

Supplementary Material

Table S1. Information of new publications on blast-resistant QTL mapping in rice*.

Mapping Population	Population Type	Population Size	Detection QTL Method	Number of QTL	References
Hokkai188×Danghang-Shali	F2	190	IM	2	Nguyen et al., 2006 [1]
SHZ-2×TXZ-13	BILs	244	SMA	3	Liu et al., 2011 [2]
Nipponbare×93-11	RILs	259	CIM	4	Yang et al., 2013 [3]
Miyazakimochi×Bikei 22	RILs	158	CIM	2	Ishihara et al., 2014 [4]
DGWG×RR9	RILs	175	SMA, CIM	6	Liu et al., 2015 [5]
DGWG×RR20	RILs	224	SMA, CIM	22	
Akhanaphou×Leimaphou	RILs	103	ICIM	2	Aglawe et al., 2017 [6]
Landraces	Landraces	314	GLM, MLM	32	Lin et al., 2018 [7]
INGR15002×BPT 5204	F2/F3	188			
INGR15002×CO-39	F2/F3	188	ICIM	4	Devi et al., 2020 [8]
INGR15002×BPT5204	BILs	188			

* Update from our previous research publication. RILs: recombinant inbred lines; DH: doubled haploid; BILs: backcross lines; IM: interval mapping; CIM: composite interval mapping; SMA : single marker analysis; MLM: Mixed linear model; GLM: generalized linear model; ICIM : inclusive composite interval mapping.

Table S2. Information of 32 publications on heat-tolerant QTL mapping in rice.

Mapping Population	Population Types	Population Size	Detection QTL Method	Number of QTL	Reference
IR64×Azucena	DH	109	Likelihood ration Chi square test	6	Cao et al. 2002 [9]
Nipponbare×Kasalath	BILs	98	MLM	3	Zhu et al. 2005 [10]
Nipponbare×Kasalath	BILs	98	MLM	9	Zhu et al. 2006 [11]
USSR5×Guangjie 9	BILs	123	MLM	7	Zhao et al. 2006 [12]
Chiyonishiki×Koshijiwase	RILs	107	CIM	4	Tabata et al. 2007 [13]
T219×T226	RILs	202	MIM, Likelihood ration Chi square test	6	Chen et al. 2008 [14]
Zhongyouzao8×Fengjin	RILs	168	MIM	3	Zhang et al. 2008 [15]
Teqing×Yuanjiangpuye	BILs	77	SMA	4	Kui et al. 2008 [16]
Bala×Azucena	RILs	181	MIM	16	Jagadish et al. 2010 [17]
996×4628	RILs	286	CIM	2	Xiao et al. 2011a [18]
996×4628	RILs	286	CIM	2	Xiao et al. 2011b [19]
Xiushui09×IR2061	BILs	240	MLM	4	Cheng et al. 2012 [20]
IR64×N22	BILs	158	CIM	16	Ye et al. 2012 [21]
HE×NW	RILs	178	CIM	12	kobayashi et al. 2013 [22]
OM5930×N22	BILs	310	SMA, IM, CIM	11	Buu et al. 2014 [23]
YJ10-03-01×Shuhui527	F2	1027	MIM	1	Cao et al. 2015 [24]
Shuhui527×6 different indica rice	BILs	131	ANOVA	43	Liu et al. 2015 [25]
Nipponbare×Kasalath	BILs	95	CIM	16	Tazib et al. 2015 [26]
Tsukushiroman×Chikushi52	RILs	88	CIM	10	Wada et al. 2015 [27]
Sasanishiki×Habataki	CSSLs	37	ANOVA	11	Zhao et al. 2016 [28]
Milyang23×Giza178	F2	96	CIM	2	Ye et al. 2015 [29]

IR64×Giza178	F2	86		4	
IR64×Milyang23×Giza178	BILs	100		5	
N22×IR64	RILs	272	ICIM	5	Ps et al. 2017 [30]
Rejing35×XieB	F2	400	ICIM	3	Zheng et al. 2017 [31]
996×4628	RILs	124	CIM	24	Zhang et al. 2017 [32]
Sasanishiki×Habataki	CSSLs	39	Dunnett's multiple comparison test	12	Zhu et al. 2017 [33]
Tsukushiroman×Chikushi52	RILs	88	Dunnett's multiple comparison test	4	Miyahara et al. 2017 [34]
IAPAR-9×Liaoyan241	RILs	200	ICIM	7	Li et.al. 2018 [35]
Bg90-2×Shuhui527	BILs	400	SMA, IM	53	Udawela et al. 2018 [36]
Mengguandamagu×Shuhui527	BILs	400			
YJ01-201×TianfengB	BILs	586	Substitution mapping	1	Cao et al. 2019 [37]
IRGC102309×9311	BILs	420	CIM	1	Cao et al. 2020 [38]
Cheongcheong×Nagdong	DH	120	CIM	19	Park et al. 2020 [39]
Cheongcheong×Nagdong	DH	120	CIM	2	Park et al. 2021 [40]

CSSLs: chromosome segment substitution lines; ANOVA: analysis of variance; MIM: multiple Interval mapping; sCIM: Simplified composite interval mapping.

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