

Supporting information

Amplification refractory mutation system (ARMS)-PCR for waxy sorghum authentication with single-nucleotide resolution to avoid contaminants

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Table S1. Oligonucleotide sequences

Name	Sequences (5' to 3')
Wxt F0	CAAATACGACGTGTCAACGG
Wxt F1	CAAATACGACGTGTCAACTG
Wxt F2	CAAATACGACGTGTCAAAGG
Wxt F3	CAAATACGACGTGTCAACAG
Wxt F4	CAAATACGACGTGTCACCGG
Wxc F0	CAAATACGACGTGTCAACGT
Wxc F1	CAAATACGACGTGTCAACTT
Wxc F2	CAAATACGACGTGTCAACCT
Wxc F3	CAAATACGACGTGTCAAAGT
Wxc F4	CAAATACGACGTGTCAACAT
R1	TTGTTGCACTCAGAACCAGC

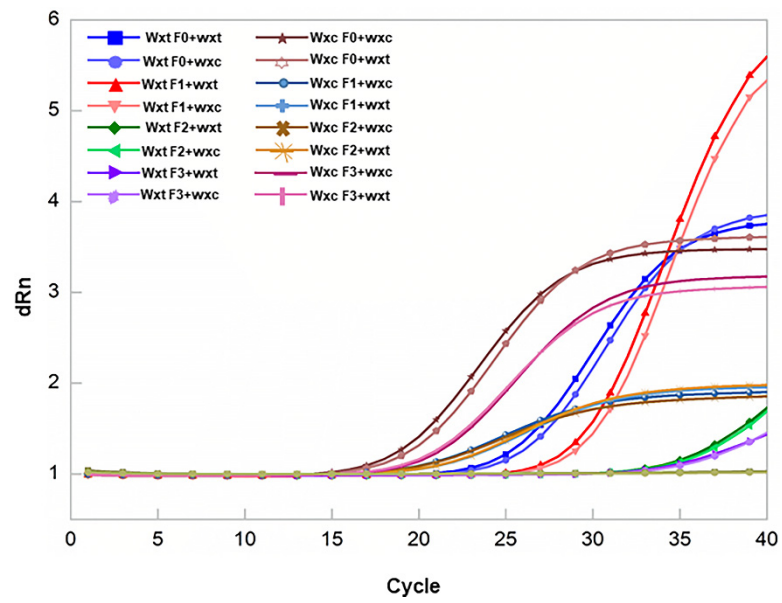


Figure S1. Primers screening. Several allele-specific forward primers designed for wx^c waxy sorghum and non- wx^c sorghum were used for qPCR amplification.

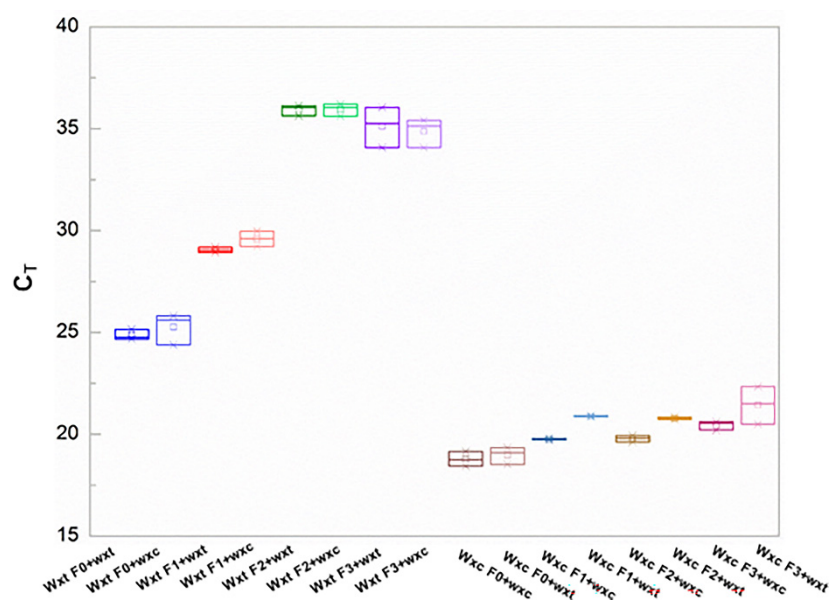


Figure S2. C_T values of qPCR amplification for screening primers that specifically identified wx^c waxy sorghum and non-wx^c sorghum. The allele-specific forward primers wx^c F0,F1,F2,F3 and wx^c F0, F1, F2 and F3 designed for wx^c waxy sorghum and non-wx^c sorghum could not specifically identify wx^c waxy sorghum or non-wx^c sorghum.

Hongyingzi.seq CTTTTGACATGTGTCTTGGTTTCTTCTGAAACTGACTGGTTGCCACTTTTCACATACTAGACGGCTTTCTGCATCCACAACTCTCTACCA@GGCAGGTTGGCTTCTGGGACTTCCCGGAGCTGAACCTCCCTGAGAGATTCAA 150
Jinnuoliang No.6.seq CTTTTGACATGTGTCTTGGTTTCTTCTGAAACTGACTGGTTGCCACTTTTCACATACTAGACGGCTTTCTGCATCCACAACTCTCTACCA@GGCAGGTTGGCTTCTGGGACTTCCCGGAGCTGAACCTCCCTGAGAGATTCAA 150
L204.seq CTTTTGACATGTGTCTTGGTTTCTTCTGAAACTGACTGGTTGCCACTTTTCACATACTAGACGGCTTTCTGCATCCACAACTCTCTACCA@GGCAGGTTGGCTTCTGGGACTTCCCGGAGCTGAACCTCCCTGAGAGATTCAA 150

Hongyingzi.seq GTCATCCTTCGATTTTCATCGACGGGTATGCAATGAATGGGCAAACTGCAATCTATCAACTATTTTTTCATCAATGGTATTGGGTTAACATAAGGTGACATGAATGTAA@CCCA@CTGGTTTGATTGCAGCTACGAGAACCCGTTGGAG 300
Jinnuoliang No.6.seq GTCATCCTTCGATTTTCATCGACGGGTATGCAATGAATGGGCAAACTGCAATCTATCAACTATTTTTTCATCAATGGTATTGGGTTAACATAAGGTGACATGAATGTAA@CCCA@CTGGTTTGATTGCAGCTACGAGAACCCGTTGGAG 300
L204.seq GTCATCCTTCGATTTTCATCGACGGGTATGCAATGAATGGGCAAACTGCAATCTATCAACTATTTTTTCATCAATGGTATTGGGTTAACATAAGGTGACATGAATGTAA@CCCA@CTGGTTTGATTGCAGCTACGAGAACCCGTTGGAG 300

Hongyingzi.seq GCCGGAAGATCAACTGGATGAAGGCCGGGATCTTGAAGCCGACAGGGTCTTCACCGTGAGCCCTACTAGCGGAGGAGCTCATCTCGGCATCGCCAGGGGCTGGAGACTCGACAMCATCATGGGCTCACCGGCATCACCGGGATCG 450
Jinnuoliang No.6.seq GCCGGAAGATCAACTGGATGAAGGCCGGGATCTTGAAGCCGACAGGGTCTTCACCGTGAGCCCTACTAGCGGAGGAGCTCATCTCGGCATCGCCAGGGGCTGGAGACTCGACAMCATCATGGGCTCACCGGCATCACCGGGATCG 450
L204.seq GCCGGAAGATCAACTGGATGAAGGCCGGGATCTTGAAGCCGACAGGGTCTTCACCGTGAGCCCTACTAGCGGAGGAGCTCATCTCGGCATCGCCAGGGGCTGGAGACTCGACAMCATCATGGGCTCACCGGCATCACCGGGATCG 450

Hongyingzi.seq TCAACGGCATGGAGCTCAGGAGTGGGATCCAGCAAGGACAGTACATCGCGCTCAATAAGAGCTGTCAAC@GAGACTTTGGCAATTGTTGCTACTCTGCTCATGTAAATCTTTCAAGGCGCTGGTTCTGAGTGCACAAATGTCCAT 600
Jinnuoliang No.6.seq TCAACGGCATGGAGCTCAGGAGTGGGATCCAGCAAGGACAGTACATCGCGCTCAATAAGAGCTGTCAACG@TGAGCTTTGGCAATTGTTGCTACTCTGCTCATGTAAATCTTTCAAGGCGCTGGTTCTGAGTGCACAAATGTCCAT 600
L204.seq TCAACGGCATGGAGCTCAGGAGTGGGATCCAGCAAGGACAGTACATCGCGCTCAATAAGAGCTGTCAACG@TGAGCTTTGGCAATTGTTGCTACTCTGCTCATGTAAATCTTTCAAGGCGCTGGTTCTGAGTGCACAAATGTCCAT 600

Figure S3. Partial DNA sequence information about ‘Hongyingzi’, ‘Jinnuoliang No.6’ and

‘Jin 204’. ‘Hongyingzi’ was wx^c, and ‘Jinnuoliang No.6’ was wx^b, and the ‘Jin 204’ was wild.

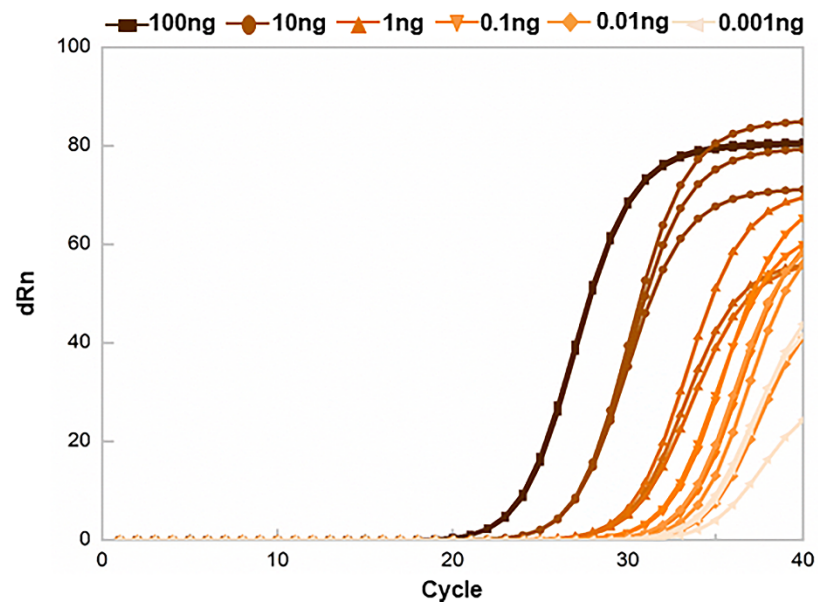


Figure S4. The amplification curves of '*Hongyingzi*' DNA samples that were continuously ten-fold diluted from 100.0 ng to 1.0 pg.

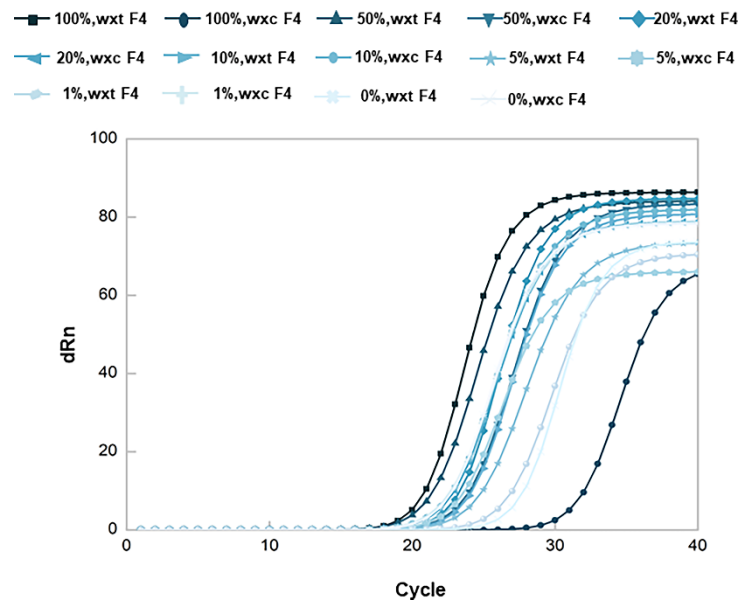


Figure S5. Amplification curves of 'Jinnuoliang No.6' with different content ratios in mixtures.