Characterization of the complete chloroplast genome of sorrel (Rumex acetosa)

Lingjian Gua**, Shaofeng Jiongb, Huaiping Wangc, Dongxin Nonga and Yingying Liua

aGuangxi Botanical Garden of Medicinal Plants, Nanning, China; bGuangdong Province Key Laboratory of Microbial Signals and Disease Control, Department of Plant Pathology, South China Agricultural University, Guangzhou, China; cCardiovascular disease hospital affiliated to Qingdao University, Shandong, China

**These authors contributed equally to this work

Rumex acetosa L. (Polygonaceae), a dioecious plant which has a multiple sex chromosome system (Shibata et al. 1999, 2000), is a perennial herb, commonly known as sheep’s sorrel, red sorrel, sour weed, and field sorrel (Lee et al. 2005). As a traditional medicine plant, it was shown to have some pharmacological activities, including anti-inflammatory, anti-oxidant (Wegiera et al. 2007), anti-tumor, antibacterial, anti-viral, and anti-fungal properties (Taylor et al. 1996; Demirezer et al. 2001; Lee et al. 2005). Meanwhile, its leaves are widely used in sauces and salads (Ahmad et al. 2006). With an aim to retrieve valuable cp molecular markers, indels, and SSRs by comparative analyses with other Rumiceae cp genomes, we assembled and analyzed the chloroplast genome of R. acetosa (Rumiceae) was determined through Illumina sequencing method. The complete chloroplast genome of R. acetosa was 160,269 bp in length and contained a pair of IR regions (30,503 bp) separated by a small single copy region (13,128 bp) and a large single copy region (86,135 bp). This cp genome is encoded with 129 genes including 83 protein-coding genes, 36 tRNA genes, and 8 ribosomal RNA genes. The overall GC content of R. acetosa cp genome is 37.2%. By phylogenetic analysis using Bayesian method, R. acetosa showed the closest relationship with other 2 Rumiceae species, Rheum palmatum and Oxystylis sinensis.

**ABSTRACT**

*Rumex acetosa*, known as sheep’s sorrel, red sorrel, sour weed, and field sorrel, is a species of flowering plant in the buckwheat family Polygonaceae. In this study, the complete chloroplast (cp) genome of *R. acetosa* (Rumiceae) was determined through Illumina sequencing method. The complete chloroplast genome of *R. acetosa* was 160,269 bp in length and contained a pair of IR regions (30,503 bp) separated by a small single copy region (13,128 bp) and a large single copy region (86,135 bp). This cp genome is encoded with 129 genes including 83 protein-coding genes, 36 tRNA genes, and 8 ribosomal RNA genes. The overall GC content of *R. acetosa* cp genome is 37.2%. By phylogenetic analysis using Bayesian method, *R. acetosa* showed the closest relationship with other 2 Rumiceae species, *Rheum palmatum* and *Oxystylis sinensis*.

**ARTICLE HISTORY**

Received 6 June 2018
Accepted 18 June 2018

**KEYWORDS**

*Rumex acetosa*; Chloroplast genome; Illumina sequencing; Phylogenetic analysis

**CONTACT** Yingying Liu yyliu816@163.com
Guangxi Botanical Garden of Medicinal Plants, Nanning 530023, China

© 2018 The Author(s). Published by Informa UK Limited, trading as Taylor & Francis Group.
This is an Open Access article distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.
heterogeneities. Four independent MCMC analyses were run for 1,000,000 cycles in PhyloBayes. Convergence was verified based on time-series plots of the likelihood scores using Tracer (http://tree.bio.ed.ac.uk/software/tracer/). The first 25% cycles were discarded as burn-in, and the maximum clade credibility (MCC) tree was constructed in TreeAnnotator v1.8.0 (Rambaut et al. 2012) depicting the maximum sum of Bayesian posterior probabilities (BPPs). The resulting tree was represented and edited using FigTree v1.4.1 (http://tree.bio.ed.ac.uk/software/figtree/). As shown in Figure 1, the phylogenetic positions of these 44 cp genomes were successfully resolved with full BPPs supports except for 6 nodes. *Rumex acetosa* belongs to the Polygonaceae as expected and exhibited the closest relationship with other 2 Rumiceae species, *Rheum palmatum* and *Oxyria sinensis*.

**Disclosure statement**

No potential conflict of interest was reported by the authors.

**References**

Ahmad S, Ullah F, Sadiq A, Ayaz M, Imran M, Ali I, Zeb A, Ullah F, Shah MR. 2016. Chemical composition, antioxidant and anticholinesterase potentials of essential oil of *Rumex hastatus* D. Don collected from the North West of Pakistan. BMC Complementary Altern Med. 16(1):29.

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 Comp Bio. 19:455–477.

Bi G, Mao Y, Xing Q, Cao M. 2018. HomBlocks: a multiple-alignment construction pipeline for organelle phylogenomics based on locally collinear block searching. Genomics. 110:18–22.

Demirezer LO. 2001. The structures of antioxidant and cytotoxic agents from natural source: anthraquinones and tannins from roots of *Rumex patientia*. Phytochemistry. 58:1213–1217.

Fan K, Sun X-J, Huang M, Wang X-M. 2015. The complete chloroplast genome sequence of the medicinal plant *Rheum palmatum* L. (Polygonaceae). Mitochondrial DNA Part A. 27:1–2936.

Hahn C, Bachmann L, Chevreux B. 2013. Reconstructing mitochondrial genomes directly from genomic next-generation sequencing reads-a baiting and iterative mapping approach. Nucleic Acids Res. Huang DI, Cronk QCB. 2015. Plann: a command-line application for annotating plastome sequences. Appl Plant Sci. 3:1500026.

Lartillot N, Lepage T, Blanquart S. 2009. PhyloBayes 3: a Bayesian software package for phylogenetic reconstruction and molecular dating. Bioinformatics. 25:2286–2288.

Lohse M, Drechsel O, Bock R. 2007. OrganellarGenomeDRAW (OGDRAW): a tool for the easy generation of high-quality custom graphical maps of plastid and mitochondrial genomes. Curr Genet. 41(13):e129–e129.

Lee N-J, Choi J-H, Koo B-S, Ryu S-Y, Han Y-H, Lee S-I, Lee D-U. 2005. Antimutagenicity and cytotoxicity of the constituents from the aerial parts of *Rumex acetosa*. Biol Pharm Bull. 28:2158–2161.

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.

Rambaut A, AJ. Drummond TreeAnnotator version 1.6. 1. University of Edinburgh, Edinburgh, UK. Available at: http://beast.bio.ed.ac.uk (2010).

Ruby JG, Bellare P, DeRisi JL. 2013. PRICE: software for the targeted assembly of components of (Meta) genomic sequence data. G3: Genes| Genomes| Genetics. 3:865–880.
Shibata F, Hizume M, Kuroki Y. 1999. Chromosome painting of Y chromosomes and isolation of a Y chromosome-specific repetitive sequence in the dioecious plant *Rumex acetosa*. Chromosoma. 108:266–270.

Shibata F, Hizume M, Kuroki Y. 2000. Differentiation and the polymorphic nature of the Y chromosomes revealed by repetitive sequences in the dioecious plant, *Rumex acetosa*. Chromosome Res. 8:229–236.

Taylor RSL. 1996. Antiviral activities of medicinal plants of southern Nepal. J Ethnopharmacol. 53:97–110.

Tillich M, Lehwark P, Pellizzer T, Ulbricht-Jones ES, Fischer A, Bock R, Greiner S. 2017. GeSeq - versatile and accurate annotation of organelle genomes Nucleic Acids Res. 31(20):3350–3352.

Wegiera M, Smolarz HD, Wianowska D, Dawidowicz AL. 2007. Anthracene derivatives in some species of Rumex L. genus. Acta Soc Bot Pol. 76:103.

Wick RR, et al. 2015. Bandage: interactive visualization of de novo genome assemblies. Bioinformatics.