Complete Plastome Sequence of *Ludwigia octovalvis* (Onagraceae), a Globally Distributed Wetland Plant

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Here, we present the first plastome of *Ludwigia octovalvis* (Onagraceae, Myrtales) as well as the first plastome in the subfamily Ludwigioideae. This genome is notable for its contracted inverted repeat regions and an expanded small single-copy region compared to other species in the orders Myrtales and Geraniaceae.

*e Ludwigia octovalvis* is distributed worldwide (1) and has a long history of usage for medicinal purposes and as herbal teas (2, 3). Presently, *L. octovalvis* is being explored in several biotherapy and anticancer studies (4–6). In some wetland ecosystems, *L. octovalvis* is also considered an invasive plant (7). In some wetland ecosystems, *L. octovalvis* is also considered an invasive plant (7, 8). The plastome sample reported here was acquired from *L. octovalvis* seedlings (voucher: Liu 2014GH96, MO) growing in the research greenhouse at the Missouri Botanical Garden (St. Louis, MO, USA) from seeds collected at Angra dos Reis, Brazil (voucher: Martins & Liu 652, MO).

The library of genomic DNA was prepared using the NEBNext Ultra library prep kit and sequenced with a 2 × 150-bp Illumina MiSeq run. Trimming and quality control were conducted using Cutadapt (9) and BBduk in BBMap (https://sourceforge.net/projects/bbmap/), respectively. To identify reads originating from the plastome of *L. octovalvis*, we mapped the trimmed reads to the plastomes of 14 species in orders Myrtales and Geraniaceae (accession numbers KC180806, KC180805, KC180804, KC180801, KP015033, KC180773, KC180782, KC180771, JQ809970, NC029808, KC118607, KC118606, KC180807, and GQ870669) and then extracted the matching reads using BWA (10) and SAMtools (11). The matching reads were then assembled de novo using SPAdes (12). Gaps among contigs were closed using an iterative mapping strategy (13) in which the contigs were extended by repeatedly mapping all trimmed reads to the contigs using the medium sensitivity/fast option in Geneious R7 (14). Sequences at the gaps and at the junctions between large single-copy (LSC)/small single-copy (SSC) regions and inverted repeats (IRs) were validated by visually inspecting the mapped reads. Gene annotations were transferred from the plastomes of three closely related species (accession numbers NC029808, KX118607, and KX118606) with a 60% or greater similarity in Geneious and then verified by BLAST searches. The tRNA genes were further confirmed using trRNAscan-SE 1.21 (15, 16).

The completed plastome of *L. octovalvis* is a circular molecule of 159,396 bp in length (198-fold coverage) with a G+C content of 37.4%. In total, 132 genes were annotated: 85 unique genes (including 22 tRNA genes) are in the LSC, 13 unique genes (including one tRNA gene) are in the SSC, and 17 genes (including 4 rRNA genes and 7 tRNA genes) are in both IRs. Introns were detected in 17 genes (including 6 tRNA genes). No genes spanned across the LSC/SSC and IRs junctions. The remarkable features of this plastome are its considerable IR contraction and SSC expansion in comparison to other plastomes in the orders Myrtales and Geraniaceae; namely, the IR of *L. octovalvis* is 24,755 kb, whereas the IR of other species in the Myrtales and Geraniaceae is 25.7 to ~28.7 kb, and the SSC of *L. octovalvis* is 19,703 kb, in contrast to other species in the Myrtales and Geraniaceae that have an SSC of 4.5 to ~19.0 kb (17, 18).

These plastome data will be useful for investigating genome rearrangements in basal lineages in the Rosids II clade as well as for phylogenomic studies of Onagraceae and *Ludwigia*.

**Accession number(s).** The annotated plastome sequence of *L. octovalvis* was deposited in GenBank under accession no. KX827312.

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**REFERENCES**

1. Raven PH. 1963. The old world species of *Ludwigia* (including *Jussiaea*), with a synopsis of the genus (Onagraceae). Reinwardtia 6:327–427.
2. Zhao X-M. 1765. Supplement to the Compendium of Materia Medica. The People’s Medical Publishing House, Beijing, China (in Chinese.)
3. Dennis PA. 1988. Herbal medicine among the Miskito of Eastern Nicaragua. Econ Bot 42:16–28. http://dx.doi.org/10.1007/BF02859024.
4. Chang CI, Kuo CC, Chang JY, Kuo YH. 2004. Three new oleanane-type triterpenes from Ludwigia octovalvis with cytotoxic activity against two human cancer cell lines. J Nat Prod 67:91–93. http://dx.doi.org/10.1021/np030267m.
5. Hsieh P, Hsu L, Lai C, Wu C, Hwang T, Lin Y, Wu Y. 2009. Evaluation of the bioactivities of extracts of endophytes isolated from Taiwanese herbal plants. World J Microbiol Biotechnol 25:1461–1469. http://dx.doi.org/10.1007/s11274-009-0036-0.
6. Kadam Yakob H, Manaf Uyub A, Fariza Sulaiman S. 2015. Immune-stimulating properties of 80% methanolic extract of Ludwigia octovalvis against Shiga toxin-producing E. coli O157:H7 in BALB/c mice following experimental infection. J Ethnopharmacol 172:30–37. http://dx.doi.org/10.1016/j.jep.2015.06.006.
7. Wagner WL, Hoch PC, Raven PH. 2007. Revised classification of the Onagraceae. Syst Bot Monogr 83:1–240.
8. Raven PH, Tai W. 1979. Observations of chromosomes in Ludwigia (Onagraceae). Ann Mo Bot Gard 66:862–879. http://dx.doi.org/10.2307/2398926.
9. Martin M. 2011. Cutadapt removes adapter sequences from high-throughput sequencing reads. EMBOlet J 17:10. http://dx.doi.org/10.14806/ej.17.1.200.
10. Li H, Durbin R. 2009. Fast and accurate short read alignment with Burrows-Wheeler transform. Bioinformatics 25:1754–1760. http://dx.doi.org/10.1093/bioinformatics/btp324.
11. Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R, 1000 Genome Project Data Processing Subgroup. 2009. The Sequence Alignment/MAP format and SAMtools. Bioinformatics 25:2078–2079. http://dx.doi.org/10.1093/bioinformatics/btp352.
12. Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Prjibelski AD, Pyshkin AV, Sirotkin AV, Vyahhi N, Tesler G, Alekseyev MA, Pevzner PA. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. J Comput Biol 19:455–477. http://dx.doi.org/10.1089/cmb.2012.0021.
13. Tsai IJ, Otto TD, Berriman M. 2010. Improving draft assemblies by iterative mapping and assembly of short reads to eliminate gaps. Genome Biol 11:R41. http://dx.doi.org/10.1186/gb-2010-11-4-r41.
14. Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran G, Thierer T, Ashton B, Meintjes P, Drummond A. 2012. Geneious basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28:1647–1649. http://dx.doi.org/10.1093/bioinformatics/bts199.
15. Schattner P, Brooks AN, Lowe TM. 2005. The tRNAscan-SE, snoGPS Web servers for the detection of tRNAs and snoRNAs. Nucleic Acids Res 33:W686–W689. http://dx.doi.org/10.1093/nar/gki366.
16. Lowe TM, Eddy SR. 1997. tRNAscan-SE: a program for improved detection of transfer RNA genes in genomic sequence. Nucleic Acids Res 25:955–964. http://dx.doi.org/10.1093/nar/25.3.0955.
17. Gu C, Tembrock LR, Johnson NG, Simmons MP, Wu Z. 2016. The complete plastid genome of Lagerstroemia fauriei and loss of rpl2 intron from Lagerstroemia (Lythraceae). PLoS One 11:e0150752. http://dx.doi.org/10.1371/journal.pone.0150752.
18. Weng M-L, Blazier JC, Govindu M, Jansen RK. 2014. Reconstruction of the ancestral plastid genome in Geraniaceae reveals a correlation between genome rearrangements, repeats, and nucleotide substitution rates. Mol Biol Evol 31:645–659. http://dx.doi.org/10.1093/molbev/msu257.