

Supplementary Table S1. Mutagenized primers for alanine substitution of selected amino acid residues on domains II and III of Cry4Ba toxin and Aa-mALP receptor.

Protein	Primer	Sequence (5' ==> 3')	Restriction site
Cry4Ba domain II	W327A-f	GAGTAGACTTCGCGACCAATACTATATA	AccI
	W327A-r	ATTGGTTCGCGAAGTCTACTCTCTTTAG	
	Y347A-f	TGGGTTCTCAGCTACAAATTCTTCTGCA	DdeI
	Y347A-r	AATTTGTAGCTGAGAACCCAATTTTATTGG	
	I358A-f	AAGTGGAGCATATGGAAGTTCTGG	NdeI
	I358A-r	TTCCATATGCTCCACTTTCTTGTCAT	
	Y359A-f	TGGAATTGCTGGATCCTCTGGTTTTGGTTC	BamHI
	Y359A-r	ACCAGAGGATCCAGCAATCCACTTTCTTG	
Cry4Ba domain III	F490A-f	AATCTAACGCTTTAAATGCAACAGCTAAA	DraI
	F490A-r	TTGCATTTAAAGCGTTAGATTTTACGGCC	
	L517A-f	TGGTACCGCATCAGGCAGAATGG	KpnI
	L517A-r	CCTGATGCGGTACCATTGCTTGTA	
Aa-mALP	L52A-f	GCACGATGCCTTATTTCGAAAAAAGGATTATACGA	BstBI
	L52A-r	TCCTTTTTTTCGAATAAAGGCATCGTGCGCCTG	
	L53A-f	GATCTCGCATTCGAAAAAAGGATTATACGA	BstBI
	L53A-r	CCTTTTTTTCGAATGCGAGATCGTGCGC	
	S490A-f	TCATGTTTGCCGGTGGCTACGAGCAAACTTC	BciVI
	S490A-r	CTCGTAGCCACCGGCAAACATGAACGCCC	
	F497A-f	GCAAAACGCGATCGCCCATGCCATC	Bsp143I
	F497A-r	ATGGGCGATCGCGTTTTGCTCGTATC	
	H500A-f	TCATTGCTGCAGCCATCTCGTTTG	PstI
	H500A-r	GATGGCTGCAGCAATGAAGTTTTGC	
	G513A-f	TGTGTGCAGGAGCTCACCACCACCAC	SacI
	G513A-r	GTGGTGAGCTCCTGCACACACGTCCG	

Bold letters indicate mutated nucleotide residues; f and r represent forward and reverse primers, respectively. Underlined and double underlined bases represent the recognition sites introduced and eliminated for restriction analysis, respectively.