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BMC Plant Biology

CORRECTION

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Correction: Comparative analysis of chloroplast genomes of *Pulsatilla* species reveals evolutionary and taxonomic status of newly discovered endangered species *Pulsatilla saxatilis*

Hefei Xue[1,2], Yanping Xing[1,4], Che Bian[1], Wenjuan Hou[1], Wenxiao Men[1], Han Zheng[3,4], Yanyun Yang[1*], Xixiang Ying[1], Tingguo Kang[1] and Liang Xu[1*]

Correction: BMC Plant Biol 24, 293 (2024)
https://doi.org/10.1186/s12870-024-04940-w

Following publication of the original article [1], the authors identified errors, specifically:

- Figure 7 – Incomplete image that seriously affects the completeness and accuracy of the figure.
- Figure 8 – Extra horizontal line was spotted.
- Table 3 – Confusing format due to inappropriate column width.

The corrections do not affect the overall Conclusion of the article but need to be corrected for the completeness and accuracy of the content of the article.

The original article [1] has been corrected.

The online version of the original article can be found at https://doi.org/10.1186/s12870-024-04940-w.

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[4]State Key Laboratory of Dao-di Herbs, Beijing 100700, China

Incorrect Figure 7

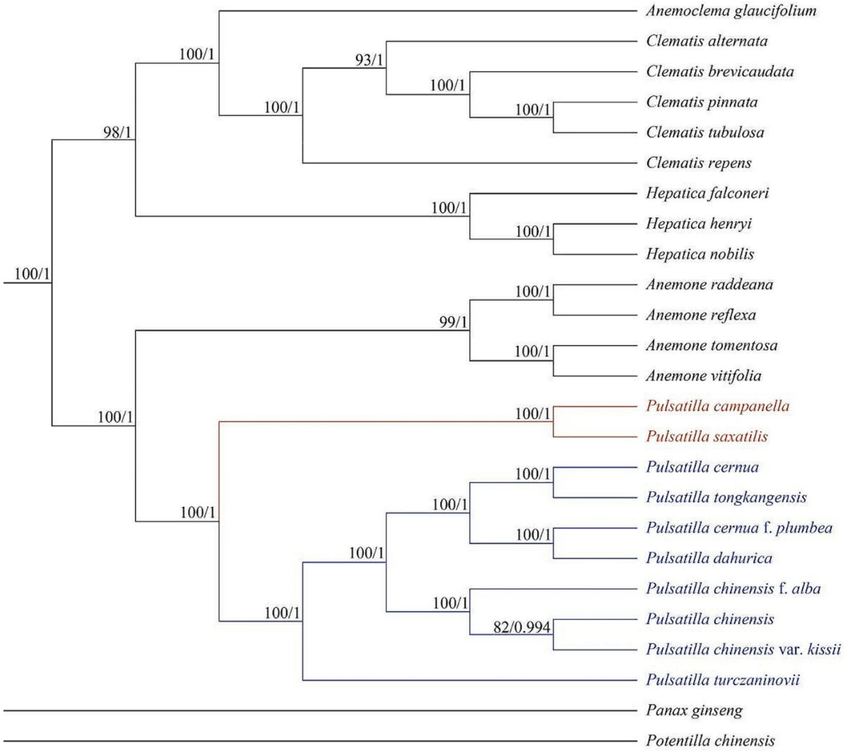


Fig. 7 Phylogenetic tree of *Pulsatilla saxatilis* and 24 other species using maximum likelihood (ML) and Bayesian inference methods based on the complete cp. genome sequences. Number of the branches indicates ML bootstrap support value/Bayesian posterior probability

Correct Figure 7

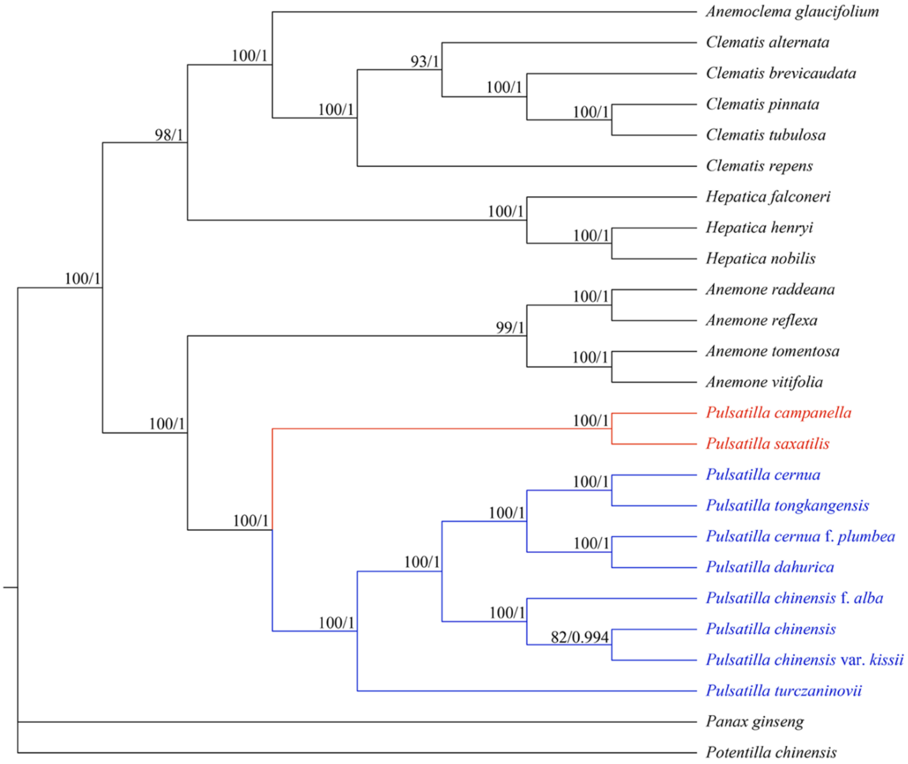


Fig. 7 Phylogenetic tree of *Pulsatilla saxatilis* and 24 other species using maximum likelihood (ML) and Bayesian inference methods based on the complete cp. genome sequences. Number of the branches indicates ML bootstrap support value/Bayesian posterior probability

Incorrect Figure 8

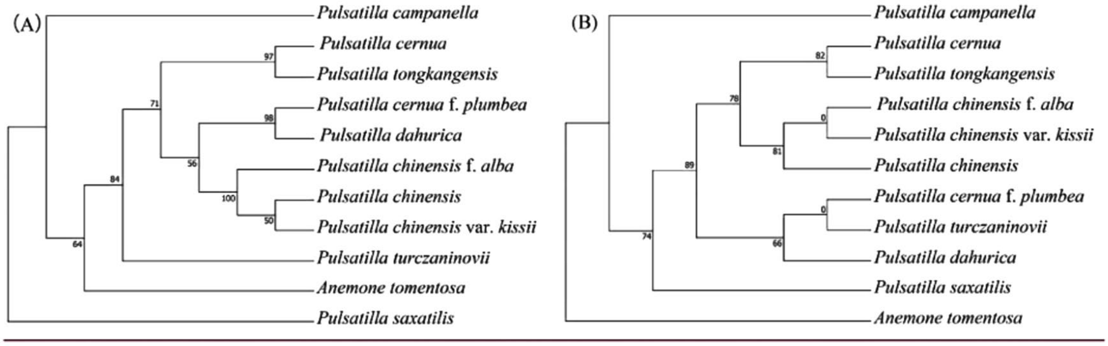


Fig. 8 Phylogenetic trees of 10 *Pulsatilla* species and outgroup Anemone tomentosa using maximum likelihood (ML) based on *rps*16_*trnK*-UUU (**A**) and *rbcL* (**B**). Number of the branches indicates ML bootstrap support value

Correct Figure 8

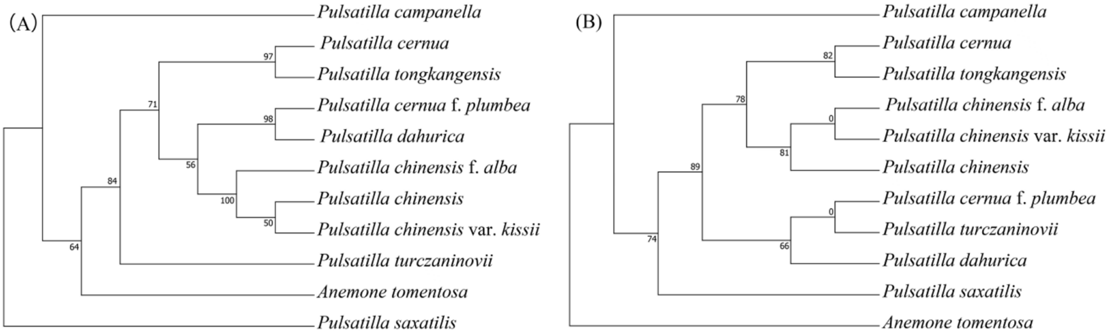


Fig. 8 Phylogenetic trees of 10 *Pulsatilla* species and outgroup Anemone tomentosa using maximum likelihood (ML) based on *rps*16_*trnK*-UUU (**A**) and *rbcL* (**B**). Number of the branches indicates ML bootstrap support value

With confusing format Table 3

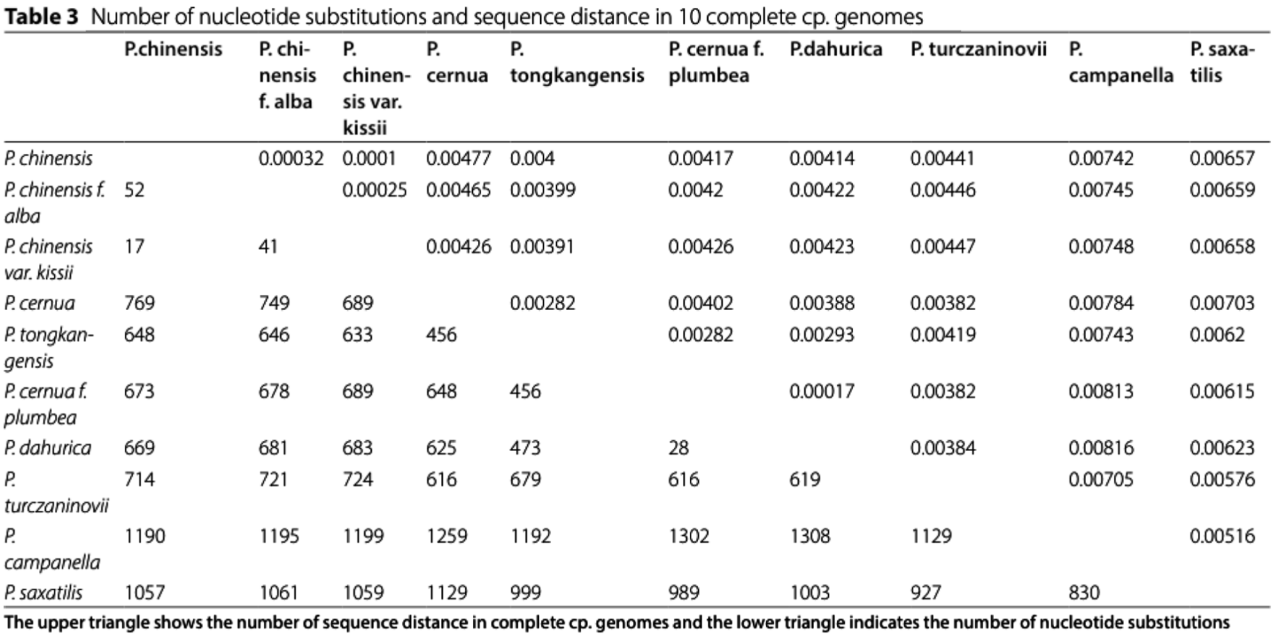
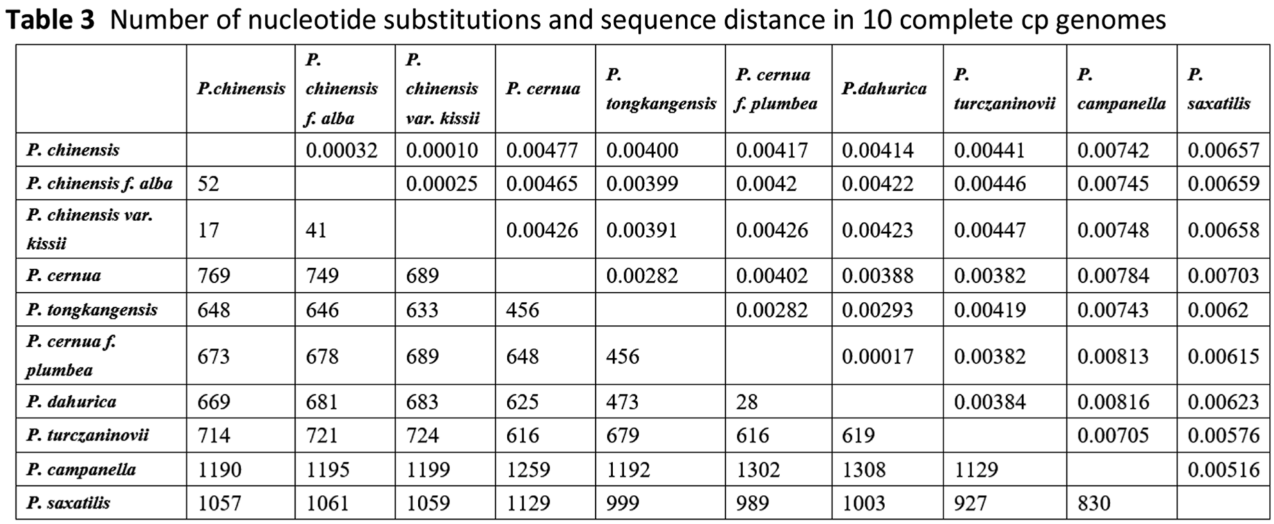


Table 3 Number of nucleotide substitutions and sequence distance in 10 complete cp. genomes

	P.chinensis	P. chinensis f. alba	P. chinensis var. kissii	P. cernua	P. tongkangensis	P. cernua f. plumbea	P.dahurica	P. turczaninovii	P. campanella	P. saxatilis
P. chinensis		0.00032	0.0001	0.00477	0.004	0.00417	0.00414	0.00441	0.00742	0.00657
P. chinensis f. alba	52		0.00025	0.00465	0.00399	0.0042	0.00422	0.00446	0.00745	0.00659
P. chinensis var. kissii	17	41		0.00426	0.00391	0.00426	0.00423	0.00447	0.00748	0.00658
P. cernua	769	749	689		0.00282	0.00402	0.00388	0.00382	0.00784	0.00703
P. tongkangensis	648	646	633	456		0.00282	0.00293	0.00419	0.00743	0.0062
P. cernua f. plumbea	673	678	689	648	456		0.00017	0.00382	0.00813	0.00615
P. dahurica	669	681	683	625	473	28		0.00384	0.00816	0.00623
P. turczaninovii	714	721	724	616	679	616	619		0.00705	0.00576
P. campanella	1190	1195	1199	1259	1192	1302	1308	1129		0.00516
P. saxatilis	1057	1061	1059	1129	999	989	1003	927	830	

The upper triangle shows the number of sequence distance in complete cp. genomes and the lower triangle indicates the number of nucleotide substitutions

Clear format Table 3



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References

1. Xue H, Xing Y, Bian C, et al. Comparative analysis of chloroplast genomes of *Pulsatilla* species reveals evolutionary and taxonomic status of newly discovered endangered species *Pulsatilla Saxatilis*. BMC Plant Biol. 2024;24:293. https://doi.org/10.1186/s12870-024-04940-w.

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