Appendix A primer sequences of genes encoding resistance related proteins

NO.	Protein accession	Gene ID	Protein name	Forward	Reverse
1	A0A1D5UVU1	TraesCS2D02G073900	Transketolase	GAACCGAGACTTCTGCTGCT	TAGCAACGCCTTCAACCGAT
2	A0A3B6B2F0	TraesCS2A02G350700	Chitinase	CCGACGCCTACTGTGGAAAA	CGGGACTTGATCCCGTTGAA
3	A0A3B6JK87	TraesCS4D02G174700	2,3-bisphosphoglycerate	ATCCCAAGGCCAATGACCAG	CGTCTCCATCCACTATGGGC
4	A0A3B6NJN5	TraesCS6A02G018200	Glycosyltransferase	GTGGAAGGAGAAAGCGGTCA	TACCCAGAGCGGCTAGGAG
5	A0A3B6MWA0	TraesCS5D02G388800	Lipoxygenase	GACCACCACGACCACATGAT	GCCGTCACCTTTCAGGAAGA
6	A0A3B6B887	TraesCS2A02G573900	Peroxidase	AGCAACATGGACCTCCTCAC	CTCGATATCCTGGACACGCC
7	A0A3B5Y7F7	TraesCS1A02G424100	Berberine bridge enzyme	CTGTCGTGGAAGGAGATGGC	TCTTGCATGAGCCGATGGAG
8	A0A077RNT9	TraesCS3B02G004500	Isoflavone reductase	AGAGCCGGATCTCCTCAAGT	CTCGACACCAAAGGATGGCT
9	AWS00780.1	MF405765.1	TaActin	TGGATCGGAGGGTCCATCTT	GAAGCACTTCCTGTGGACGA

Appendix B Enriched biological processes in the two varieties after inoculation

Time Point	Sample	GO（Biological Process）	P.value	Up regulated proteins	Down regulated proteins
24 hpi	Xinmai 26	glycerophospholipid metabolic process	0.017515628	A0A3B6EIE9 W5CPW0	A0A3B6QCS8
		glycerolipid biosynthetic process	0.02282289	A0A3B6EIE9 W5CPW0	
		glycerolipid metabolic process	0.023372686	A0A3B6EIE9 W5CPW0	A0A3B6QCS8
		dephosphorylation	0.033911506		A0A3B6QCS8 D8L9K9 W5C050
		phospholipid metabolic process	0.039961311	A0A3B6EIE9 W5CPW0	A0A3B6QCS8
		oxidoreduction coenzyme metabolic process	0.043820096	A0A3B6MUF0	A0A3B6TMY1 W5FL09 A0A3B6RJK8 W5G4A2
		phospholipid biosynthetic process	0.046745614	A0A3B6EIE9 W5CPW0	
	04 Zhong 36	aminoglycan catabolic process	0.002114396	A0A3B6B2F0 Q4Z8L8 A0A3B6GXR9	
		amino sugar catabolic process	0.002114396	A0A3B6B2F0 Q4Z8L8 A0A3B6GXR9	
		chitin metabolic process	0.002114396	A0A3B6B2F0 Q4Z8L8 A0A3B6GXR9	
		glucosamine-containing compound metabolic process	0.002114396	A0A3B6B2F0 Q4Z8L8 A0A3B6GXR9	
		glucosamine-containing compound catabolic process	0.002114396	A0A3B6B2F0 Q4Z8L8 A0A3B6GXR9	
		cell wall macromolecule catabolic process	0.002114396	A0A3B6B2F0 Q4Z8L8 A0A3B6GXR9	
		protein-DNA complex assembly	0.021122854		A0A3B6KRY8 A0A3B5Z6V4
		nucleosome organization	0.021122854		A0A3B6KRY8 A0A3B5Z6V4
		chromatin assembly or disassembly	0.022627029		A0A3B6KRY8 A0A3B5Z6V4
		DNA packaging	0.024174271		A0A3B6KRY8 A0A3B5Z6V4
		cell wall macromolecule metabolic process	0.024529982	A0A3B6B2F0 Q4Z8L8 A0A3B6GXR9	
		DNA conformation change	0.049928101		A0A3B6KRY8 A0A3B5Z6V4

Appendix B Enriched biological processes in the two varieties after inoculation

Time Point	Sample	GO（Biological Process）	P.value	Up regulated proteins	Down regulated proteins
48 hpi	Xinmai 26	glycerolipid biosynthetic process	0.02282289	A0A3B6EIE9 W5CPW0	
		hydrogen transport	0.02812331		P06528A0 A3B6HQK1 B2B9U2 A0A3B6TRT4
		monovalent inorganic cation transport	0.040614224		P06528A0 A3B6HQK1 B2B9U2 A0A3B6TRT4
		regulation of proteolysis	0.042930621		W5D700 A0A077RFQ1
		phospholipid biosynthetic process	0.046745614	A0A3B6EIE9 W5CPW0	
		negative regulation of hydrolase activity	0.046745614		W5D700 A0A077RFQ1
	04 Zhong 36	aminoglycan catabolic process	7.64261E-05	A0A3B5ZUP1 A0A3B6B2F0 A0A3B5ZVX5 A0A3B6GXR9 A0A3B5Y2G4	
		amino sugar catabolic process	7.64261E-05	A0A3B5ZUP1 A0A3B6B2F0 A0A3B5ZVX5 A0A3B6GXR9 A0A3B5Y2G4	
		chitin metabolic process	7.64261E-05	A0A3B5ZUP1 A0A3B6B2F0 A0A3B5ZVX5 A0A3B6GXR9 A0A3B5Y2G4	
		glucosamine-containing compound metabolic process	7.64261E-05	A0A3B5ZUP1 A0A3B6B2F0 A0A3B5ZVX5 A0A3B6GXR9 A0A3B5Y2G4	

Appendix B Enriched biological processes in the two varieties after inoculation

Time Point	Sample	GO（Biological Process）	P.value	Up regulated proteins	Down regulated proteins
48 hpi	04 Zhong 36	glucosamine-containing compound catabolic process	7.64261E-05	A0A3B5ZUP1 A0A3B6B2F0 A0A3B5ZVX5 A0A3B6GXR9 A0A3B5Y2G4	
		cell wall macromolecule catabolic process	7.64261E-05	A0A3B5ZUP1 A0A3B6B2F0 A0A3B5ZVX5 A0A3B6GXR9 A0A3B5Y2G4	
		cell wall macromolecule metabolic process	0.000754478	A0A3B5ZUP1 A0A3B6B2F0 A0A3B5ZVX5 A0A3B6GXR9 A0A3B5Y2G4	A0A3B6JS11
		cellular oxidant detoxification	0.003750717	A0A1D5UL37 D0PRB4	Q43206 Q5S1S6
		cellular detoxification	0.003750717	A0A1D5UL37 D0PRB4	Q43206 Q5S1S6
		hydrogen peroxide catabolic process	0.01924246	A0A3B6CH98 A0A1D5UL37 A0A3B6FYA0 A0A3B6B887	Q43206 A0A3B6DFB4
		glycerolipid biosynthetic process	0.019694865	A0A3B6EIE9 W5CPW0	
		regulation of proteolysis	0.037219197	A0A077RPC2	P01085
		phospholipid biosynthetic process	0.040557745	A0A3B6EIE9 W5CPW0	
		negative regulation of hydrolase activity	0.040557745	A0A077RPC2	P01085
72 hpi	Xinmai 26	lipid transport	0.006364163	A0A3B6HVU8 A0A3B6JF64 A0A3B6IRG5	

Appendix B Enriched biological processes in the two varieties after inoculation

Time Point	Sample	GO（Biological Process）	P.value	Up regulated proteins	Down regulated proteins
72 hpi	Xinmai 26	polysaccharide catabolic process	0.000459921		A0A3B6IYD4 A0A3B6U9P0 A0A3B6C4B2
		regulation of proteolysis	0.013953072		W5D700 P01085
		negative regulation of hydrolase activity	0.015263691		W5D700 P01085
		negative regulation of protein metabolic process	0.018036625		W5D700 P01085
		negative regulation of cellular metabolic process	0.022561212		W5D700 P01085
		regulation of cellular protein metabolic process	0.048808082		W5D700 P01085
72 hpi	04 Zhong 36	response to water deprivation	0.013826072	A0A3B6ED63 A0A3B6GU21	
		response to desiccation	0.013826072	A0A3B6ED63 A0A3B6GU21	
		aminoglycan catabolic process	0.025319909	A0A3B6B2F0 A0A3B6API9 Q8W428	
		amino sugar catabolic process	0.025319909	A0A3B6B2F0 A0A3B6API9 Q8W428	
		chitin metabolic process	0.025319909	A0A3B6B2F0 A0A3B6API9 Q8W428	
		glucosamine-containing compound metabolic process	0.025319909	A0A3B6B2F0 A0A3B6API9 Q8W428	
		glucosamine-containing compound catabolic process	0.025319909	A0A3B6B2F0 A0A3B6API9 Q8W428	
		cell wall macromolecule catabolic process	0.025319909	A0A3B6B2F0 A0A3B6API9 Q8W428	
		hexose metabolic process	0.038498358	A0A3B6JJ78 A0A3B6JK87 A0A3B6CCY3	A0A1D5TTT2
		regulation of signal transduction	0.041953732	A0A3B6JCK6	A0A3B6SMF7

Appendix C Enriched KEGG pathways in the two varieties after inoculation

Time Point	Sample	KEGG pathway	P.value	Up regulated proteins	Down regulated proteins
24 hpi	Xinmai 26	Glyoxylate and dicarboxylate metabolism	5.48504E-07	F1DKC1	A0A3B6LUD5 A0A3B6KNX6 A0A3B6SHQ4 A0A3B6EJX1 W5C050 A0A3B6GU52 A0A3B6C5R2 Q43206 A0A3B5ZQM6 A0A3B6KQP3
		MAPK signaling pathway - plant	0.00517315	F1DKC1 A0A3B6GXR9 A0A3B5ZVX5	Q43206 A0A3B6KQP3
		Alanine, aspartate and glutamate metabolism	0.036678158	A0A3B6ITK8 A0A3B6HQX0	A0A3B6SHQ4 A0A3B6C5R2
		Carbon fixation in photosynthetic organisms	1.48327E-07	A0A3B6MUF0	A0A1D5TTT2 A0A3B6TMY1 A0A3B6GYS8 A0A3B6RJK8 W5FL09 P26302 W5G4A2 A0A3B6JMT4 A0A3B6C5R2 D8L9K9 A0A3B6ECY0
		Pentose phosphate pathway	0.00014393	A0A3B6MUF0	D8L9K9 A0A3B6TMY1 A0A3B6DA58 A0A3B6RJK8 W5FL09
		Peroxisome	0.000931432	F1DKC1	A0A3B6KNX6 A0A3B6MVP8 A0A3B6SHQ4 Q43206 A0A3B6LUD5 A0A3B6KQP3
		Glycolysis / Gluconeogenesis	0.00497562	A0A3B6QD94	A0A3B6TMY1 A0A3B6DA58 A0A3B6RJK8 W5FL09 W5G4A2 D8L9K9 A0A3B5ZQM6
		Tryptophan metabolism	0.005404266	F1DKC1	Q43206 A0A3B5ZQM6 A0A3B6KQP3
		Fructose and mannose metabolism	0.006551911		D8L9K9 A0A3B6TMY1 A0A3B6RJK8 W5FL09 W5G4A2
		Glycine, serine and threonine metabolism	0.01466453		A0A3B6GU52 A0A3B6SHQ4 A0A3B6C5R2 A0A3B5ZQM6 A0A3B6EJX1

Appendix C Enriched KEGG pathways in the two varieties after inoculation

Time Point	Sample	KEGG pathway	P.value	Up regulated proteins	Down regulated proteins
24 hpi	Xinmai 26	Steroid biosynthesis	0.019984734	A0A3B6U6D1 A0A3B6JG02	
		Cutin, suberine and wax biosynthesis	0.02471337	A0A3B6MVP8	A0A3B5XXV3
	04 Zhong 36	Glyoxylate and dicarboxylate metabolism	0.024022461	F1DKC1 A0A3B6DQ04	A0A3B6LUD5 A0A3B6BYP2
		MAPK signaling pathway - plant	0.03888815	F1DKC1 A0A3B6GXR9 Q4Z8L8	
		Alanine, aspartate and glutamate metabolism	0.009461508	A0A3B6ITK8 A0A3B6FIG0 A0A3B6MPP1A0A3B6KEE9	
		Photosynthesis - antenna proteins	3.63608E-05		A0A1D5V1G5 A0A3B6DA68 A0A341YEW4 A0A3B5ZZE4 A0A3B6C6E5
		Arginine and proline metabolism	0.019020221	A0A3B6ELC5 A0A3B6QLG0	W5BQT6
		Nitrogen metabolism	0.030913433		A0A3B6NUX9 A0A3B6GWA0
48 hpi	Xinmai 26	Ribosome	0.014387023	A0A3B6TJ62	A0A3B6QPH2 A0A3B5XY38 A0A3B6MYX8 A0A3B6NSN4 A0A3B6QHZ8 A0A3B6QIS6 Q95H51 A0A3B6QG11 A0A3B6MXK0
		Ribosome biogenesis in eukaryotes	2.33072E-07	A0A3B6QFZ4 A0A3B6RSD0 A0A3B6SL10 A0A3B6MMB8 A0A3B6RFZ8 W5BV40 A0A3B6C277 A0A3B5Y4C6 A0A3B6ATW2 A0A1D5YA13	
		Nitrogen metabolism	0.012828293	A0A3B6JQ25	A0A3B6NUX9 Q6RUJ0

Appendix C Enriched KEGG pathways in the two varieties after inoculation

Time Point	Sample	KEGG pathway	P.value	Up regulated proteins	Down regulated proteins
48 hpi	04 Zhong 36	Ribosome	0.029796989	A0A3B6ISR9 A1YE34	A0A3B6QPH2 A0A3B5XY38 A0A3B6PPE3 A0A3B6CHH4 A0A3B6JK17 W5CQ20
		Phenylpropanoid biosynthesis	0.003698186	Q1XH05 D0PRB4 A0A3B6CH98 A0A1D5UL37 A0A3B6FYA0 A0A3B6B887	A0A3B6MSU8 A0A3B6LM09 A0A3B6DFB4
		MAPK signaling pathway - plant	0.004502871	A0A3B5ZUP1 A0A3B5ZVX5 A0A3B6GXR9 A0A3B5Y2G4	Q43206
		Taurine and hypotaurine metabolism	0.023264793	A0A3B6FIG0 W5DRS3	
		Carbon fixation in photosynthetic organisms	0.029832168	A0A3B6GYC1 A0A1D5UVU1	A0A3B6D693 A0A3B6QCR5 A0A3B6LSL8
		Oxidative phosphorylation	0.047706916	A0A3B6NIS3	Q95H60 A0A3B6NUT1 P20858 Q95H46
72 hpi	Xinmai 26	Glyoxylate and dicarboxylate metabolism	0.009444343	F1DKC1 A0A3B6PQR7 A0A3B6B901	A0A3B6GZQ6
		Cyanoamino acid metabolism	7.5843E-05	A0A3B6KSF9 D5MTF8 A0A3B6U6E7 A0A3B6MZB9	A0A3B6GZQ6
		Pyruvate metabolism	0.002813518	A0A3B6GYC1 A0A3B5YYW4 A0A3B6TNY0 A0A3B6JJ78	A0A3B6MUW2
		Alanine, aspartate and glutamate metabolism	0.025400133	A0A3B6FIG0 A0A3B6MPP1 A0A3B6ITK8	
		Citrate cycle (TCA cycle)	0.028204613	A0A3B6TNY0 A0A3B6JJ78	A0A3B6MUW2
		Starch and sucrose metabolism	0.03106613	D5MTF8 D8L9G6 A0A3B6MZB9	A0A3B6QIH9

Appendix C Enriched KEGG pathways in the two varieties after inoculation

时间	品种	KEGG 途径	P 值	上调蛋白	下调蛋白
Time Point	Sample	KEGG pathway	P.value	Up regulated proteins	Down regulated proteins
72 hpi	04 Zhong 36	Glyoxylate and dicarboxylate metabolism	0.042425959	F1DKC1 A0A3B6PQR7 A0A3B6B901 A0A3B6EAD8 A0A3B6DQ04	A0A3B6KNX6
		Cyanoamino acid metabolism	0.048663262	A0A3B6KSF9 D5MTF8 A0A3B6C1C0	A0A3B6ERB4
		Ribosome biogenesis in eukaryotes	0.00444746	A0A3B6QFZ4 A0A3B6B461 A0A3B6JNL3 A0A3B5Y4C6 A0A3B6MMB8	A0A3B6C739
		Ribosome	0.005374167		A0A3B6HY18 P69661 A0A3B6KU60 Q95H48 A0A3B6QPH2 A0A3B6IR85 Q95H51 A0A3B5XY38 A0A3B5YQM4 A0A3B6IX07 W5D1S8 A0A3B6JJU4 A0A3B6ISN2
		Carbon fixation in photosynthetic organisms	0.00633774	A0A3B6GYC1 A0A1D5UVU1 A0A3B5XX22 A0A3B6JJ78	A0A1D5TTT2 W5E5Z3 W5FL09 A0A3B6QCR5
		Flavonoid biosynthesis	0.032110756	Q0WYI8	A0A3B6KG55 A0A3B6MP18