



OPEN ACCESS

EDITED AND REVIEWED BY

Subhojit Datta,
Central Research Institute for Jute and
Allied Fibres (ICAR), India

*CORRESPONDENCE

Nripendra Vikram Singh,
nripendras72@gmail.com
Umesh K. Reddy,
ureddy@wvstateu.edu

[†]These authors have contributed equally
to this work and share first authorship

SPECIALTY SECTION

This article was submitted to Plant
Genomics,
a section of the journal
Frontiers in Genetics

RECEIVED 19 September 2022

ACCEPTED 28 September 2022

PUBLISHED 17 October 2022

CITATION

Singh NV, Patil PG, Roopa Sowjanya P,
Parashuram S, Natarajan P, Babu KD,
Pal RK, Sharma J and Reddy UK (2022),
Corrigendum: Chloroplast genome
sequencing, comparative analysis, and
discovery of unique cytoplasmic
variants in pomegranate (*Punica
granatum* L.).
Front. Genet. 13:1047979.
doi: 10.3389/fgene.2022.1047979

COPYRIGHT

© 2022 Singh, Patil, Roopa Sowjanya,
Parashuram, Natarajan, Babu, Pal,
Sharma and Reddy. This is an open-
access article distributed under the
terms of the [Creative Commons
Attribution License \(CC BY\)](https://creativecommons.org/licenses/by/4.0/). The use,
distribution or reproduction in other
forums is permitted, provided the
original author(s) and the copyright
owner(s) are credited and that the
original publication in this journal is
cited, in accordance with accepted
academic practice. No use, distribution
or reproduction is permitted which does
not comply with these terms.

Corrigendum: Chloroplast genome sequencing, comparative analysis, and discovery of unique cytoplasmic variants in pomegranate (*Punica granatum* L.)

Nripendra Vikram Singh^{1*†}, Prakash Goudappa Patil^{1†},
P. Roopa Sowjanya^{1†}, Shilpa Parashuram^{1†},
Purushothaman Natarajan², Karuppannan Dhinesh Babu¹,
Ram Krishna Pal¹, Jyotsana Sharma¹ and Umesh K. Reddy^{2*}

¹ICAR-National Research Centre on Pomegranate (NRCP), Solapur, India, ²Gus R. Douglass Institute
and Department of Biology, West Virginia State University, West Virginia, WV, United States

KEYWORDS

chloroplast, plastid genome, pomegranate, phylogenetic, sequence diversity

A Corrigendum on Chloroplast genome sequencing, comparative analysis, and discovery of unique cytoplasmic variants in pomegranate (*Punica granatum* L.)

by Singh NV, Patil PG, P RS, Parashuram S, Natarajan P, Babu KD, Pal RK, Sharma J and Reddy UK
(2021). *Front. Genet.* 12:704075. doi: 10.3389/fgene.2021.704075

In the original article, there was an error in [Table 2](#). Parameters “Gene Size(bp)” & “tRNA size (bp) values” were not relevant and have been removed. The corrected table appears below.

There was also an error in [Table 4](#). For Parameters “tRNA size (bp)” and “rRNA size (bp)”, the value for “Bhagawa (NRCP)” was modified from “9043” and “10606” to “-” and “9043” respectively. The corrected table appears below.

The authors apologize for this error and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

Publisher's note

All claims expressed in this article are solely those of the authors and do not necessarily represent those of their affiliated organizations, or those of the publisher, the editors and the reviewers. Any product that may be evaluated in this article, or claim that may be made by its manufacturer, is not guaranteed or endorsed by the publisher.

TABLE 2 Summary of complete chloroplast genomes of 16 pomegranate genotypes.

Parameters	<i>Punica granatum</i> (Pg)															
	Cultivars												Wild			
	SL	SA	B	DF	RN	SB	M	W	A	R	J	G	GR	1201	1181	8718
Genome Size (bp)	158,641	158,641	158,641	158,639	158,638	158,641	158,641	158,643	158,641	158,633	158,641	158,641	158,662	158,593	158,593	158,633
Overall GC content (%)	36.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9	36.9
LSC size (bp)	89,025	89,025	89,025	89,021	89,020	89,025	89,025	89,027	89,025	89,014	89,025	89,025	89,044	88,976	88,976	89,016
IR-A size (bp)	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467
IR-B size (bp)	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467	25,467
SSC size (bp)	18,682	18,682	18,682	18,684	18,684	18,682	18,682	18,682	18,682	18,685	18,682	18,682	18,684	18,683	18,683	18,683
Protein coding regions (bp)	77,059	77,083	77,083	77,059	77,059	77,181	77,083	77,059	77,083	77,083	77,059	77,083	77,083	77,059	77,083	77,059
rRNA size (bp)	9,043	9,043	9,043	9,043	9,043	9,050	9,043	9,043	9,043	9,043	9,043	9,043	9,043	9,043	9,043	9,043
Number of Protein coding genes	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82	82
Number of tRNA	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37	37
Number of rRNA	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8	8
Total Number of genes	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127	127

SL, Solapur Lal; SA, Solapur Anardana; B, Bhagawa; DF, double-flowering type (ornamental)*; RN, Red Nana (ornamental)*; SB, Super Bhagawa; M, Mridula; W, Wonderful; A, Arakta; R, Ruby; J, Jyoti; G, Ganesh; GR, Gul-e-Shah Red; 8718, IC-318718.

TABLE 4 Comparison of the “Bhagawa (NRCP)” chloroplast genome with other genotypes.

Parameters	<i>Punica granatum</i>			Other species		
	Bhagawa (NRCP)	Bhagawa (R)	Helow	Tunisia (NC035240)	<i>L. intermedia</i> (NC034662)	<i>L. speciosa</i> (NC031414)
Genome Size (bp)	158,641	158,641	158,630	158,633	152,330	152,476
Overall GC content (%)	36.9	36.9	36.9	36.9	37.6	37.6
LSC size (bp)	89,026	89,026	89,015	89,017	83,987	84,051
SSC size (bp)	18,682	18,682	18,686	18,687	16,873	16,979
IR size (bp)	25,467	25,467	25,466	25,465	25,736	25,723
Protein coding regions (bp)	77,083	-	78,159	78,816	81,300	81,309
tRNA size (bp)	-	-	2,816	2,790	2,810	2,742
rRNA size (bp)	9,043	-	9,050	9,050	9,050	9,046
Number of genes	127	112	131	129	130	129
Number of protein coding genes	82	78	86	84	85	85
Number of rRNA	8	4	8	8	8	8
Number of tRNA	37	30	37	37	37	36
Genes with introns	18	-	11	11	13	13