

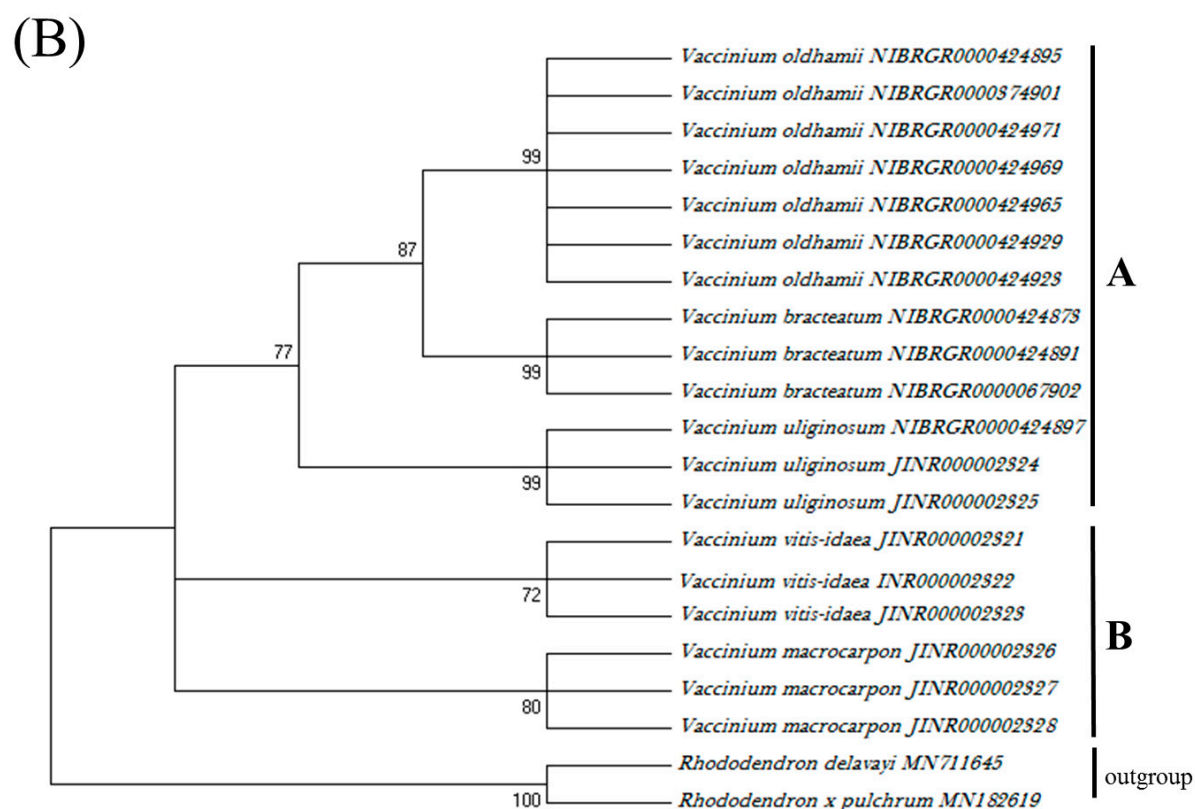
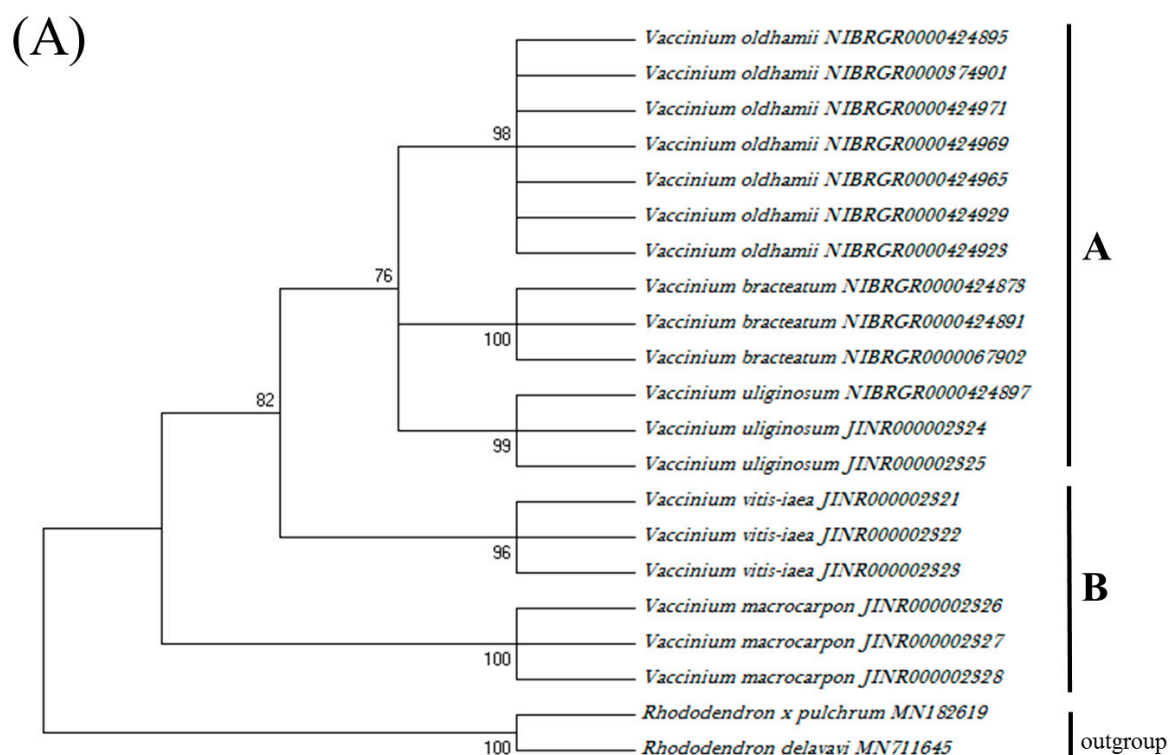
Table S1. Hypervariable InDels of 12 intergenic spacer regions among five *Vaccinium* cp genomes. Vb, *Vaccinium bracteatum* cp genome; Vu, *Vaccinium uliginosum* cp genome; Vv, *Vaccinium vitis-idaea* cp genome; Vm, *Vaccinium macrocarpon* cp genome; Vo, *Vaccinium oldhamii* cp genome.

Gene	Region	Nucleotide diversity (<i>Pi</i>)	InDel		
			Motif	Insertion (size)	Deletion (size)
<i>trnT-UGU</i>	IGS, gene	0.021	ta atataagttcttatataaaatataaaaaatat taa aaa a	Vm (2) Vu (35) Vm (3) -	- - - Vo (1)
<i>psbM-petN</i>	IGS	0.02	tagtaataacctctaa t	Vb (15) Vu (1)	- -
<i>trnC-GCA-rps12</i>	IGS	0.02	gttttaccattt c a	Vv (12) - Vm (1), Vu (1)	- Vu (1) Vm (1)
<i>accD-trnT-GGU</i>	IGS	0.035	t tt ataacg agtctt cttgaagc tctctt catttt ttct(c/a)aaa	- - Vv (6) Vu (6) - Vv (6) Vu (6) -	Vv (1) Vm (2) - - Vo (9) - - Vv (8)
<i>psaA-trnQ-UUG</i>	IGS	0.021	aataataatataaaataataatataa atttaaa ta tattttattat aa t	Vb (26) - - Vm (12) Vm (2) Vb (1)	- Vu (7) Vu (2) - - -
<i>rpoB-rpoA (1)</i>	IGS	0.081	(t/g)gaaatataaaa cta aaaata gat t	Vo, Vb (12) Vo (3) Vv (6) Vo (3) Vu (1)	- - - - -
<i>rpoB-rpoA(2)</i>	IGS	0.053	cta aaaata gat t ctt tt(t/g)(a/g) acgatatcgcataaaaaaacta acatatctttcataaaaacatacctttcata aaaacatatctt acac aaa acatatctttcataaaaa taaaattctaaaatatttttc catatctttcat c	Vo (3) Vv (6) Vo (3) Vu (1) - - Vm (22) Vm (43) Vm (4) Vm, Vo (3) Vm (18) Vo (21) Vm, Vo (12) Vm (1)	- - - - Vb (3) Vv (4) - - - - - -
<i>rpoB-rpoA(3)</i>	IGS	0.031	aagaaa(a/g)(g/t)aaatccc tatcgaaatgagagttgactatatcgaaat gagagttgacta tccgc gaatttgactttctgctcaatt tcaatcgcatctttcactttgtgg	- Vm (42) - - - Vb (23)	Vu (15) - - Vu (5) Vm, Vv (23) -

			t ttatt	- -	Vb (1) Vm, Vo (5)
<i>ycf2-trnL-CAA</i>	IGS	0.02	ctctaatagcttcgaataaat	Vm (21)	-
			taatcatgggttgcggtac(c/t)acgagat	-	Vm (78)
			cttctagcacttaccgctgaggccctatca	Vo, Vu (16)	-
			tcaatcaatttcgattaat		-
			attccacaacagaaga		-
			attccacaacagaagaaaaatttttagag	-	Vm (182)
			actaatacaattcgattcgccttcatagac	-	-
			aaactttggatttgcgaagcctgtgtaagtc	-	-
			gggtgtgatggggtccttttcgatccgtag	-	-
			gaagggctgctgcacaaagtatacttcta	-	-
			agtaatggcttcatagaacttatattatctt	-	-
			a	-	Vm, Vo (5)
tctat	-	Vm (28)			
at(c/a)ggatgaaatgaaatt(a/c)tgt	-	Vo (1)			
a	Vv (1)	-			
g	Vo (1)	-			
gt	Vm (2)	-			
aaa(a/t)	-	Vm, Vv (4)			
aggacgaa	-	Vo (8)			
<i>rps12-ycf15</i>	IGS, gene	0.025	aata	Vo (4)	-
			a	-	Vm, Vu (1)
			ataa	-	Vm (4)
			t/a	Vm (1)	-
			t	Vm (1)	-
ttagta	-	Vu (6)			
<i>trnV-GAC</i>	IGS, gene	0.028	a	-	Vu, Vm (1)
			g/t	Vu, Vv (1)	-
			tatt	Vo (4)	-
			a	Vo (1)	-
			ta	Vo (2)	-
			ac	-	Vb (2)
			taataaat	-	Vb (8)
			attaata	Vv (7)	-,
			gttaattt	Vu (8)	-
			ag(g/t)g	-	Vb (4)
gagagg(g/c)	-	Vv (7)			
<i>ndhE-ndhF</i>	IGS, gene	0.027	tt	Vo, Vv (2)	-
			tta	Vo, Vv (3)	-
			taatgatcta	Vo (10)	-
			atagaaagac(g/a)taggacttatag(t/a)aa(a/g)(t/a)(a/c)gta(a/g)g	Vo, Vu (34)	-
			tta	Vo (3)	-
			gtaa/actt	Vo, Vu (4)	-
			aa	Vu (2)	-

Table S2. Intra- and interspecific variation of K2P genetic distances of *rpoB-rpoA* (2), *ycf2-trnL-CAA*, and *ndhE-ndhF* sequences for five *Vaccinium* species; Vb, *Vaccinium bracteatum*; Vu, *Vaccinium uliginosum*; Vv, *Vaccinium vitis-idaea*; Vm, *Vaccinium macrocarpon*; Vo, *Vaccinium oldhamii* .

Vaccinium (n)	K2P genetic distance		
	<i>rpoB-rpoA</i> (2)	<i>ycf2-trnL-CAA</i>	<i>ndhE-ndhF</i>
Vb (3)	0.0-0.4	0.0-0.5	0.0-0.6
Vu (3)	0.0-0.6	0.0-0.4	0.0-0.5
Vv (3)	0.0-0.5	0.0-0.7	0.0-0.4
Vm (3)	0.0-0.7	0.0-0.4	0.0-0.7
Vo (7)	0.0-1.0	0.0-0.9	0.0-1.9
Vb vs Vu	1.4-2.2	1.3-2.0	2.2-3.4
Vb vs Vv	4.6-5.5	3.5-4.6	3.6-4.7
Vb vs Vm	4.2-5.8	3.7-4.7	5.7-6.2
Vb vs Vo	1.2-2.0	1.6-2.7	1.5-2.7
Vu vs Vv	4.4-5.6	3.2-4.1	3.2-4.1
Vu vs Vm	3.3-4.0	4.7-5.5	5.3-6.2
Vu vs Vo	2.2-3.4	1.4-2.8	3.3-4.1
Vv vs Vm	1.9-2.6	1.1-2.2	5.4-6.8
Vv vs Vo	4.7-5.2	4.3-5.2	2.1-3.0
Vm vs Vo	4.0-5.5	5.5-6.4	4.4-5.8



(C)

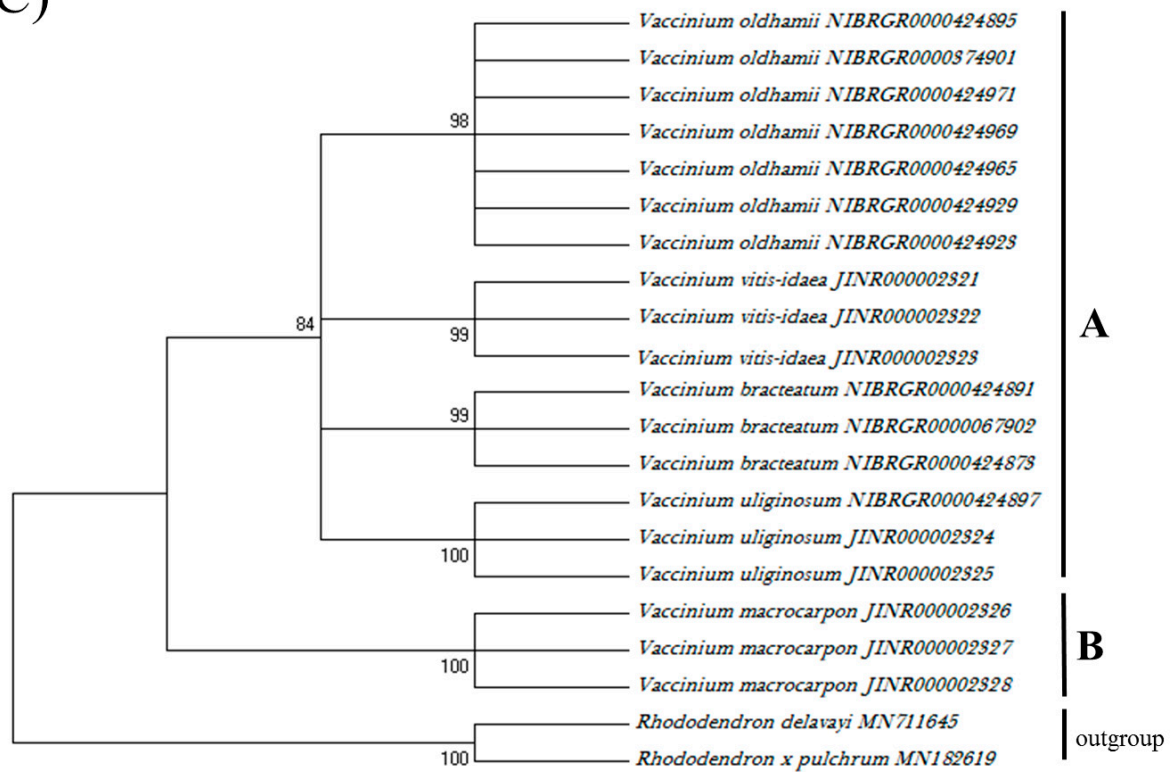


Figure S1. Phylogenetic tree derived from (A) *rpoB-rpoA* (2), (B) *ycf2-trnL-CAA*, and (C) *ndhE-ndhF* sequences of specimens of the *V. bracteatum*, *V. uliginosum*, *V. vitis-idaea*, *V. macrocarpon*, *V. oldhamii* .and outgroup *Rh. delavayi* and *Rh. pulchrum*. See details in Table 1.