

Table S3. Genomic structure of Wisteria vein mosaic virus (WVMV), isolate Bari with putatively encoded proteins and predicted cleavage sites.

Genomic region	Putative product	Position (nt)		Size		Cleavage site
		start	end	nt	aa	
5'-UTR		1	163	163	-	-
ORF1	polyprotein	164	9,442	9,279	3,092	-
↓	P1-Pro	164	1,114	951	317	-
	HC-Pro	1,115	2,485	1,371	457	IQHY/S
	P3	2,486	3,526	1,041	347	YRVG/G
	6K1	3,527	3,682	156	52	VSIQ/A
	CI	3,683	5,584	1902	634	VKIQ/S
	6K2	5,585	5,743	159	53	VQLQ/S
	VPg	5,744	6,313	570	190	VSTQ/G
	NIa-Pro	6,314	7,042	729	243	VEVE/S
	NIb	7,043	8,593	1551	517	VSVQ/S
	CP	8,594	9,442	849	282	VSLQ/S
ORF2	<i>pipo</i> protein	2,941	3,168	228	75	-
3'-UTR		9,443	9,694	252	-	

P1-Pro: P1 proteinase; **HC-Pro:** helper component proteinase; **P3:** P3 protein; **6K1:** 6K1 protein; **CI:** cylindrical inclusion; **6K2:** 6K2 protein; **VPg:** viral protein genome-linked; **NIa-Pro:** nuclear inclusion proteinase a; **NIb:** nuclear inclusion body b protein; **CP:** coat protein; **pipo:** Pretty Interesting Potyviridae ORF protein. Cleavage sites were predicted according to [33] and using the ExPASy PeptideCutter tool [34].