Taylor & Francis
Taylor & Francis Group

Mitochondrial DNA Part B
Resources

ISSN: 2380-2359 (Online) Journal homepage: www.tandfonline.com/journals/tmdn20

# The complete plastome sequence of *Polylepis rugulosa* Bitter 1911 (Rosaceae), an endangered tree species native of the Andean cordillera of South America

**Roberto Contreras-Díaz , Julio César Chávez-Galarza & Wilson Huanca-Mamani**

**To cite this article:** Roberto Contreras-Díaz , Julio César Chávez-Galarza & Wilson Huanca-Mamani (2025) The complete plastome sequence of *Polylepis rugulosa* Bitter 1911 (Rosaceae), an endangered tree species native of the Andean cordillera of South America, Mitochondrial DNA Part B, 10:12, 1174-1179, DOI: 10.1080/23802359.2025.2528566

**To link to this article:** https://doi.org/10.1080/23802359.2025.2528566

MITOCHONDRIAL DNA PART B: RESOURCES
2025, VOL. 10, NO. 12, 1174–1179
https://doi.org/10.1080/23802359.2025.2528566

Taylor & Francis
Taylor & Francis Group

PLASTOME REPORT

# The complete plastome sequence of *Polylepis rugulosa* Bitter 1911 (Rosaceae), an endangered tree species native of the Andean cordillera of South America

Roberto Contreras-Díaz[a,b], Julio César Chávez-Galarza[c] and Wilson Huanca-Mamani[d,e]

[a]Centro Regional de Investigación y Desarrollo Sustentable de Atacama (CRIDESAT), Universidad de Atacama, Copiapó, Chile; [b]Núcleo Milenio de Ecología Histórica Aplicada para los Bosques Áridos (AFOREST), Santiago, Chile; [c]Departamento de Ciencias Básicas y Afines, Universidad Nacional de Barranca, La Florida, Barranca, Perú; [d]Laboratorio de Biología Molecular de Plantas, Facultad de Ciencias Agronómicas, Universidad de Tarapacá, Arica, Chile; [e]Centro de Genética y Genómica Uasara (CGGU), Universidad de Tarapacá, Arica, Chile

**ABSTRACT**

*Polylepis rugulosa* Bitter is an endangered species native to the central and northern Andes and is one of the woody species that form the highest altitude woodlands in the world. Despite its ecological importance, genomic information for *P. rugulosa* is scarce, which limits our understanding of its evolutionary relationships and hinders the development of conservation strategies. In this study, we assembled the complete chloroplast genome of *P. rugulosa* and conducted phylogenetic analyses using 25 chloroplast genomes. The chloroplast genome is composed of 155,163 bp, with a typical quadripartite structure: a large single copy (85,290 bp), a small single copy (18,761 bp), and two inverted repeats (26,556 bp each). A total of 129 genes were identified, including 84 protein-coding genes, 37 tRNA genes, and 8 rRNA genes. Phylogenetic analysis confirmed the placement of *P. rugulosa* within the Sanguisorbinae clade (Sanguisorbeae tribe). This is the first report of the complete plastome genome of a *Polylepis* species, providing valuable genomic data for conservation strategies and for reconstructing the biogeographical history of the genus *Polylepis* in South America.

**ARTICLE HISTORY**
Received 23 January 2025
Accepted 27 June 2025

**KEYWORDS**
Plastome genome; Rosaceae; *Polylepis rugulosa*; endangered species

## Introduction

The *Rosaceae* family comprises about 90 genera containing approximately 3000 species (Longhi et al. 2014). In the genus *Polylepis* (*Rosaceae*), 45 species have been currently recognized, grouped in five sections and distributed in the central and northern Andes (Espinoza and Kessler 2022). *Polylepis rugulosa* Bitter. is a tree or shrub characteristic of semiarid Andean cordillera from south-western Peru and north-western Chile and is one of the woody species that grows at the highest altitude in the world, between 3400 and 4100 m a.s.l. (Schmidt-Lebuhn et al. 2006). *Polylepis* species provide valuable ecological services such as biodiversity conservation, soil erosion control, carbon capture, protection of water sources, and as medicinal plant for local communities (Cuyckens et al. 2016; Espinoza and Kessler 2022).

In Chile, the conservation status of *P. rugulosa* is categorized as endangered species (MMA 2023). Adaptations such as small, thick leaflets with wax layers and sunken stomata, the development of protective pigments, and higher efficiency in net photosynthetic rate due to the effects of water and temperature stress limitations have contributed to a better ability of the response of *Polylepis* species to the extreme environmental conditions in high Andean regions (García-Núñez et al. 2004; González et al. 2007; Rodriguez-Caton et al. 2021). Unfortunately, the highly complicated taxonomic situation within the genus causes difficulties in the species classification (Espinoza et al. 2019), making it necessary to search for new approaches that support a precise delimitation. For example, plastome genomes are highly valuable in taxonomy and phylogeny, as they are mainly maternally inherited and highly conserved (Chávez-Galarza et al. 2021; Díaz et al. 2022) and offer valuable information regarding evolutionary processes and species delimitation (Wang et al. 2024). For this reason, we used NGS and assembled the complete chloroplast genome of *P. rugulosa* to determine its phylogenetic relationship compared to other species of the *Rosacea* family.

## Materials and methods

The fresh samples of *P. rugulosa* were collected near Chapiquiña town of Provincia de Putre in Chile (GPS: 18°24′29.0′′S, 69°30′28.0′′W; 3,641 masl) (Figure 1). Moreover, the voucher specimens (EIF17383) were deposited in the Herbarium EIF of the Facultad de Ciencias Forestales y de la Conservación de la Naturaleza (https://sweetgum.nybg.org/

**CONTACT** Wilson Huanca-Mamani whuanca@academicos.uta.cl Laboratorio de Biología Molecular de Plantas, Facultad de Ciencias Agronómicas, Universidad de Tarapacá, Arica, Chile. Centro de Genética y Genómica Uasara (CGGU), Universidad de Tarapacá, Arica, Chile.

Supplemental data for this article can be accessed online at https://doi.org/10.1080/23802359.2025.2528566.

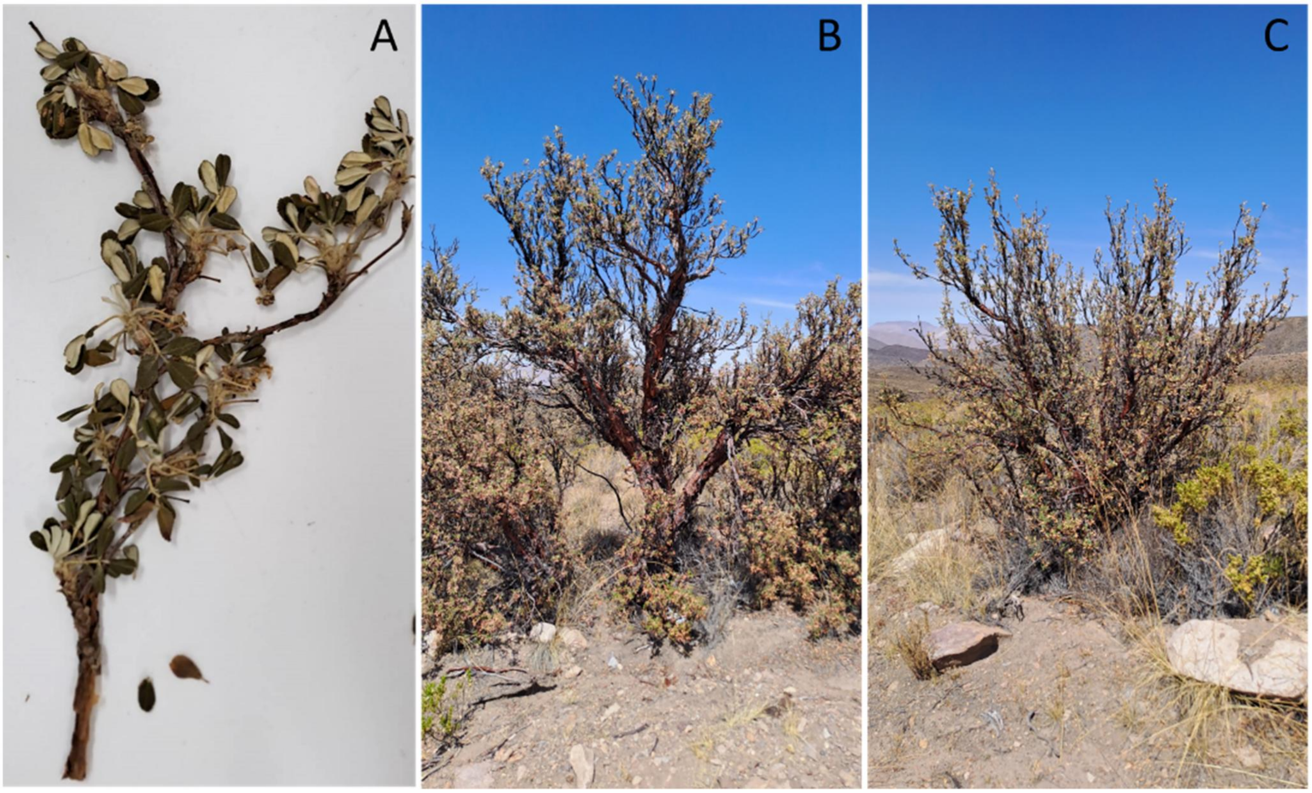

**Figure 1.** Photographs of *Polylepis rugulosa* Bitter, taken by Wilson Huanca-Mamani, near Chapiquiña, Provincia de Putre, Chile (18°24’29.0”S, 69°30’28.0”W). (A) Flowers and leaves branch, (B and C) field photos of two complete trees. It is a perennial tree, reaching a height of between 3 and 7 meters. It has reddish-brown bark that peels off in fragments and a diameter that can reach up to 1 m. Its leaves are pinnately compound, with 1 to 3 leaflets, ranging from oval to circular in shape. The upper surface is glossy, while the underside has whitish hairs. The inflorescences, measuring between 4.5 and 10 cm in length, are hanging and consist of hermaphroditic, actinomorphic flowers that lack petals.

science/ih/herbarium-details/?irn=126262), Universidad de Chile (Nicolás García; ngarcia@uchile.cl).

The total DNA of *P. rugulosa* was extracted using a modified CTAB method (Contreras-Díaz et al. 2022). Genomic paired-end sequencing (PE150) was performed on an Illumina NovaSeq 6000, generating approximately 24GB clean reads. Trim Galore (Krueger 2019) was used to filter low-quality reads and sequencing adapters. The paired-end reads were qualitatively assessed and assembled using SPAdes software 3.15.5 (Bankevich et al. 2012). Contigs related to chloroplast were mapped to the reference genome of *Sanguisorba officinalis* (NC_044694) (Meng et al. 2018) using Geneious Prime 2023.2 (https://www.geneious.com/) (Kearse et al. 2012). The complete plastome genome was annotated using the online tool CPGAVAS2 (Shi et al. 2019) and the circular map of the plastome genome was generated using the CPGView program (Liu et al. 2023). The annotated plastome genome was submitted to GenBank with the accession number OQ834952.

Phylogenetic analyses were conducted using complete plastome genome sequences of 23 species of the family *Rosaceae*, and two species of the family *Rhamnaceae* were included as outgroups. The complete plastome genome sequences with default parameters were aligned using MAFFT software (Katoh and Standley 2013). The best-fitting nucleotide substitution model of sequence evolution, model TVM+G4, was determined using the Corrected Akaike Information Criterion (AICc) through Modeltest-NG on XSEDE (Darriba et al. 2020). The maximum-likelihood (ML) inference was carried out using RAxML-HPC BlackBox v.8.1.12 (Stamatakis 2014) with 1,000 bootstrap replicates, using the CIPRES Science Gateway v3.3 (Miller et al. 2010). Non-parametric bootstrap support (BS) values were used to measure the internal nodes of the resulting trees.

## Results

We sequenced the plastome genome of *P. rugulosa* (GenBank accession number: OQ834952) using Illumina NovaSeq 6000 platform with an average coverage of 8117x (Supplemetal Figure S1). The plastome genome is composed of four regions, with a total length of 155,163 bp (Figure 2). The two inverted repeat regions (IRs) contain 26,556 bp and are separated by a large single copy region (LSC) of 85,290 bp and a small single copy region (SSC) of 18,761 bp (Figure 2). The GC content in the plastome genome was 37.3%. A total of 129 genes were predicted, including 84 protein-coding genes (PCGs), eight rRNA genes, and 37 tRNA genes. Six unique PCGs (*rps12*, *rps7*, *rpl2*, *rpl23*, *ndhB*, and *ycf2*), seven unique tRNA genes (*trnA-UGC*, *trnI-GAU*, *trnL-CAA*, *trnI-CAU*, *trnN-GUU*, *trnR-UGC* and *trnV-GAC*) and four unique rRNA genes (*rrn16S*, *rrn23S*, *rrn4.5S*, *rrn5S*) were located at the IR regions. In the complete plastome, fourteen genes (*rps16*, *rpoC1*, *petB*, *petD*, *rpl16*, *rpl2*, *ndhB*, *ndhA*, *trnK-UUU*, *trnG-UCC*, *trnL-UAA*, *trnV-UAC*, *trnI-GAU* and *trnA-UGC*) contained one intron each, whereas two genes (*ycf3* and *clpP*) contain two introns

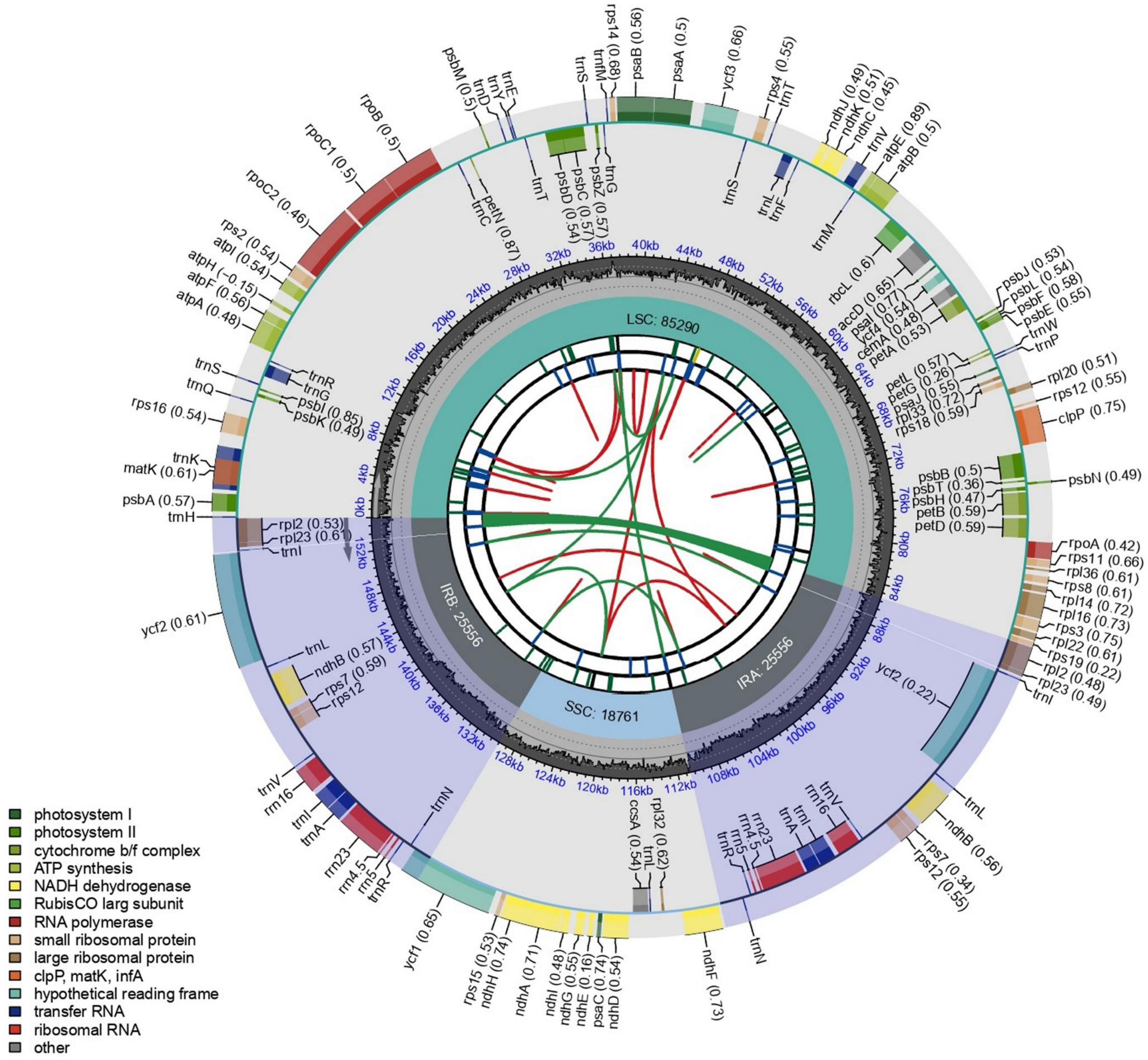

**Figure 2.** Schematic map of overall features of the chloroplast genome of *Polylepis rugulosa*. The map contains six tracks in default. From the center outward, the first track represents the forward and reverse repeats indicated by red and green arcs, respectively. The second and third tracks are represented by short bars, indicating tandem repeats and microsatellite sequences, respectively. The fourth track shows the plastome structure: large single-copy (LSC) region, small single-copy (SSC) region, and inverted repeated regions (IRA, and IRB). The fifth track shows the GC ratio in dark gray. The genes are shown on the sixth track. The optional codon usage bias is displayed in the parenthesis after the gene name. Genes are color-coded by their functional classification. The transcription directions of the inner and outer genes are clockwise and counterclockwise, respectively. The functional classification of the genes is shown in the bottom left corner.

(Supplemetal Figure S2). The *rps12* gene was a trans-splicing gene (Supplemetal Figure S3).

The resulting ML tree revealed two main clades with high bootstrap value (BS = 100): one containing the outgroup species *Barchemiella wilsonii* and *Spyridium villosum* (*Rhamnaceae*), and the other containing all 23 *Rosaceae* species (Figure 3). Within the *Rosaceae* cluster, three subclades were identified: the *Potentilleae* clade consisting of *P. lineata*, *S. adpressa*, *P. mongolica*, *P. glabra*, *F. iturupensis*, *F. viridis*, *F. nipponica* and *F. pentaphylla* (BS = 100); the *Colurieae* clade including *G. japonicum*, *G. aleppicum*, *C. longifolia*, *G. macrophyllum*, *G. rupestre* and *G. urbanum* (BS = 100); and the Sanguisorbeae clade, corresponding of *H. abyssinica*, *A. nipponica*, *A. pilosa*, *A. coreana* (*Agrimoniinae*), *P. rugulosa*, *S. tenuifolia*, *S. officinalis*, *S. stipulata* and *B. extipulata* (*Sanguisorbinae*) (BS = 100). This analysis strongly supported *P. rugulosa* as a sister species of *Sanguisorba* species (BS = 100) (Figure 3).

## Discussion and conclusion

Genomic research with NGS technology has revolutionized the field of genomics, allowing efficient sequencing of complete chloroplast genomes (Moore et al. 2006). Here, we successfully assembled and annotated the chloroplast genome sequence of *P. rugulosa* for the first time. In fact, no complete chloroplast genome sequencing data have been publicly available in the *Polylepis* genus.

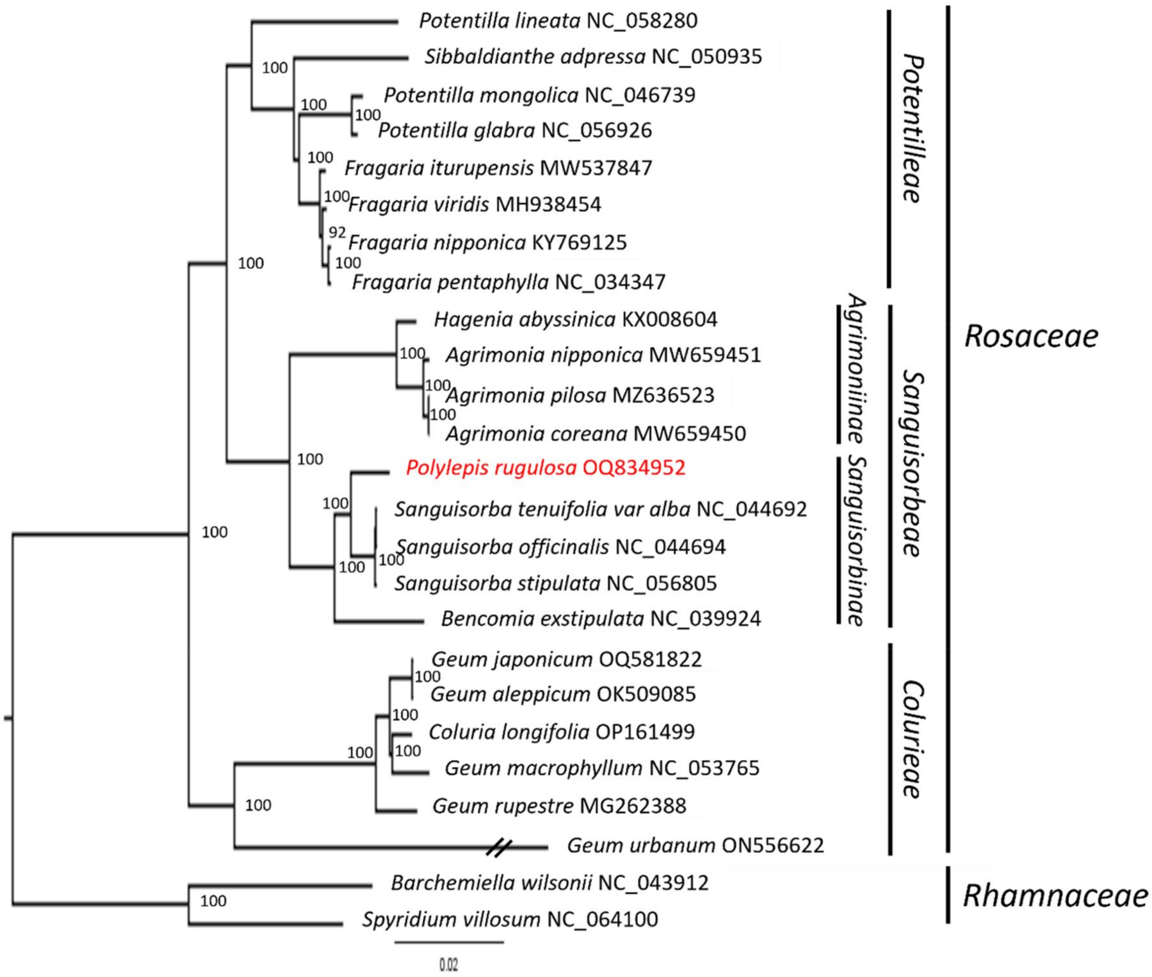

**Figure 3.** The maximum-likelihood tree was constructed based on the twenty-three chloroplast genome sequences of *Rosaceae* species. The following sequences were used: *Potentilla lineata* Treviranus NC_058280 (Zhang and Zhang 2021), *Sibbaldianthe adpressa* (Bunge) Juz. NC_050935 (Tian et al. 2020), *P. mongolica* Maxim NC_046739 (Cong and Jiang 2020), *P. glabra* Lodd NC_056926 (Yu et al. 2021), *Fragaria iturupensis* J. Gay MW537847, *F. viridis* Duchesne MH938454, *F. nipponica* var. yakusimensis KY769125, *F. pentaphylla* Losinsk NC_034347 (Bai et al. 2017), *Hagenia abyssinica* (Bruce) J.F.Gmel KX008604 (Gichira et al. 2017), *Agrimonia nipponica* Koidz. MW659451, *A. Pilosa* MZ636523, *A. coreana* MW659450, *Polylepis rugulosa* Bitter OQ834952 (this study), *Sanguisorba tenuifolia* var alba NC_044692, *S. officinalis* L. NC_044694 (Meng et al. 2018), *S. stipulata* NC_056805, *Bencomia exstipulata* Svent. NC_039924, *Geum japonicum* Thunb. OQ581822, *G. aleppicum* Jacq. OK509085 (Zhang et al. 2022), *Coluria longifolia* Maxim. OP161499 (Guo et al. 2023), *G. macrophyllum* Willd. NC_053765 (Q. Q. Li and Wen 2021), *G. rupestre* (T.T.Yu & C.L.Li) Smedmark MG262388 (Duan et al. 2018), *G. urbanum* L. ON556622. *Barchemiella wilsonii* (C.K.Schneid.) Koidz. NC_043912 (Li et al. 2019) and *Spyridium villosum* (Turcz.) Benth. NC_064100 (Clowes et al. 2022) from the *Rhamnaceae*, served as the outgroup. The bootstrap support values are place on the nodes.

Our results showed within the *Sanguisorbinae* clade that *P. rugulosa* formed a highly supported clade with *Sanguisorba* species (BS = 100). A phylogenetic analysis study of whole plastomes showed a like relationship between *Polylepis* species and *Sanguisorba* species, however *P. rugulosa* was not included on this study, and the more than 130 whole plastomes of *Rosaceae* reconstructed not available for analysis from GenBank (Zhang et al. 2017). In our study, the ML analyses of plastome data strongly supported *P. rugulosa* and *Sanguisorba* species as monophyletic groups, which were placed within the *Sanguisorbinae* clade (*Sanguisorbeae* tribe). Thus, these molecular results are compatible with previous studies of the genus *Polylepis* and *Rosaceae* family (Potter et al. 2007; Longhi et al. 2014).

With this study about the chloroplast genome of *P. rugulosa*, we improve our understanding of its phylogeny in the hope of aiding the conservation of this valuable species.

## Acknowledgements

We thank the Educación Superior Regional program ESR UTA2295. RC thanks AFOREST, a Millenium Nucleus supported by ANID – MILENIO – NCS2022_024. WHM designed and conceived the research; JChG and RC assembled the chloroplast genome; RC annotated the chloroplast genome and drafted the manuscript; WHM collected the samples in fields, analyzed the phylogenetic results. All authors discussed the results and revised the final manuscript.

## Authors contributions

CRediT: **Roberto Contreras-Díaz**: Methodology, Writing – original draft; **Julio César Chávez-Galarza**: Methodology; **Wilson Huanca-Mamani**: Investigation, Methodology, Writing – original draft, Writing – review & editing.

## Disclosure statement

No potential conflict of interest was reported by the author(s).

## Ethical approval

The authors comply with the IUCN policies research involving species at risk of extinction, the Convention on Biological Diversity, and the Convention on the Trade in Endangered Species of Wild Fauna and Flora. The collection of plant materials of *Polylepis rugulosa* was conducted according to the guidelines provided by Corporación Nacional Forestal (CONAF) and did not cause any damage to this endangered species. A permit for sample collection and scientific research on wild flora (AyP No 009/2024) was provided by CONAF.

## Funding

This work was supported by the Educacion Superior Regional under Grant ESR2295.

## Data availability statement

The data that supports this study is openly available in GenBank of NCBI (https://www.ncbi.nlm.nih.gov) under the accession number OQ834952. The associated Bio project, Biosample, and SRA numbers are PRJNA1049573, SAMN38701603, and SRR27124996, respectively.

## References

Bai LJ, Ye YT, Chen Q, Tang HR. 2017. The complete chloroplast genome sequence of the white strawberry *Fragaria pentaphylla*. Conservation Genet Resour. 9(4):659–661. doi:10.1007/s12686-017-0713-5.

Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol. 19(5):455–477. doi:10.1089/cmb.2012.0021.

Chávez-Galarza JC, Cardenas-Ninasivincha S, Contreras R, Ferro-Mauricio R, Huanca-Mamani W. 2021. Chloroplast genome of *Tillandsia landbeckii* Phil. (Bromeliaceae) a species adapted to the hyper-arid conditions of the Atacama and Peruvian desert. Mitochondrial DNA B Resour. 6(12):3375–3377. doi:10.1080/23802359.2021.1997122.

Clowes C, Fowler RM, Fahey PS, Kellermann J, Brown GK, Bayly MJ. 2022. Big trees of small baskets: phylogeny of the Australian genus. Aust Syst Bot. 35(2):95–119. doi:10.1071/SB21034.

Cong L, Jiang H. 2020. The complete chloroplast genome of *Potaninia mongolica* (Rosaceae) from China. Mitochondrial DNA B Resour. 5(1): 574–575. doi:10.1080/23802359.2019.1710295.

Contreras-Díaz R, Carevic FS, Huanca-Mamani W, Oses R, Arias-Aburto M, Navarrete-Fuentes M. 2022. Chloroplast genome structure and phylogeny of *Geoffroea decorticans*, a native tree from Atacama Desert. Electron J Biotechnol. 60:19–25. doi:10.1016/j.ejbt.2022.09.005.

Cuyckens GAE, Christie DA, Domic AI, Malizia LR, Renison D. 2016. Climate change and the distribution and conservation of the world's highest elevation woodlands in the South American Altiplano. Global Planet Change. 137:79–87. doi:10.1016/j.gloplacha.2015.12.010.

Darriba D, Posada D, Kozlov AM, Stamatakis A, Morel B, Flouri T. 2020. ModelTest-NG: a new and scalable tool for the selection of DNA and protein evolutionary models. Mol Biol Evol. 37(1):291–294. doi:10.1093/molbev/msz189.

Díaz RC, Mamani WH, Brink L, van den Fuentes MN, Aburto MA. 2022. The complete chloroplast genome of the endangered species garra de león [*Bomarea ovallei* (Phil.) Ravenna] from Chile. IJGPB. 82(03): 365–368. doi:10.31742/ISGPB.82.3.14.

Duan N, Liu S, Liu BB. 2018. Complete chloroplast genome of *Taihangia rupestris* var. rupestris (Rosaceae), a rare cliff flower endemic to China. Conservation Genet Resour. 10(4):809–811. doi:10.1007/s12686-017-0936-5.

Espinoza TEB, Kessler M. 2022. A monograph of the genus Polylepis (Rosaceae). PhytoKeys. 203:1–274. doi:10.3897/phytokeys.203.83529.

Espinoza TEB, Quispe-Melgar HR, Kessler M. 2019. Taxonomic reevaluation of the *Polylepis sericea* complex (Rosaceae), with the description of a new species. Systematic Botany. 44(2):324–334. doi:10.1600/036364419X15562052252225.

García-Núñez C, Rada F, Boero C, González J, Gallardo M, Azócar A, Liberman-Cruz M, Hilal M, Prado F. 2004. Leaf gas exchange and water relations in *Polylepis tarapacana* at extreme altitudes in the Bolivian Andes. Photosynt. 42(1):133–138. doi:10.1023/B:PHOT.0000040581.94641.ed.

Gichira AW, Li Z, Saina JK, Long Z, Hu G, Gituru RW, Wang Q, Chen J. 2017. The complete chloroplast genome sequence of an endemic monotypic genus Hagenia (Rosaceae): structural comparative analysis, gene content and microsatellite detection. PeerJ. 5(1):e2846. doi:10.7717/peerj.2846.

González JA, Gallardo MG, Boero C, Liberman Cruz M, Prado FE. 2007. Altitudinal and seasonal variation of protective and photosynthetic pigments in leaves of the world's highest elevation trees *Polylepis tarapacana* (Rosaceae). Acta Oecologica. 32(1):36–41. doi:10.1016/j.actao.2007.03.002.

Guo J-J, Zhang Z-P, Li Q-Q, Khasbagan, Soyolt. (2023). The complete chloroplast genome of *Geum longifolium* (Maxim.) Smedmark 2006 (Rosaceae: colurieae) and its phylogenomic implications. Mitochondrial DNA B Resour. 8(10), 1124–1127. doi:10.1080/23802359.2023.2270212.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30(4):772–780. doi:10.1093/molbev/mst010.

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, et al. 2012. Geneious Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics. 28(12): 1647–1649. doi:10.1093/bioinformatics/bts199.

Krueger F. 2019. Trim Galore. https://github.com/FelixKrueger/TrimGalore.

Liu S, Ni Y, Li J, Zhang X, Yang H, Chen H, Liu C. 2023. CPGView: a package for visualizing detailed chloroplast genome structures. Mol Ecol Resour. 23(3):694–704. doi:10.1111/1755-0998.13729.

Li Y, Wang J, Li P, Cheng S, Wang F. 2019. The complete chloroplast genome sequence of *Berchemiella wilsonii* (Rhamnaceae), an endangered endemic species. Mitochondrial DNA Part B: resources. 4(1):452–454. doi:10.1080/23802359.2018.1555018.

Li QQ, Wen J. 2021. The complete chloroplast genome of *Geum macrophyllum* (Rosaceae: colurieae). Mitochondrial DNA B Resour. 6(2):297–298. doi:10.1080/23802359.2020.1861562.

Longhi S, Giongo L, Buti M, Surbanovski N, Viola R, Velasco R, Ward JA, Sargent DJ. 2014. Molecular genetics and genomics of the Rosoideae: State of the art and future perspectives. Hortic Res. 1(1):1. doi:10.1038/hortres.2014.1.

Meng XX, Xian YF, Xiang L, Zhang D, Shi YH, Wu ML, Dong GQ, Ip SP, Lin ZX, Wu L, et al. 2018. Complete chloroplast genomes from Sanguisorba: identity and variation among four species. Molecules. 23(9), 2137. doi:10.3390/molecules23092137.

Miller MA, Pfeiffer W, Schwartz T. 2010. Creating the CIPRES Science Gateway for inference of large phylogenetic trees. 2010 Gateway Computing Environments Workshop, GCE 2010. doi:10.1109/GCE.2010.5676129.

MMA. 2023. *Categoría de Conservación Polylepis tarapacana, ID especie N°260*. Ministerio de Medio Ambiente, *Reporte Res Ex 199/MMA 2023 (19$^{no}$ Proceso RCE)*, Santiago, Chile.

Moore MJ, Dhingra A, Soltis PS, Shaw R, Farmerie WG, Folta KM, Soltis DE. 2006. Rapid and accurate pyrosequencing of angiosperm chloroplast genome s. BMC Plant Biol. 6(1):17. doi:10.1186/1471-2229-6-17.

Potter D, Eriksson T, Evans RC, Oh S, Smedmark JEE, Morgan DR, Kerr M, Robertson KR, Arsenault M, Dickinson TA, et al. 2007. Phylogeny and classification of Rosaceae. Plant Syst Evol. 266(1–2):5–43. doi:10.1007/s00606-007-0539-9.

Rodriguez-Caton M, Andreu-Hayles L, Morales MS, Daux V, Christie DA, Coopman RE, Alvarez C, Rao MP, Aliste D, Flores F, et al. 2021. Different climate sensitivity for radial growth, but uniform for tree-ring stable isotopes along an aridity gradient in *Polylepis tarapacana*, the world's highest elevation tree species. Tree Physiol. 41(8):1353–1371. doi:10.1093/treephys/tpab021.

Schmidt-Lebuhn AN, Kumar M, Kessler M. 2006. An assessment of the genetic population structure of two species of *Polylepis* Ruiz & Pav. (Rosaceae) in the Chilean Andes. Flora. 201(4):317–325. doi:10.1016/j.flora.2005.07.007.

Shi L, Chen H, Jiang M, Wang L, Wu X, Huang L, Liu C. 2019. CPGAVAS2, an integrated plastome sequence annotator and analyzer. Nucleic Acids Res. 47(W1):W65–W73. doi:10.1093/nar/gkz345.

Stamatakis A. 2014. RAxML version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 30(9):1312–1313. doi:10.1093/bioinformatics/btu033.

Tian W-J, Li Q-Q, Khasbagan. (2020). The complete chloroplast genome of *Sibbaldianthe adpressa* (Rosaceae: potentilleae). Mitochondrial DNA Part B Res. 5(2), 1563–1564. doi:10.1080/23802359.2020.1742601.

Wang LL, Li Y, Zheng SS, Kozlowski G, Xu J, Song YG. 2024. Complete chloroplast genomes of four oaks from the section *Cyclobalanopsis* improve the phylogenetic analysis and understanding of evolutionary processes in the genus *Quercus*. Genes (Basel). 15(2):230. doi:10.3390/genes15020230.

Yu S, Kang WJ, Yang F, Li FX. 2021. The complete chloroplast genome sequence of *Potentilla glabra* Lodd. Mitochondrial DNA B Resour. 6(7): 1873–1874. doi:10.1080/23802359.2021.1934141.

Zhang SD, Jin JJ, Chen SY, Chase MW, Soltis DE, Li HT, Yang JB, Li DZ, Yi TS. 2017. Diversification of Rosaceae since the Late Cretaceous based on plastid phylogenomics. New Phytol. 214(3):1355–1367. doi:10.1111/nph.14461.

Zhang P, Wang L, Lu X. 2022. Complete chloroplast genome of *Geum aleppicum* (Rosaceae). Mitochondrial DNA B Resour. 7(1):234–235. doi:10.1080/23802359.2021.2024461.

Zhang Q, Zhang D. 2021. Complete chloroplast genome sequence of medicinal plant *Potentilla lineata* Treviranus (Rosaceae) from Yunnan, China. Mitochondrial DNA B Resour. 6(8):2422–2424. doi:10.1080/23802359.2021.1951137.