

See discussions, stats, and author profiles for this publication at: <https://www.researchgate.net/publication/322403878>

Characterization and phylogenetic analysis of the chloroplast genome of *Lupinus westianus*, a endemic species to Florida, United States

Article in *Conservation Genetics Resources* · January 2018

DOI: 10.1007/s12686-017-0965-0

CITATIONS

0

READS

43

6 authors, including:



Xu Zhenggang

43 PUBLICATIONS 53 CITATIONS

SEE PROFILE



Yang Guiyan

Northwest A & F University

34 PUBLICATIONS 149 CITATIONS

SEE PROFILE

Some of the authors of this publication are also working on these related projects:



ecology [View project](#)



Characterization and phylogenetic analysis of the chloroplast genome of *Lupinus westianus*, a endemic species to Florida, United States

Zhenggang Xu^{1,2} · Yunlin Zhao¹ · Meng Dong^{1,2} · Chaojie Dong² · Yun Xue² · Guiyan Yang^{1,3}

Received: 22 December 2017 / Accepted: 30 December 2017
© Springer Science+Business Media B.V., part of Springer Nature 2018

Abstract

The complete chloroplast genome sequence of *Lupinus westianus*, an endangered and endemic species to Florida, United States, has been assembled from Illumina pair-end sequencing. The chloroplast genome structure of *L. westianus* is a circular molecule of 154,270 bp in length, with a large single copy (LSC) region of 82,437 bp, a small single copy (SSC) region of 15,853 bp, and a pair of inverted repeats (IRs) regions of 27,990 bp. The total G+C content of chloroplast genome is 36.47%, and while it is 41.56% of IRs, which was higher than LSC and SSC regions. The genome contained 130 genes, including 85 protein coding genes, 37 tRNA genes and 8 rRNA genes, of which 18 were duplicated in the IRs region. The phylogenetic analysis indicated that *L. westianus* was clustered together with other two genus of *Lupinus*, *L. luteus* and *L. albus*. The chloroplast genome of *L. westianus* laid a good foundation for genetic resources conservation. The chloroplast genome reported provided useful genomic resources not only for the exchange of information between different species, but also for the population genetics of *L. westianus* and its phylogenetic and evolutionary studies.

Keywords *Lupinus westianus* · Endangered species · Endemic species · Illumina sequencing · Chloroplast genome

Lupinus, commonly known as lupin or lupine (North America), is a genus of flowering plants in the legume family, Fabaceae. The scrub lupine is a federally listed endangered species of the United States. *L. westianus*, mainly distribute in subtropical, tropical dry or coastal sand dunes habitat and is a endemic species to Florida, United States. Before the 1930s, the distribution of *L. aridorum* was described as “infrequent to locally abundant”, while the population showed a continuing downward trends basing on annual surveys since 2002 (Bupp et al. 2017). The main survived populations were found in scrub habitat on two ridge systems in northern Florida. *L. westianus* were evaluated as

near threatened (NT) species and the decreasing population be noted in the IUCN Red List of Threatened Species (IUCN). The main threatened pressure come from human development, leading to loss of natural habitat. Low genetic diversity and gene flow were find out in the fragmentation habitat of *L. westianus* (Bupp et al. 2017). Aside from reduction of viable habitat, remaining habitat is affected by fire suppression. Other threats, such as disease caused bacterium would improve the species wilt. *L. westianus* population is important not only for biodiversity, but the species can supply medicinal materials (Goldberg and Sahli 1967). Germplasm resources information is helpful to its effective management, conservation and exploitation. Chloroplast genomes of *L. westianus* were got based on the Illumina paired-end sequencing data and characterization and phylogenetic analysis were done in the study. The annotated have been deposited into GenBank under the accession numbers MG252262.

Leaf samples of *L. westianus* were collected from ridge systems in northern Florida (83.9689°E, 30.3866°N, United States). Total genomic DNA was extracted from one or two leaf samples per individual, using a QIAquick DNA Mini Kit (QIAGEN, Valencia, California, USA). Shotgun libraries were constructed, and high-throughput sequencing was

✉ Guiyan Yang
yangguiyan@yahoo.com

¹ Hunan Research Center of Engineering Technology for Utilization of Environmental and Resources Plant, Central South University of Forestry and Technology, Changsha 410004, Hunan, People’s Republic of China

² School of Material and Chemical Engineering, Hunan City University, Yiyang 413000, Hunan, People’s Republic of China

³ College of Forestry, Northwest A&F University, Yangling 712100, Shaanxi, People’s Republic of China

carried out on the Illumina HiSeq 2500 sequencing system following the manufacturer’s protocol (Illumina, CA,USA). Chloroplast genome data were filtered, annotated and the circular map was generated as Zhang et al. described (2017).

The chloroplast genome structure of *L. westianus* is a circular molecule of 154,270 bp in length, with a large single copy (LSC) region of 82,437 bp, a small single copy (SSC) region of 15,853 bp, and a pair of inverted repeats

(IRs) regions of 27,990 bp (Fig. 1). The total G+C content of chloroplast genome is 36.47%, and while it is 41.56% of IRs, which was higher than LSC and SSC regions (34.20 and 30.32%, respectively). The genome contained 130 genes, including 85 protein coding genes, 37 tRNA genes and 8 rRNA genes, of which 18 were duplicated in the IRs region, including 7 PCG species [*ndhB*, *rpl2*, *rpl23*, *rps7*, *rps12*, *ycf1* and *ycf2*], 7 tRNA [*trnI-CAU*, *trnL-CAA*, *trnV-GAC*,

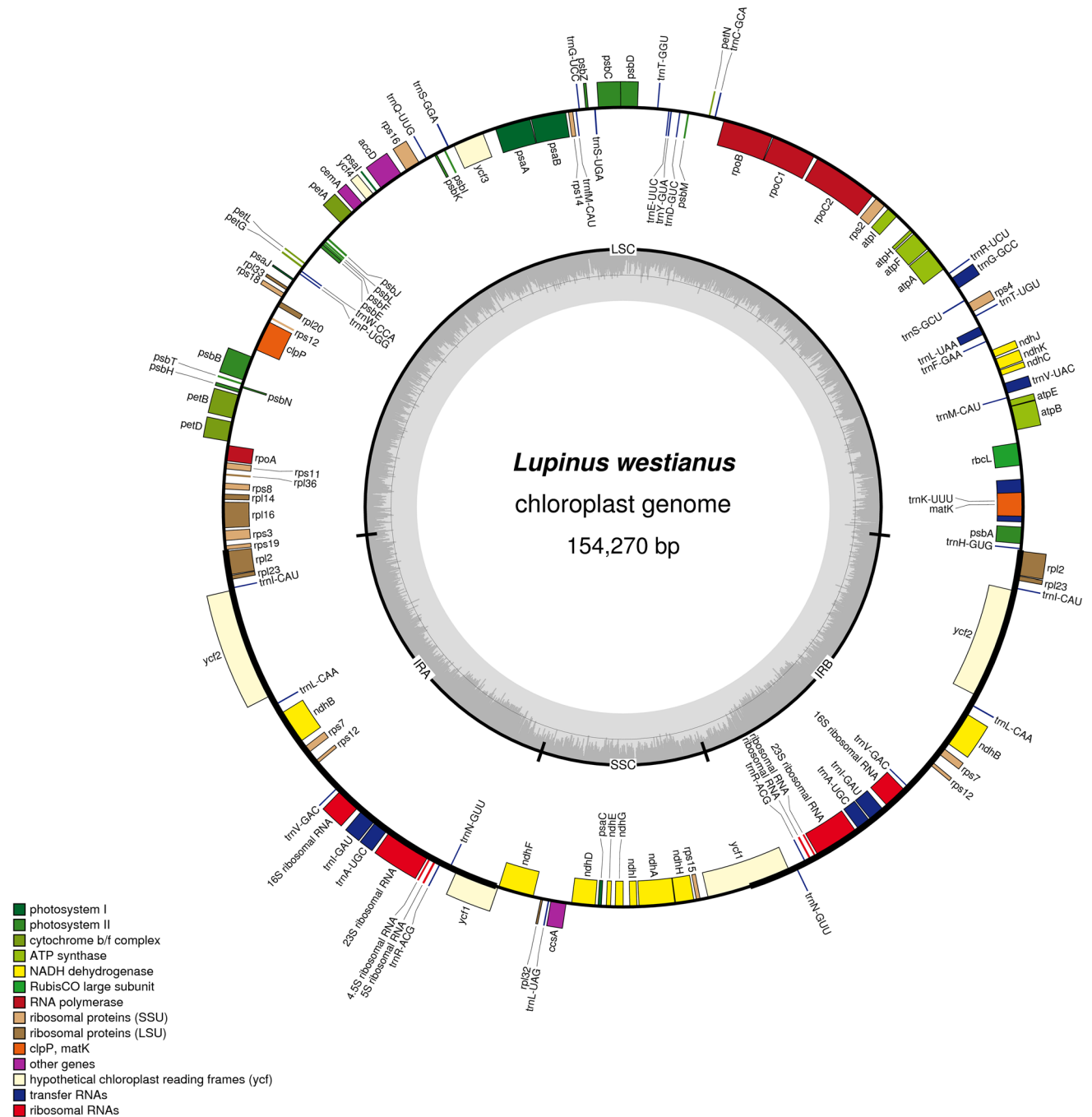


Fig. 1 Gene map of the *Lupinus westianus* chloroplast genome

Acknowledgements The study was financially supported by the Key Technology R&D Program of Hunan Province (2016NK2148, 2016TP2007, 2016TP1014), Forestry Science and Technology Project of Hunan Province (XKL201731) and Science and Technology Major project of Hunan province (2017NK1014).

References

- Bupp G, Ricono A, Peterson CL, Pruett CL (2017) Conservation implications of small population size and habitat fragmentation in an endangered lupine. *Conserv Genet* 18(1):77–88
- Goldberg SI, Sahli MS (1967) Leguminosae Alkaloids. II. Alkaloids of *Lupinus westianus* small. *J Med Chem* 10(1):124–125
- IUCN (2017) The IUCN Red List of Threatened Species. Version 2017-3. <http://www.iucnredlist.org>. Accessed 13 Dec 2017
- Kumar S, Stecher G, Tamura K (2016) MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. *Mol Biol Evol* 33(7):1870–1874
- Zhang W, Zhao Y, Yang G, Tang Y, Xu Z (2017) Characterization of the complete chloroplast genome sequence of *Camellia oleifera* in Hainan, China. *Mitochondrial DNA B* 2(2):843–844