

Supplementary Table 1 Overview of molecular markers, QTLs and candidate genes/proteins involved in PM, DM and FW resistance in cucumber.

Disease	Causal agent	Typical symptoms	Resistance donor	Mapping Population	QTLs / candidate genes/proteins	Involved pathways	Function verification	References
Powdery mildew	<i>Podosphaera xanthii</i> (<i>Sphaerotheca fuliginea</i>) and <i>Golovinomyces cichoracearum</i> (<i>Erysiphe cichoracearum</i>)	mainly invades cotyledon, leaves and stems occur in the whole development period of cucumber, and the disease is serious in the middle and late stages of plant growth, resulting in yellow leaves, crisp and dry, seriously affecting the photosynthesis of cucumber leaves and	WI 2757 and True Lemon H136 and BK2 S1003 and S1001 H136 and BK2	F _{2:3} populations F ₂ population F ₂ population F ₂ population	<i>Pm1.1</i> and <i>Pm1.2</i> for leaf resistance; <i>pm3.1</i> and <i>pm4.1</i> for leaf or hypocotyls; <i>pm5.1</i> for cotyledon, <i>pm5.2</i> for hypocotyl <i>pm5.3</i> and <i>pm6.1</i> <i>pm5.1</i> <i>Pm1.1</i> , <i>pm6.1</i>	- - - defense response, toxin metabolism, cell stress response,	- - - -	He et al., 2013 Zhang et al., 2015 Nie et al., 2015 Zhang et al., 2015

reducing yield.	cucumber					and injury response	
	PI 197088	and	RILs population	<i>pm1.1, pm2.1, pm5.1,</i>	-	-	Wang et al., 2018
	Coolgreen			<i>pm6.1</i>			
	a cucumber	core	-	<i>pmG1.1,</i>	<i>pmG1.2,</i>	-	Liu et al., 2021
	germplasm			<i>pmG2.1, pmG2.2,</i>			
	(CG) consisting of 94			<i>pmG3.1,</i>	<i>pmG4.1,</i>		
	resequenced lines			<i>pmG4.2,</i>	<i>pmG5.1,</i>		
				<i>pmG5.2,</i>	<i>pmG5.3,</i>		
				<i>pmG5.4,</i>	<i>pmG6.1,</i>		
				and <i>pmG6.2</i>			
	SSSL0.7 and Jin5-508		F ₂ population	<i>Pm1.1</i>	cysteine-rich	-	Xu et al., 2016
				(<i>Csa1M064780</i> and	receptor-like		
				<i>Csa1M064790</i>)	protein kinase		
	NCG122 and NCG121		F ₂ population	<i>pm-s</i> (Csa5G623470)	encoding	-	Liu et al., 2017
					Mlo-related		
					protein.		

Changchunmici IL52	and	F ₂ and RILs	<i>Pm/dm5.2</i> , <i>Csa5M622830.1</i>	encodes a transcriptional factor	-	Zhang et al., 2018
PM-R and PM-S		F ₂ populations	<i>pm5.2</i> and <i>pm6.1</i> , <i>CsGy5G015660</i>	encoding a putative leucine-rich repeat receptor-like serine/threonine-protein kinase (RPK2)	-	Zhang et al., 2021
S1003 and S05		-	<i>CsaMLO1</i>	a cell membrane protein	Ectopic expression in <i>Atmlo2 Atmlo12</i> double mutants	Nie et al., 2015
9930, cv. <i>Anaxo</i>		no	<i>CsaMLO1</i> , <i>CsaMLO8</i> , <i>CsaMLO11</i>	encode a plasma membrane-anchored	Heterologous overexpression in the	Schouten et al., 2014; Berg et

			ored protein with	tomato <i>mlo</i> mutant	al., 2017
			seven		
			transmembrane		
			helices		
SSL508-28, Jin5-508	-	8 candidate genes	encoding	-	Xu et al., 2017
and D8		underlie the <i>Pm5.1</i> (receptor protein		
		<i>Csa5G569350</i> ,	kinases,		
		<i>Csa5G606310</i> ,	transcription		
		<i>Csa5G600370</i> ,	factors, remorin		
		<i>Csa5G600380</i> ,	proteins, a		
		<i>Csa5G604040</i> ,	P-type ATPase		
		<i>Csa5G606540</i> ,	and a 70 kDa		
		<i>Csa5G606730</i> ,	heat shock		
		<i>Csa5G512930</i>)	protein.		
BK2 and H136	-	2312 DEGs	Hormone	-	Zhang et al., 2021
			signaling,		
			defense		

			response,pathog	
			en response, and	
			peroxidase,	
			NBS, glucanase	
			and chitinase	
			pathways	
XY09-118 and Q10	-	5478 DEGs	plant hormone	Zheng et al., 2021
			signal	
			transduction,	
			phenylpropanoid	
			biosynthesis,	
			plant-	
			pathogen	
			interaction and	
			the MAPK	
			signalling	
			pathway ,	

			encoding		
			WRKY, NAC		
			and TCP		
BK2 and H136	-	5832 DEGs and 971 DAMs	flavonoid, hormone, fatty acid and diterpenoid metabolisms.	-	Zhang et al., 2021
Rijiecheng	-	miR319a-JRL3, miR6300-BEE1, miR6300-DAHP1 and miR6300-PERK2	JRL3 contains three jacalin-like lectin domains, BEE1 encoded a bHLH domain, DAHP1 encodes a 3-deoxy-D-arabi no-heptulosonate	-	Xu et al., 2020

					7-phosphate		
					synthase		
S1003	and	NIL	-	119	phenylpropanoid	-	Nie et al., 2021
(<i>Pm5.1</i>)				lncRNAs and 136	biosynthesis,		
				mRNAs	phenylalanine		
					metabolism,		
					ubiquinone and		
					other		
					terpenoid-quinon		
					e		
					biosynthesis, and		
					endocytosis.		
D8 and SSL508-28.			-	<i>NRPI</i> (<i>Csa5G606550</i>	nodulin-related	-	Xu et al., 2019
)	protein 1		
XinTaiMiCi, JinYan4,			-	Cs TCTP1, Cs	Defense	Transient	Meng et al., 2018
B21-a-2-2-2,				TCTP2	response	or transformation	
B21-a-2-1-2					ABA	or TOR	

							signaling			
							pathways			
			B21-a-2-1-2	and	-	<i>CsRSF1</i> and <i>CsRSF2</i>	nucleotide-binding	transient silencing and	Wang et al., 2020	
			B21-a-2-2-2				ng	Transient		
							site-leucinerich	transformation		
							repeats			
							(NBS-LRR)			
							proteins			
Downy mildew	<i>Pseudoperonospora cubensis</i>	mainly infects leaves and can also harm stems and inflorescences. It can occur from seedling stage to adult stage, especially when cucumber enters the harvest stage.	CS-PMR1 and Santou PI 197087 and WI7120 (PI330628) and 9930 TH118FLM and WMEJ PI 197088 and	RILs F ₂ F _{2:3} population F ₂ and F _{2:3} F ₂		<i>dm1.1</i> , <i>dm5.1</i> and <i>dm5.3</i> <i>Dm1</i> , <i>Dm2</i> , <i>Dm3</i> <i>dm2.1</i> , <i>dm4.1</i> , <i>dm5.1</i> and <i>dm6.1</i> <i>dm2.2</i> , <i>dm4.1</i> , <i>dm5.1</i> , <i>dm5.2</i> , and <i>dm6.1</i> <i>dm1.1</i> , <i>dm3.1</i> , <i>dm4.1</i> ,	-	-	Yoshioka et al., 2014 Szczeczura et al., 2015 Wang et al., 2016 Win et al., 2017 Li et al., 2018	

Changchunmici			<i>dm5.1, dm5.2</i>			
CSL0067	and F ₂		<i>Cot7_5.1_1,</i>	-	-	Innark et al., 2020
CSL0139			<i>Cot7_5.1_2,</i>			
			<i>Cot10_5.1,</i>			
			<i>Cot14_5.1</i>			
			<i>First7_1.1</i>			
			<i>First7_6</i>	,		
			<i>First14_5.1_1,</i>			
			<i>First14_5.1_2,</i>			
			<i>First14_6,</i>			
			<i>Second10_6,</i>			
			<i>Second14_2,</i>			
			<i>Second14_5.1,</i>			
			<i>Second14_6,</i>			
a cucumber core	-		<i>dmG1.4, dmG4.1,</i>	-	-	Liu et al., 2020
germplasm			<i>dmG4.3, dmG5.2,</i>			
(CG) consisting of 94			<i>dmG7.1, and dmG7.2</i>			

resequenced lines						
PI 197088 and HS279	NILs	<i>subQTL DM4.1.1</i> , <i>subQTLDM4.1.2</i> , <i>subQTLDM4.1.3</i> , <i>CsLRK10L2</i>	plays a role as a receptor of the DAMP oligogalacturona n, breakdown product of pectin in the plant cell wall.	loss-of-function mutation and heterologous expression in N. benthamiana		Berg et al., 2020
Gy14 and WI2757	F _{2:3} population	<i>CsSGR</i>	in the chlorophyll degradation pathway	-		Wang et al., 2019
Changchunmici and IL57		58 unique expressed sequence tags (ESTs)	nearly the whole process of plant defense	-		Li et al., 2011

such as signal
transduction
and cell defense,
transcription,
cell cycle and
DNA
processing,
protein
synthesis,
protein fate,
proteins with
binding
functions,
transport,
metabolism and
energy

dmG1.4, was WRKY
Csa2G060360 for transcription
dmG2.1, factor
Csa4G064680 for
dmG4.1,
Csa5G606470 for
dmG5.2, and
Csa7G004020 for
dmG7.1

IL53 and IL51 F₂ population Different expressed multiple Gao et al., 2021
genes functions of
defense
response:
pathogen-associa
ted molecular
pattern
recognition,

			signal	
			transduction,	
			reactive oxygen	
			species and	
			lignin	
			accumulation,	
			and transcription	
			regulators.	
Jinyou Sihao and -	17	differentially	enhanced energy	Sun et al., 2021
Changchun Mici		expressed proteins	supply and	
			resistance	
			related proteins,	
			balanced ROS	
			production and	
			clearance,	
			accelerated	
			protein	

				metabolism and photorespiration The function of reducing photosynthesis, inducing photosystem repair and programmed cell death.		
9930	-	13 <i>ZF-HD</i> genes(<i>Cs</i> <i>MIF1-CsMIF3</i> , <i>CsZHD1-CsZHD10</i>)	Zinc	-	Lai et al., 2021	
			finger-homeodo main (ZF-HD) proteins encode a family of plant-specific transcription			

							factors	
			PI 197088 and -			different expressed of	hormones and -	Burkhardt and
			Vlaspik			mRNA and siRNA	regulation of	Day 2016
							nutrient supply	
			R1461	-		<i>CsIVP</i>	a negative RNAi	Yan et al., 2020
							regulator in SA	
							signaling	
							pathway	
Fusarium wilt	<i>Fusarium oxysporum</i> f.sp. <i>cucumerinum</i>	a systemic infection of soil-borne fungal diseases and the hyphae of this pathogen penetrated cucumber root, which can cause vascular wilt, leads to necrotic lesions on the stem	9110Gt and 9930 cv.SMR-18 and cv.Ashley Superina and Rijiecheng Cvs Straight-8 and SMR-18	F ₉ RILs and F ₂ population and F ₂ population	<i>Foc2.1</i> <i>Foc</i> gene <i>fw2.1</i>	- - -	- - -	Zhang et al., 2014 Vakalounakis and Lamprou 2018 Dong et al., 2019
						SCAR markers for	-	Jaber et al., 2020
						SCE12M50 _A and		
						SCE12M50 _B linker to		
						<i>Foc</i>		

base, foliar wilting and eventually whole plant wilt and even death, and occur throughout the growth period of cucumber	WIS2757 and Jinyan No. 2	F ₂ population	<i>Foc-4</i>	-	-	Zhou et al., 2015
	Superina and Rijiecheng	F ₂ population	QTL <i>fw2.1</i>	-	-	Dong et al., 2019
	Rijiecheng and Superina	-	4116 differentially expressed genes	ethylene signaling	-	Dong et al., 2020
	Rijiecheng	-	miR319a-JRL3, miR6300-BEE1, miR6300-DAHP1 and miR6300-PERK2	JRL3 contains three jacalin-like lectin domains, TaJRL1 encodes mannosespecific jacalin-like lectin domains and regulates the salicylic acid-dependent and jasmonic acid-dependent pathways, The BEE1 gene encodes a bHLH	-	Xu et al., 2021

			domain, DAHP1		
			encodes a		
			3-deoxy-D-arabi		
			no-heptulosonate		
			7-phosphate		
			synthase		
9930	-	14 chitinase genes, Especially <i>CsChi23</i>	Pathogenesis-rel ated proteins, and catalyzed the hydrolysis of chitin	-	Bartholomew et al., 2019
Jinchun No.2	-	56 differentially expressed proteins	Carbohydrate metabolism, amino acid metabolism, defense and stress responses, oxidation		Du et al., 2016

				reduction, metabolism and transport and other process	
995 and F9	F ₂ population	15 over-accumulated proteins	defense and stress responses, oxidation reduction, metabolism and transport and other process	Zhang et al., 2016	
Rijiecheng Superina	and -	32 differentially regulated proteins, three proteins with higher expression, <i>TMEM115</i> (<i>CsaV3_5G025750</i>),	MEM115 encoding a transmembrane protein, TET8 encoding function as a	Xu et al., 2021	

<i>TET8(CsaV3_2G007</i>	tetraspanin,	
<i>840),TPS10</i>	TPS10	
<i>(CsaV3_2G017980),</i>	encoding	a
<i>MGT2</i>	terpene	
<i>(CsaV3_7G006660)</i>	synthaseand,	
	MGT2	
	encoding	a
	glycosyltransfera	
	se	
