

Supplementary Materials

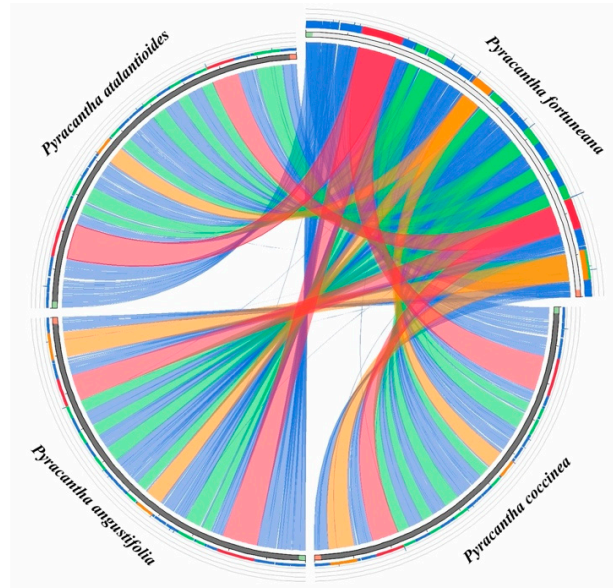


Figure S1. Synteny comparison among the chloroplast genomes of *P. fortuneana* and another three *Pyracantha* species. The colored blocks outside the sequences refer to the score/max bit core ration, with red > 0.75, orange > 0.50, green > 0.25, and blue ≤ 0.25 .

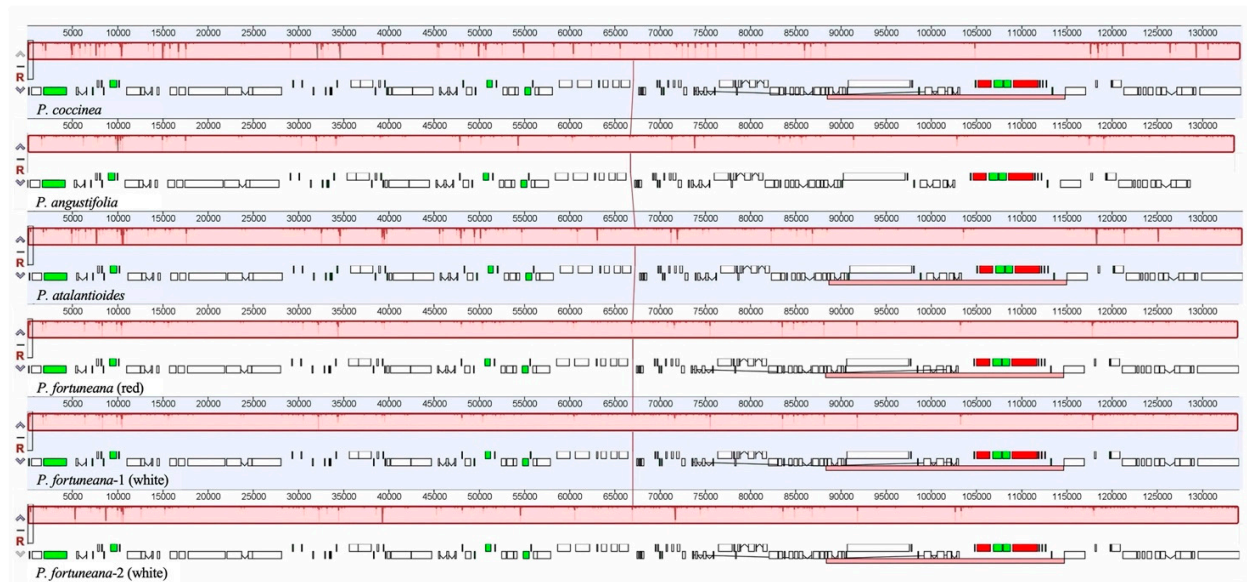


Figure S2. The structural rearrangement analysis of six *Pyracantha* chloroplast genomes using the mauve multiple alignment algorithm.

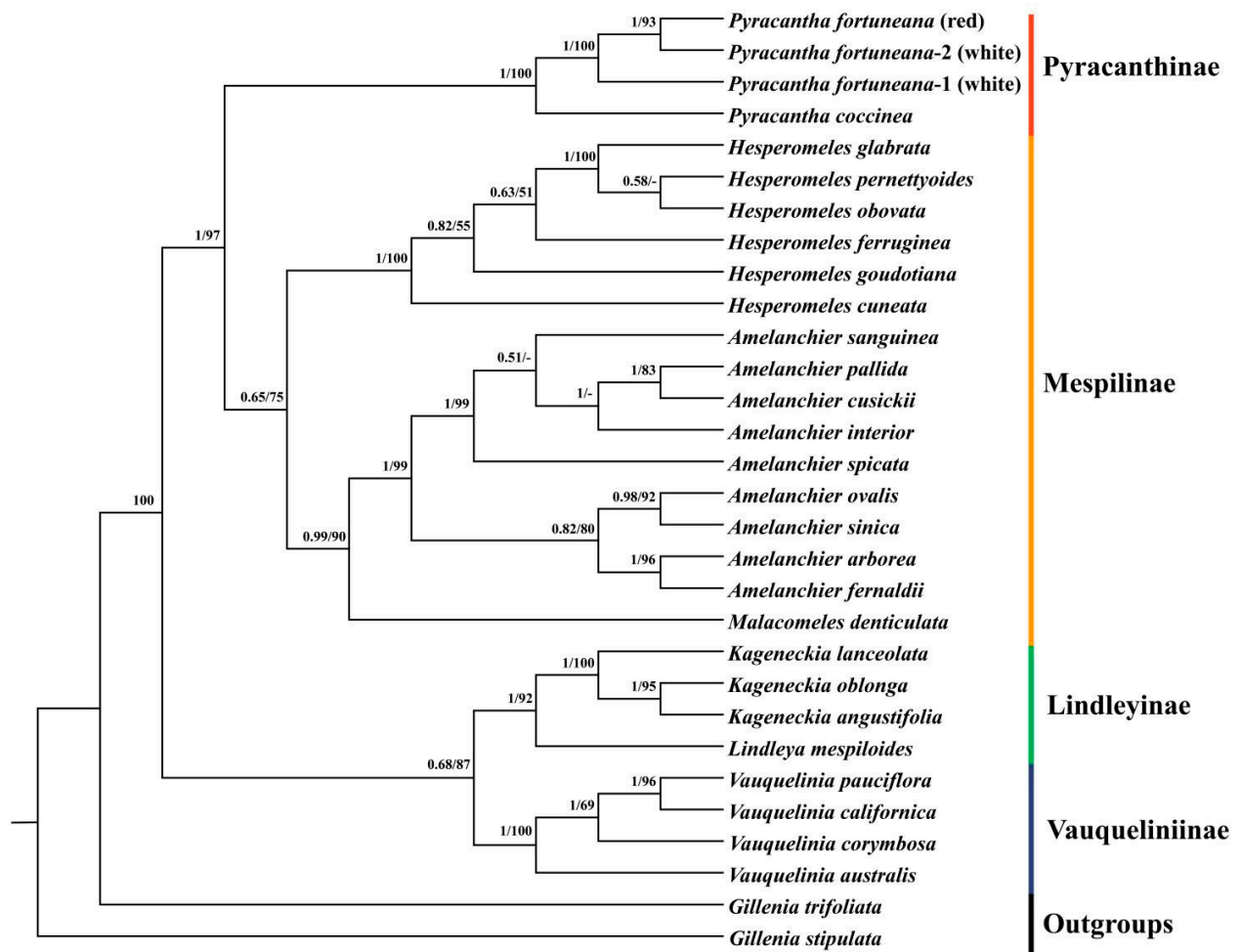


Figure S3. The phylogenetic tree of the genus *Pyracantha* based on 30 nrDNA ITS sequences using both ML and BI methods. The BI posterior probabilities / ML bootstrap values are displayed above the lines ("-" stands for the value less than 0.5/50).

Table S1. Sample list of chloroplast genomes used in this study.

Species Name	Accession	Species Name	Accession
<i>Amelanchier sinica</i>	MK920291	<i>Pyracantha fortuneana</i> -1 (white)	NC_059101
<i>Malacomeles denticulata</i>	NC_045325	<i>Pyracantha fortuneana</i> -2 (white)	MW596361
<i>Hesperomeles ferruginea</i>	NC_045328	<i>Pyracantha atalantioides</i>	MW801001
<i>Hesperomeles glabrata</i>	MK920298	<i>Vauquelinia australis</i>	NC_045309
<i>Hesperomeles obovata</i>	MK920299	<i>Vauquelinia californica</i>	NC_062344
<i>Hesperomeles goudotiana</i>	NC_045327	<i>Vauquelinia californica</i> -1	KY419925
<i>Hesperomeles pernettyoides</i>	NC_045329	<i>Vauquelinia californica</i> -2	MN068269
<i>Crataegus cuneata</i>	NC_058896	<i>Vauquelinia corymbosa</i>	MN068249
<i>Crataegus pinnatifida</i>	NC_057086	<i>Kageneckia angustifolia</i>	NC_045322
<i>Crataegus hupehensis</i>	NC_054155	<i>Kageneckia crataegifolia</i>	KY420027
<i>Crataegus laevigata</i>	NC_062347	<i>Kageneckia oblonga</i>	NC_045324
<i>Crataegus rhipidophylla</i>	NC_062345	<i>Kageneckia lanceolata</i>	MN068265
<i>Crataegus kansuensis</i>	NC_039374	<i>Lindleya mespiloides</i>	MN068248
<i>Pyracantha coccinea</i>	NC_062343	<i>Gillenia stipulata</i>	NC_045321
<i>Pyracantha angustifolia</i>	KY419957	<i>Gillenia trifoliata</i>	NC_045311

Table S2. Sample list of rDNA ITS sequences used in this study.

Species Name	Accession	Species Name	Accession
<i>Amelanchier sanguinea</i>	MN905587	<i>Lindleya mespiloides</i>	MN577906
<i>Amelanchier pallida</i>	MN905586	<i>Kageneckia angustifolia</i>	MN905589
<i>Amelanchier interior</i>	MN905585	<i>Kageneckia oblonga</i>	MN577932
<i>Amelanchier fernaldii</i>	MN905583	<i>Kageneckia lanceolata</i>	MN068265
<i>Amelanchier cusickii</i>	MN905582	<i>Malacomeles denticulata</i>	MN905591
<i>Amelanchier arborea</i>	MN905579	<i>Pyracantha fortuneana</i> (red)	OP821228
<i>Amelanchier ovalis</i>	MN215988	<i>Pyracantha fortuneana</i> -1 (white)	MN216013
<i>Amelanchier sinica</i>	MN216016	<i>Pyracantha fortuneana</i> -2 (white)	SRR17631715
<i>Amelanchier spicata</i>	MN215976	<i>Pyracantha coccinea</i>	SRR13004386
<i>Hesperomeles pernettyoides</i>	MN905597	<i>Vauquelinia californica</i> subsp. <i>sonorensis</i>	MN905593
<i>Hesperomeles ferruginea</i>	MN905596	<i>Vauquelinia pauciflora</i>	MN905577
<i>Hesperomeles goudotiana</i>	MN905595	<i>Vauquelinia corymbosa</i> subsp. <i>heterodon</i>	MN905576
<i>Hesperomeles cuneata</i>	MN905594	<i>Vauquelinia australis</i>	MN577917
<i>Hesperomeles obovata</i>	MN216004	<i>Gillenia stipulata</i>	MN905588
<i>Hesperomeles glabrata</i>	MN216003	<i>Gillenia trifoliata</i>	MN577923

Table S3. The codon number in six *Pyracantha* chloroplast genomes.

Species	Codons
<i>Pyracantha atalantioides</i>	26,288
<i>Pyracantha angustifolia</i>	26,317
<i>Pyracantha coccinea</i>	26,291
<i>Pyracantha fortuneana</i> (red)	26,292
<i>Pyracantha fortuneana</i> -1 (white)	26,291
<i>Pyracantha fortuneana</i> -2 (white)	26,292

Table S4. List of the potential RNA editing sites in the chloroplast protein-coding genes of *Pyracantha fortuneana* (red) and two individuals of *P. fortuneana* (white).

Nt Pos	AA Pos	Align Col	Effect	Score	Gene
64	22	22	CGG (R) => TGG (W)	1	<i>accD</i>
1463	488	519	CCT (P) => CTT (L)	1	<i>accD</i>
773	258	258	TCA (S) => TTA (L)	1	<i>atpA</i>
914	305	305	TCA (S) => TTA (L)	1	<i>atpA</i>
1148	383	383	TCA (S) => TTA (L)	1	<i>atpA</i>
37	13	13	CCT (P) => TCT (S)	1	<i>atpB</i>
629	210	213	TCA (S) => TTA (L)	1	<i>atpI</i>
559	187	187	CAT (H) => TAT (Y)	1	<i>clpP</i>
634	212	227	CAT (H) => TAT (Y)	1	<i>matK</i>
149	50	50	TCA (S) => TTA (L)	1	<i>ndhB</i>
467	156	156	CCA (P) => CTA (L)	1	<i>ndhB</i>
542	181	181	ACG (T) => ATG (M)	1	<i>ndhB</i>
586	196	196	CAC (H) => TAC (Y)	1	<i>ndhB</i>
737	246	246	CCA (P) => CTA (L)	1	<i>ndhB</i>
746	249	249	TCT (S) => TTT (F)	1	<i>ndhB</i>
830	277	277	TCA (S) => TTA (L)	1	<i>ndhB</i>
1112	371	371	TCA (S) => TTA (L)	1	<i>ndhB</i>
1255	419	419	CAT (H) => TAT (Y)	1	<i>ndhB</i>
1481	494	494	CCA (P) => CTA (L)	1	<i>ndhB</i>
383	128	128	CCA (P) => CTA (L)	1	<i>ndhD</i>
599	200	200	TCA (S) => TTA (L)	1	<i>ndhD</i>
674	225	225	TCA (S) => TTA (L)	1	<i>ndhD</i>
878	293	293	TCA (S) => TTA (L)	1	<i>ndhD</i>
290	97	97	TCG (S) => TTG (L)	1	<i>ndhF</i>
392	131	131	TCC (S) => TTC (F)	1	<i>ndhF</i>
1876	626	631	CTT (L) => TTT (F)	1	<i>ndhF</i>
418	140	140	CGG (R) => TGG (W)	1	<i>petB</i>
611	204	204	CCA (P) => CTA (L)	1	<i>petB</i>
214	72	72	CCT (P) => TCT (S)	1	<i>psbE</i>
77	26	26	TCT (S) => TTT (F)	1	<i>psbF</i>
2	1	1	ACG (T) => ATG (M)	1	<i>psbL</i>
830	277	279	TCA (S) => TTA (L)	1	<i>rpoA</i>
338	113	113	TCT (S) => TTT (F)	1	<i>rpoB</i>
566	189	190	TCG (S) => TTG (L)	1	<i>rpoB</i>
1994	665	684	TCT (S) => TTT (F)	1	<i>rpoB</i>
248	83	83	TCA (S) => TTA (L)	1	<i>rps2</i>
80	27	27	TCA (S) => TTA (L)	1	<i>rps14</i>
149	50	53	CCA (P) => CTA (L)	1	<i>rps14</i>

Table S5. Summary of SSRs in six *Pyracantha* chloroplast genomes.

Repeat types	A/T	C/G	AG/CT	AT/AT	AAAT/ATTT	AATT/AATT	AAGG C/CCTT G	AATCC/ATTGG	AATATT/AATATT	AACTAT/AGTTAT	Total
3					7			1			8
5			1	15							16
6				1							1
7				1							1
10	23										23
11	11	2									13
12	13										13
13	7										7
14	3	1									4
15	4										4
16	1										1
17	2										2
18	2										2
19	1										1
25	1										1
Total	68	3	1	17	7	0	0	1	0	0	97
<i>Pyracantha angustifolia</i>											
3					7	1		1		1	10
5			1	22							23
6				4							4
10	21	2									23
11	9	1									10
12	13										13
13	5										5
14	5	1									6
15	2										2
16	5	1									6
17	5										5
18	1										1
20	1										1
24	1										1
34	1										1
Total	69	5	1	26	7	1	0	1	0	1	111
<i>Pyracantha atalantioides</i>											
3					6	1		1	1		9
4							2				2
5			1	20							21
6				4							4
10	21										21
11	11										11

12	10	2									12
13	3										3
14	7										7
15	8										8
16	1										1
17	3										3
18	1										1
19	2										2
Total	67	2	1	24	6	1	2	1	1	0	105

Pyracantha coccinea

3					7			1			8
5			1	20							21
6				3							3
7				1							1
10	20	3									23
11	8										8
12	12										12
13	6										6
14	4										4
15	2										2
16	5										5
17	3										3
18	1										1
19	2										2
22	1										1
23	1										1
Total	65	3	1	24	7	0	0	1	0	0	101

Pyracantha fortuneana (red)

3					7			1			8
5			1	20							21
6				3							3
7				1							1
10	20	2									22
11	8	1									9
12	13										13
13	5										5
14	3										3
15	2										2
16	6										6
17	4										4
18	1										1
19	1										1
21	1										1
23	1										1
Total	65	3	1	24	7	0	0	1			101

Pyracantha fortuneana-1 (white)

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3					7			1			8
5			1	23							24
6				2							2
7				1							1
10	19	2									21
11	11	1									12
12	16										16
13	2										2
14	5	1									6
15	4										4
16	5										5
17	1										1
20	1										1
21	2										2
22	1										1
Total	67	4	1	26	7	0	0	1	0	0	106
<i>Pyracantha fortuneana</i> -2 (white)											

Table S6. The neutral selected sites detected in the 78 CDSs of six *Pyracantha* chloroplast genomes.

Rate estimate	LRT	p-value	Gene	Region	Rate estimate	LRT	p-value	Gene	Region
189.581	1.307	0.2529	<i>accD</i>	LSC	279.163	0.513	0.4739	<i>petB</i>	LSC
337.637	1.081	0.2984			277.363	0.631	0.4268		
110.059	1.415	0.2342	<i>atpA</i>	LSC	281.809	-0.045	1	<i>petL</i>	LSC
118.066	1.91	0.167			148.181	0.403	0.5255		
118.104	1.756	0.1852	<i>ccsA</i>	SSC	219.006	0.483	0.4872	<i>psaB</i>	LSC
196.862	2.192	0.1387	<i>cemA</i>	LSC	240.572	0.369	0.5434		
202.472	0.223	0.6369			285.467	1.792	0.1807	<i>psbA</i>	LSC
138.283	0.377	0.539	<i>matK</i>	LSC	254.254	2.681	0.1015	<i>psbC</i>	LSC
249.616	-0.001	1			322.933	0.631	0.4271	<i>psbK</i>	LSC
140.031	1.352	0.245	<i>ndhA</i>	SSC	221.789	2.031	0.1542	<i>rpl14</i>	LSC
229.471	0.5	0.4794	<i>ndhC</i>	SSC	241.761	0.824	0.3639	<i>rpl32</i>	SSC
174.035	0.62	0.4309			196.116	1.123	0.2892	<i>rpl33</i>	LSC
161.961	1.09	0.2965	<i>ndhD</i>	SSC	368.073	0.736	0.3911	<i>rpoA</i>	LSC
141.525	0.427	0.5136			194.096	2.568	0.1091	<i>rps11</i>	LSC
157.918	0.951	0.3294			199.376	1.308	0.2528	<i>rps12</i>	IR
0.008	-0.034	1			342.758	0.681	0.4094	<i>rps15</i>	SSC
219.006	0.483	0.4872			266.225	0.556	0.456	<i>rps18</i>	LSC
324.996	0.579	0.4467	<i>ndhF</i>	SSC	309.785	2.234	0.135	<i>ycf2</i>	IR
374.718	2.502	0.1137			271.046	0.535	0.4646	<i>ycf3</i>	LSC
250.479	1.343	0.2465			264.924	0.514	0.4733		
238.061	0.599	0.4389	<i>ndhJ</i>	LSC	468.867	0.432	0.511	<i>rpoC2</i>	LSC