millet (*Panicum miliaceum* L.) in China

Ruiyun Wang^{a,b,*}, Haigang Wang^{b,1}, Xiaohuan Liu^a, Xu Ji^a, Ling Chen^b, Ping Lu^f, Minxuan Liu^f, Bin Teng^d, Zhijun Qiao^{b,*}

^aCollege of Agriculture, Shanxi Agricultural University, Taigu 030801, Shanxi, China

^bInstitute of Crop Germplasm Resources of Shanxi Academy of Agricultural Sciences, Key Laboratory of Crop Gene Resources and Germplasm Enhancement on Loess Plateau, Ministry of Agriculture, Shanxi Key Laboratory of Genetic Resources and Genetic Improvement of Minor Crops, Taiyuan 030001, Shanxi, China

^cInstitute of Crop Science, Chinese Academy of Agricultural Sciences, Beijing 100081, China

^dAnhui Provincial Key Lab of Rice Genetics and Breeding, Institute of Rice Research, Anhui Academy of Agricultural Sciences, Hefei 230001, Anhui, China

ARTICLE INFO

Article history:

Received 21 November 2017

Received in revised form 9 February 2018

Accepted 1 March 2018

Available online xxx

Keywords:

Common millet

Waxy gene

SNP

Starch

ABSTRACT

A set of 132 accessions of common millet, *Panicum miliaceum* L., from 12 provinces of China were assessed for endosperm starch type (waxy or non-waxy) using I₂-KI staining, amylose and amylopectin contents using the dual-wavelength colorimetric method, and genotype of Waxy genes conditioning amylose content by gene sequencing. Endosperm starch content varied from 57.69% to 74.70%, while the amylose and amylopectin contents of the starch ranged from 0 to 23.29% and from 41.99% to 70.24%, respectively. Sequencing two Wx genes, including Wx-L (intron 5–exon 7 and intron 8–9) and Wx-S (exon 9–intron 10) revealed several polymorphisms (S₀, S₋₁₅, L_C, L_F, L_Y). Marker M5-R11 linking to the Wx-S gene may be used to discriminate waxy common millet accessions from non-waxy ones. Among the 132 accessions, 68 with the S₋₁₅ allele had waxy endosperm starch with the amylose content range 0–2.58% and 64 accessions with the S₀ allele had non-waxy endosperm starch with amylose content range 3.94%–23.29%. Five genotypes including S₋₁₅/L_F (45% of the accessions), S₀/L_F (25%), S₀/L_Y (12%), S₀/L_C (11%), and S₋₁₅/L_Y (7%) were identified. Six new SNPs were detected at the Wx-L locus. These results will facilitate common millet breeding, especially of cultivars free of amylose.

© 2018 "Crop Science Society of China and Institute of Crop Science, CAAS". Production and hosting by Elsevier B.V. on behalf of KeAi Communications Co., Ltd. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

1. Introduction

Starch is an important component of the endosperm in cereal grain, and is composed of amylose and amylopectin. Many cereals are rich in amylopectin [1–11]. High-amylopectin

kernels of waxy sorghum [*Sorghum bicolor* (L.) Moench] have high economic value in the food and bioenergy industries because of their increased starch digestibility and higher ethanol conversion rate compared with those of wild-type sorghum [1]. High-amylopectin grains of waxy common millet

* Corresponding authors.

E-mail addresses: wry925@126.com, (R. Wang), nkypzs@126.com. (Z. Qiao).

Peer review under responsibility of Crop Science Society of China and Institute of Crop Science, CAAS.

¹ These authors contributed equally to this work.

<https://doi.org/10.1016/j.cj.2018.02.004>

2214-5141 © 2018 "Crop Science Society of China and Institute of Crop Science, CAAS". Production and hosting by Elsevier B.V. on behalf of KeAi Communications Co., Ltd. This is an open access article under the CC BY-NC-ND license (<http://creativecommons.org/licenses/by-nc-nd/4.0/>).

Please cite this article as: R. Wang, et al., Waxy allelic diversity in common millet (*Panicum miliaceum* L.) in China, The Crop Journal (2018), <https://doi.org/10.1016/j.cj.2018.02.004>

show high adhesiveness after cooking, properties that are preferred by people of East Asia [2]. Amylose content affects the edible quality of the grain: waxy starch has a lower amylose content, resulting in a glutinous nature. For this reason, waxy types are preferred, and non-waxy types contain a higher amylose content. Waxy and non-waxy endosperm occur in many plants including rice (*Oryza sativa*), wheat (*Triticum aestivum*), maize (*Zea mays*), barley (*Hordeum vulgare*), foxtail millet [*Setaria italica* (L.) P. Beauv] and Job's tears (*Coix lacryma-jobi* L.) [3–11]. In rice, a G–T mutation at the fifth splicing site of the first intron of the Waxy (Wx) gene was associated with low amylose content and glutinous phenotype [5,12]. In wheat, an insertion of a 173-bp transposable element in Wx-A1b was detected [4,13]. In maize, DNA insertions of 1–131 bp and five spontaneous deletions were determined and insertion of transposable elements resulted in the expression of the Wx gene [3]. In barley, a C (nucleotide 2453) to T mutation in the fifth exon, as well as 191-bp and 15-bp insertions in the first intron and second exon, respectively, together with the deletion of a 403-bp sequence of Wx gene, were detected in waxy endosperm accessions. These alterations gave rise to waxy protein expression and produced an amylose-free phenotype [7,14–16]. Four classes of Wx alleles, Wx (a)–Wx (d), have been generated in sorghum [1,6]. Among them, a Glu/His polymorphism was detected at the Wx locus in the waxy line BTxARG1. The Wx (c) allele has a G deletion at the 5' splicing site of the ninth intron, causing a shift of the 5' cleavage position, and the resulting reading frame shift led to premature translation termination. The Wx (d) allele contains a mutation at the splice site of the 10th intron, leading to a splicing site shift and the deletion of five amino acids (GTGKK). All of the above mutations in the Wx gene contributed to the waxy phenotype. In foxtail millet, seven kinds of transposons inserted in the Wx gene were detected in several waxy endosperm phenotypes [9,10]. Types IV, IVa, and IVb harbored TSI-2, TSI-4&TSI-2, TSI-5&TSI-2, respectively, in the first intron [9,10]. Type VII harbored TSI-9 in the 10th exon [9,10]. Type VIII was characterized by TSI-11&TSI-10 in the 12th intron [10]. Types V and X were characterized by TSI-7 and TSI-8, respectively, in the third exon [9,10]. In Job's tears, a 275-bp deletion in exons 10–11 of the Wx gene was detected, corresponded to the amylose-free phenotype, and caused a lack of the Wx protein [11].

Common millet originated in China and is widely grown in the northern part of the country. It is drought-resistant and plays an important role in local people's daily life and diet. Many studies of this crop have focused on genetic diversity, common millet-specific SSR marker development, and drought-induced transcription [17–21], but research into the starch properties of this minor grain crop has lagged behind. Previous studies have revealed starch contents ranging from 67.6% to 75.1% in common millet [22]. Common millet is tetraploid with $2n = 4x = 36$ and carries two Wx loci, as revealed by crossing experiments and DNA sequencing of lines [2,23]. The waxy trait is controlled by the Wx gene, which encodes the GBSSI enzyme regulating amylose synthesis. Graybosch and Baltensperger [2] found that the amylose content of waxy endosperm starch was 3.5% and that the waxy trait was controlled by the recessive alleles *wx-1/wx-2*; the amylose content of non-waxy endosperm starch was

25.3%, and the non-waxy trait was controlled by the dominant alleles Wx-1 and Wx-2. Hunt et al. [23] named the two Wx loci Wx-S and Wx-L and identified five alleles: S₀, S₋₁₅, L₀, L_F, and L_Y. Starch composition and protein function assays showed that these two loci were responsible for amylose content and reduced synthesis capacity of GBSSI protein [24]. However, only 17 accessions from China were investigated in that study.

A total of 9885 germplasm resources are maintained in the National Gene Bank of the Institute of Crop Science, Chinese Academy of Agricultural Sciences (Beijing, China). There may be new alleles at the Wx locus. To further elucidate the genetic regulation of starch production, we assessed the genotypes and phenotypes of 132 common millet accessions from different provinces of China. New single-nucleotide polymorphisms (SNPs) identified in the process could enhance our understanding of the genomic regulation of starch properties in this old species.

2. Materials and methods

2.1. Plant materials and endosperm type evaluation

Table 1 describes the 132 common millet accessions originating in 12 provinces of China (Table S1). Seeds of each accession were sown in plastic pots (diameter, 10 cm), and grown under greenhouse conditions at the experimental station of the Agronomy College, Shanxi Agricultural University (37°25'N, 112°35'E), Taigu, Shanxi, China. The endosperm type (waxy or non-waxy) was determined by an iodine color reaction using milled grain. Five seeds obtained from self-pollinated plants were cracked and soaked in a 3% KI and 1% I₂ solution, and the non-waxy and waxy phenotypes in the endosperm starch were classified by their blue-black and reddish-brown colors, respectively.

2.2. Measurement of amylose and amylopectin contents

The amylose and amylopectin contents of starch were detected using a dual-wavelength colorimetric method [22]. The absorbance of the solution was measured with a UV1601 spectrophotometer (Ruili Corp., Beijing, China), detection wavelengths of amylose and amylopectin were evaluated at

Table 1 – The types of starch in the endosperm of common millet.

Type	Amylose content (%)	Number of accessions
Waxy germplasm with high nutritional quality and palatability	0 <0.5	2
Waxy germplasm	<3.7	68
Non-waxy germplasm with high nutritional quality and palatability	3.7–7.5	11
Non-waxy germplasm	3.7–21.9	64

The types are classified as described previously [28,29].

Download English Version:

<https://daneshyari.com/en/article/8408665>

Download Persian Version:

<https://daneshyari.com/article/8408665>

[Daneshyari.com](https://daneshyari.com)