**Appendix A.** Oligonucleotide primers used in this study. Primers were designed based on the reference sequence of a German *Cherry virus A* (CVA) isolate (GenBank accession X82547.1).

Primer		Primer sequence (5′-3′)	Position	Product size (bp)
CVA	5′RACE	AGAAGTCACCAATCAACAGAAG	1147-1126	
		CCAACAGACTCAAGAAGACCTAT	872-850	
CVA	2862F	GCCAACCTCAATAGAAGATTCA	511-532	2862
	2862R	ATCCATCTCACCTTGTATAGCA	3372-3351	
CVA	4291F	CATAGCAGTGACAGGTGATACATT	2892-2915	4291
	4291R	TGATTGGTGACGGTGAAGGAT	7182-7162	
CVA	7124F	GATGGCATAGGTCTTGGATT	7124-7143	
	Oligo (dT)	TTTTTTTTTTTTTTTTTT		
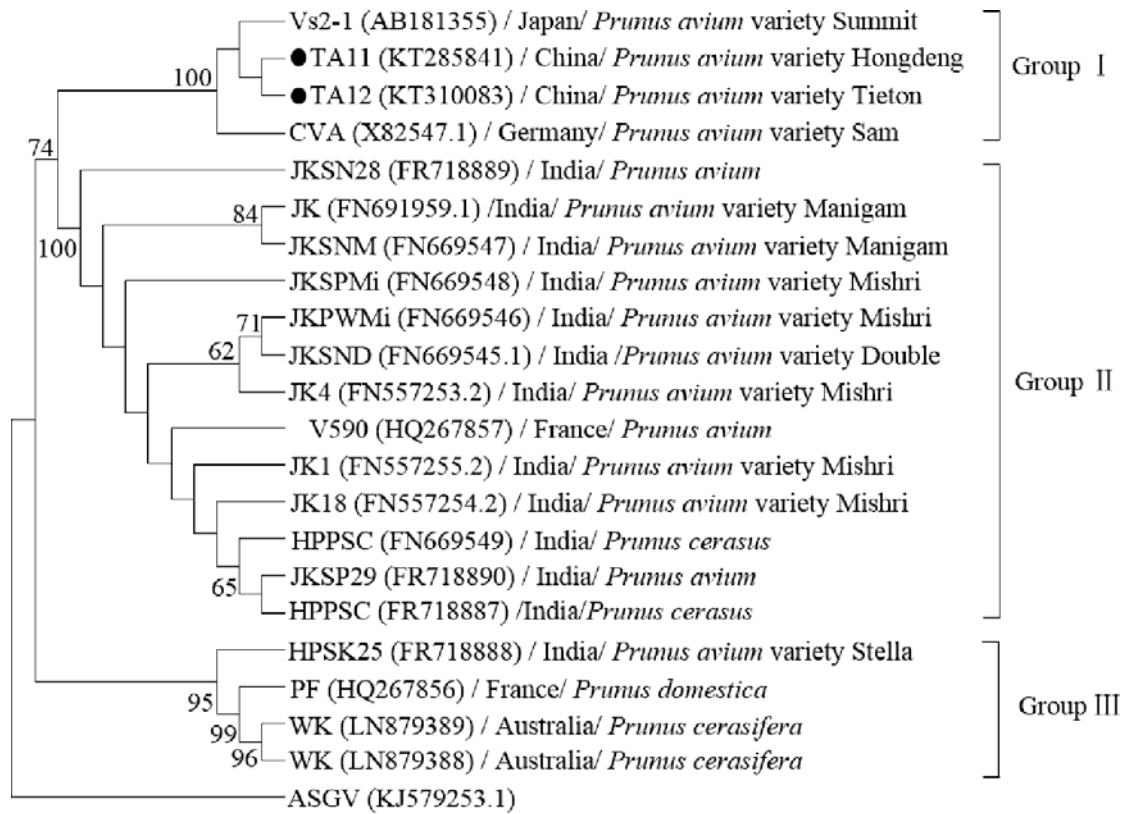
Appendix B. Phylogenetic analysis based on the partial coat protein (CP) gene sequences of CVA

isolates ChTA11 and ChTA12 from sweet cherry in China and 19 previously reported CVA isolates in

GenBank. Single CP gene sequence of *Apple stem grooving virus* (ASGV) was used to construct the

phylogenetic tree as an outgroup. The two CVA genome sequences from this study are indicated by

" ● " . Bootstrap values below 60% are not shown.