

Supplementary Materials

Supplementary Table S1. QTLs associated with WBPH resistance in the CNDH populations.

Characteristics	Year	QTLs	Chromosome	Interval Markers ^z	LOD	Additive effect ^y	R^2 ^x	Increasing effects ^w
Resistant score	2018	<i>qWBPH1</i>	1	RM3482-RM11966	4.0	-0.3	0.3	Nagdong
		<i>qWBPH1-1</i>	1	RM3709-RM11694	3.5	0.3	0.3	Cheongcheong
		<i>qWBPH1-2</i>	1	RM11694-RM11669	3.3	0.5	0.3	Cheongcheong
		<i>qWBPH4</i>	4	RM280-RM127	3.2	1.1	0.3	Cheongcheong
		<i>qWBPH8</i>	8	RM17699-RM264	3.3	0.7	0.3	Cheongcheong
	2019	<i>qWBPH4-1</i>	4	RM280-RM6909	3.5	1.1	0.3	Cheongcheong
		<i>qWBPH7</i>	7	RM248-RM1134	3.0	1.2	0.3	Cheongcheong

^zInterval markers are those within the significance threshold on each border of the QTL range; ^yThe proportion of evaluated phenotypic change attributable to a particular QTL was estimated using the coefficient of determination (R^2); ^x Positive values of the additive effect indicate that alleles from Cheongcheong are in the direction of increasing the traits; ^w Increase allele is the source of the allele that causes an increase in the measured trait.

Supplementary Table S2. Twenty-seven candidate genes identified between RM280 and RM6909 markers and their ORFs, which include various proteins associated with WBPH resistance.

Function	Chr.	Gene locus	Description
Cell function	4	<i>LOC_Os04g55090</i>	Protein prenyltransferase domain containing protein.
	4	<i>LOC_Os04g57670</i>	Protein prenyltransferase domain containing protein.
	4	<i>LOC_Os04g57900</i>	Protein prenyltransferase domain containing protein.
	4	<i>LOC_Os04g58980</i>	Protein prenyltransferase domain containing protein.
Kinase	4	<i>LOC_Os04g55620</i>	Protein kinase domain containing protein.
	4	<i>LOC_Os04g56060</i>	Protein kinase-like domain containing protein.
	4	<i>LOC_Os04g56110</i>	Protein kinase-like domain containing protein.
	4	<i>LOC_Os04g56360</i>	Protein kinase-like domain containing protein.
	4	<i>LOC_Os04g56530</i>	Protein kinase-like domain containing protein.
	4	<i>LOC_Os04g58990</i>	Protein kinase domain containing protein.
Signaling	4	<i>LOC_Os04g55230</i>	Tetratricopeptide-like helical domain containing protein.
	4	<i>LOC_Os04g55240</i>	VQ domain containing protein.
	4	<i>LOC_Os04g55440</i>	Leucine-rich repeat, plant specific containing protein.
	4	<i>LOC_Os04g56680</i>	Auxin responsive SAUR protein family protein.
	4	<i>LOC_Os04g56690</i>	Auxin responsive SAUR protein family protein.

	4	<i>LOC_Os04g57430</i>	Leucine-rich repeat, plant specific containing protein.
	4	<i>LOC_Os04g57660</i>	Leucine rich repeat, N-terminal domain containing protein.
	4	<i>LOC_Os04g57940</i>	Tetratricopeptide-like helical domain containing protein.
	4	<i>LOC_Os04g58080</i>	Leucine-rich repeat, plant specific containing protein.
	4	<i>LOC_Os04g58180</i>	WD40-like domain containing protein.
Secondary Metabolite	4	<i>LOC_Os04g56700</i>	Similar to Naringenin,2-oxoglutarate 3-dioxygenase (EC 1.14.11.9) (Flavanone 3- hydroxylase)
	4	<i>LOC_Os04g56950</i>	Similar to S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase-like protein.
Transcription factor	4	<i>LOC_Os04g55510</i>	Zinc finger, RING-type domain containing protein.
	4	<i>LOC_Os04g55560</i>	Pathogenesis-related transcriptional factor and ERF domain containing protein.
	4	<i>LOC_Os04g56750</i>	Zinc finger, CCCH-type domain containing protein.
	4	<i>LOC_Os04g57010</i>	Zinc finger, CCCH-type domain containing protein.
	4	<i>LOC_Os04g57600</i>	Zinc finger, CCCH-type domain containing protein.

Supplementary Table S3. WBPH resistance gene-specific primers for qRT-PCR.

Gene		Sequence (5' to 3')	GC contents (%)	Annealing T _m (°C)	Product size (bp)
<i>F3H</i>	Forward	TTCTCGTACCCGGTGAAGTC	55	59.5	84
	Reverse	GCTGTACTGCTCCACCACTG	60	59.5	
<i>PAL1</i>	Forward	TGCACGGTGGCAACTCCAG	60	59.5	95
	Reverse	CTGCGCGAACATGAGCTTGC	60	59.5	
<i>NPR1</i>	Forward	CCGAGCTTTTGGATCTCGCAC	57	59.8	85
	Reverse	TTTAGGCTCTCTTCGCCTCGC	57	59.8	
<i>EIN2</i>	Forward	GCAGCTCCCTTGGCGTTTGA	60	59.5	89
	Reverse	CTTGCACTTGGGTTTGGGCTTTG	52	60.2	
<i>PRB1</i>	Forward	CGAGAACCTGTCGTGGAACC	60	59.5	91
	Reverse	GTAGTCGTAGGAGCCCTTCTC	57	59.8	
<i>HPL3</i>	Forward	CAGCAAGGAGGAGGCCATCA	60	59.5	88
	Reverse	GACCAGGAACGGCAGGAACA	60	59.5	
<i>WRKY45</i>	Forward	AGGACATGGAGAAGGGGAAGG	57	59.8	92
	Reverse	GAGAATCTGGTCGACGAAGCG	57	59.8	
<i>COI1</i>	Forward	GCTGCACCTCGTGATGGGC	68	61.4	92
	Reverse	TGAGCGCGTCGATGCGGTG	68	61.4	
<i>CAS</i>	Forward	ACGACAGGCAGGAGGCCAAT	60	59.5	93
	Reverse	CCAGCTCCATCTCCGCGAAAA	57	59.8	