

Table S1. List of qRT-PCR primer sequences for validation of candidate genes.

Gene	Gene ID (Glyma.Wm82. Gnm4)	Primer (5' – 3')	Annealing temperature	Purpose
GmUKN1		Forward primer (5' → 3') : TGGTGCTGCCGCTATTTACTG Reverse primer (5' → 3') : GGTGGAAGGAACTGCTAACAATC		qRT-PCR
03g171500	Glyma03G171500	Forward primer (5' → 3') : GCATGTATCCACGGCCCAAA Reverse primer (5' → 3') : GTGGGACCGGCTGAAGAAAG	60	qRT-PCR
03g171600	Glyma03G171600	Forward primer (5' → 3') : GGATTACTGGCTTCCCGCTT Reverse primer (5' → 3') : ACAACCTCCATCTTCAAATTCATCT	60	qRT-PCR
03g171700	Glyma03G171700	Forward primer (5' → 3') : ATGGCAGGAGACTGTGGAGT Reverse primer (5' → 3') : TCCCAGCTCTTCATTCCCGT	60	qRT-PCR

Table S2. SNP markers used for linkage mapping.

Chr.	Marker no.	Length (cM)	Average spacing (cM)	Chr.	Marker no.	Length (cM)	Average spacing (cM)
1	73	151.7	2.1	11	80	172.1	2.2
2	101	200.8	2.0	12	68	91.2	1.3
3	47	57.6	1.2	13	88	166.1	1.9
4	54	141.7	2.6	14	92	124.7	1.4
5	91	125.9	1.4	15	38	84.4	2.2
6	71	121.3	1.7	16	36	79.9	2.2
7	72	104.9	1.5	17	36	96.4	2.7
8	66	95.9	1.5	18	109	109.5	1.0
9	94	151.8	1.6	19	97	145.3	1.5
10	82	168.1	2.1	20	57	133.8	2.3
				Total	1452	2523.1	1.7

Table S3. Summary of genome re-sequencing and DNA sequence variants identified in Kwangan, KA-1285, and PI483463.

	Kwangan	KA-1285	PI483463
Total reads	197,216,576	231,945,086	152,115,370
Average sequence length (bp)	151	151	90
Total size (Mb)	29,779	35,024	13,690
Sequencing depth (X)	27.07x	31.84 x	12.45x
Mapped reads	179,874,598	220,303,485	139,426,290
Genome coverage (%)	95.56	95.67	92.62
Number of SNPs	1,675,560	1,675,675	3,105,458
Number of indels	335,327	334,039	613,605
Total variation	2,010,887	2,009,714	3,719,063

