Table S2 NLB QTL mapping studies.

Reference	Parents	Resistance source	Population	QTL mapping	Trait	Flanking markers		Lower CI*	Upper CI*
Balint-Kurti *et al.* 2010	B73 x Mo17	B73	RIL	Composite interval mapping	AUDPC (AU06WMD)	bnlg1598	umc1396	187.8	191.1
Freymark *et al.* 1993	B52 x Mo17	B52	$F_{2:3}$	Interval mapping	Average Number of lesions/leaf	umc157	umc67	12.2	175.6
					Average percentage leaf tissue diseased	umc157	umc67	12.2	175.6
Welz *et al.* 1999	D32 x D145	D32	F_3	Composite interval mapping	% diseased leaf area	csu61b	dup12 (dupssr12)	181.0	239.6
Wisser *et al.* 2008	-	-	Recurrent selection	Selection mapping	-	bnlg615		201.0	
Chung *et al.* 2010	B73 x Tx303	Tx303	NILs	-	IP, AUDPC	umc1754	umc2234	180.0	187.4
Chung *et al*. 2011	B73 x CML52	CML52	HIFs	-	IP, lesion number, diseased leaf area, AUDPC			182.6	189.8
	B73 x CML52	CML52	RIL	ICIM	3 diseased leaf area ratings			200.4	205.8
Zwonitzer *et al.* 2010	Ki14 × B73	Ki14	RIL	Multiple interval mapping	sAUDPC	PZA01041.2	bnlg1057	157.1	190.0
Poland *et al.* 2011	NAM	B97 CML103 CML247 CML52 CML69	NAM	Joint linkage mapping	AUDPC	PZA02191.1	PZA00619.3	182.5	195.6

Ki11
Ki3
M37W
Mo17
Mo18W
NC358
Tzi8

Previous QTL studies that identified QTL for NLB resistance at maize bin 1.06 are listed. Confidence interval (CI) locations are based on AGP_V2.

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