•研究报告•

极小种群濒危植物广西火桐、丹霞梧桐的叶绿体基因组特征

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摘要: 广西火桐(*Firmiana kwangsiensis*)和丹霞梧桐(*F. danxiaensis*)是我国南方特有物种, 其分布范围狭窄, 种群数量少。为了了解其叶绿体基因组结构及系统发生关系, 本文通过高通量测序方法获得广西火桐和丹霞梧桐的浅层基因组数据, 通过生物信息学方法对叶绿体全基因组进行组装, 并对其结构特征进行分析。结果表明: 广西火桐和丹霞梧桐的叶绿体基因组大小分别为160,836 bp和161,253 bp, 具有典型被子植物叶绿体基因组环状四分体结构, 包含长度分别为89,700 bp、90,142 bp的大单拷贝区(large single copy, LSC), 长度分别为19,970 bp、20,067 bp的小单拷贝区(small single copy, SSC)及长度分别为25,583 bp、25,522 bp的2个反向重复序列区(inverted repeat sequence, IR)。两个物种的叶绿体基因组共注释得到131个基因, 包括86个蛋白编码基因、37个tRNA基因和8个rRNA基因。广西火桐的叶绿体基因组中共检测出26个正向重复序列、2个反向重复序列、21个回文重复序列、21个串联重复序列和98个简单重复序列; 丹霞梧桐叶绿体基因组中共检测出23个正向重复序列、5个反向重复序列、21个回文重复序列、30个串联重复序列和107个简单重复序列。系统发生分析结果表明5种梧桐属(*Firmiana*)植物构成两个强烈支持的分支(支持率100%), 一个分支为广西火桐、美丽火桐(*F. pulcherrima*)和火桐(*F. colorata*), 其中广西火桐与美丽火桐构成姐妹群; 另一分支是互为姐妹群的丹霞梧桐和云南梧桐(*F. major*)。综上所述, 广西火桐和丹霞梧桐的叶绿体基因组结构、基因排列及重复序列具有较高的相似性, 系统进化树将5种梧桐属物种分为两个分支, 其中广西火桐和美丽火桐最近; 而丹霞梧桐与云南梧桐关系最近。本研究鉴定的SSR位点可为梧桐属物种系统发生、进化关系的研究提供遗传信息。

关键词: 广西火桐; 丹霞梧桐; 叶绿体全基因组; 高通量测序; 重复序列; 系统发生分析

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Characterization of complete chloroplast genome in *Firmiana kwangsiensis* and *F. danxiaensis* with extremely small populations

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ABSTRACT

Aims: *Firmiana kwangsiensis* and *F. danxiaensis* are endemic plant species with narrow distribution and small population in southern China, which have important ecological and economic value. However, our knowledge of the chloroplast genome level of *F. kwangsiensis* and *F. danxiaensis* are still limited. Also, the phylogenetic relationships among the *Firmiana* genus remain unclear.

Methods: The genome skimming sequencing data of *F. kwangsiensis* and *F. danxiaensis* were obtained by using the high-throughput sequencing, and the complete chloroplast genomes were assembled and then the structures were analyzed by bioinformatics methods.

Results: The results revealed that complete chloroplast genomes of the *F. kwangsiensis* and *F. danxiaensis* show a

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typical quadripartite structure of 160,836 bp and 161,253 bp in length, consisting of a large single copy region (89,700 bp and 90,142 bp) and a small single copy region (19,970 bp and 20,067 bp) that were separated by a pair of inverted repeat regions (25,583 bp and 25,522 bp each). The annotation results showed that chloroplast genomes of both species contain 131 genes, including 86 protein-coding, 37 transfer RNA (tRNA), and eight ribosomal RNA (rRNA) genes. In *F. kwangsiensis*, 26 forward repeats, two reverse repeats, 21 palindromic repeats, 23 tandem repeats, and 98 simple sequence repeats were found, and 23 forward repeats, five reverse repeats, 21 palindromic repeats, 30 tandem repeats, and 107 simple sequence repeats were found in *F. danxiaensis*. Phylogenetic analyses revealed that five *Firmiana* species were clustered into two branches with strong supports. *Firmiana kwangsiensis*, *F. pulcherrima* and *F. colorata* formed a branch, and the *F. kwangsiensis* was a sister relationship to *F. pulcherrima* in this branch, the other branch was *F. danxiaensis* and *F. major*.

Conclusion: The structures, gene arrangement and repeat sequences in *F. kwangsiensis* and *F. danxiaensis* chloroplast genome were high similar. Phylogenetic analyses revealed that five *Firmiana* species were clustered into two clades, *F. kwangsiensis* was closely related to *F. pulcherrima*, and *F. danxiaensis* was closely related to *F. major*. In addition, the SSRs in this study will provides important genetic information for phylogenetic, evolution for *Firmiana* species.

Key words: *Firmiana kwangsiensis*; *Firmiana danxiaensis*; chloroplast genome; high-throughput sequencing; repeat sequence; phylogenetic analysis

叶绿体是植物细胞内进行光合固碳和胁迫应答的重要半自主性细胞器(Ivanova et al, 2017), 它具有一套可独立自主复制的遗传系统, 可编码与光合作用相关的蛋白。陆生植物中的叶绿体基因组主要为单亲遗传, 其基因组一般为107–218 kb的环状DNA分子, 包括1个大单拷贝区(large single copy, LSC)、1个小单拷贝区(small single copy, SSC)及被其分隔开的2个反向重复区(inverted repeat, IR)(Daniell et al, 2016; 李倩等, 2020)。与核基因组相比, 叶绿体基因组具有重组率较低、后代遗传稳定等特点(Birky, 1995; 于涛等, 2019)。因此, 研究叶绿体基因组数据有助于揭示物种的系统发生关系。然而, 在以往的研究中, 所选择的核基因组和叶绿体基因片段较少且获得有效信息偏少, 对物种进化关系的全面解析产生了一定的影响。随着测序技术的提升和成本的下降, 利用叶绿体全基因组解析物种系统发生关系已成为有效的手段。叶绿体基因组信息的挖掘不仅有助于物种鉴定和分子育种等方面的研究, 还可为重要经济作物、园艺品种改良、珍稀濒危植物保育提供分子基础(Nie et al, 2012)。

梧桐属(*Firmiana*)隶属于锦葵科梧桐亚科, 包含12–18种(Chen et al, 2015), 中国分布有7种, 分别为梧桐(*F. simplex*)、海南梧桐(*F. hainanensis*)、丹霞梧桐(*F. danxiaensis*)、云南梧桐(*F. major*)、火桐(*F. colorata*)、广西火桐(*F. kwangsiensis*)和美丽火桐(*F. pulcherrima*), 其中除梧桐因栽培而分布较广外, 其余6种均为狭域分布种(Wang et al, 2018; Ya et al, 2018; 武星彤等, 2018)。随着观赏植物物种需求的

增加, 梧桐属部分物种因其优美的树形和鲜艳的花色而被推广栽培。有研究发现梧桐属植物的提取物不仅具有抗微生物、抗炎症和抗癌的药理作用(Ajaib et al, 2014; Woo et al, 2015; Lim et al, 2017), 还具有保护神经系统和护肝的作用(Kim et al, 2015; Lim et al, 2017)。目前, 对梧桐属的系统发生关系已有相关报道, 凡强等(2011)利用ITS片段对梧桐属的系统发生关系进行了研究; Abdullah等(2019)基于火桐、云南梧桐和美丽火桐的叶绿体全基因组进行了系统发生关系分析。为了更准确全面地了解梧桐属的系统发生关系, 还需要更多物种的相关基因信息。

广西火桐和丹霞梧桐均为梧桐属内重要的落叶树种, 其自然分布狭窄, 野外种群数量少, 被列为国家二级重点保护野生植物(国家林业局和农业部, 1999)以及《中国物种红色目录》的濒危等级物种(汪松和解焱, 2004), 并被列入《全国极小种群野生植物拯救保护工程规划(2011–2015年)》名录。其中广西火桐仅分布于广西中部至南部的石灰岩地区, 丹霞梧桐主要分布于广东丹霞山自然保护区, 是丹霞山特征种及丹霞地貌特有种。这两种植物树形优美、花色艳丽, 极具园林观赏价值。近年来, 对这两种植物的相关研究主要集中于资源调查和群落特征(骆文华等, 2010; 陈璐等, 2018)、群体遗传分析(Chen et al, 2014; 骆文华等, 2015; 武星彤等, 2018)等方面, 尚未发现利用叶绿体全基因组信息对广西火桐和丹霞梧桐的系统发生进行研究的相关报道。因此, 本文以广西火桐和丹霞梧桐的叶片

为研究材料,利用高通量测序技术,对两个物种的叶绿体全基因组进行组装,并对其结构特征进行分析,希望有助于理解广西火桐和丹霞梧桐的系统发生关系,为后续开展其遗传多样性的保护和种群恢复研究提供分子基础信息。

1 材料和方法

1.1 植物材料及DNA提取

广西火桐叶片样品于2018年6月采集于桂林植物园(25°04' N, 110°17' E), 并使用硅胶干燥保存。丹霞梧桐叶片样品于2019年7月采集于桂林植物园幼苗, 该幼苗为2017年7月引种于广东丹霞山自然保护区(25°02' N, 113°43' E), 叶片样品置于硅胶内干燥保存。利用改良CTAB法(Doyle, 1987)提取广西火桐和丹霞梧桐的叶片DNA。随后, 利用琼脂糖凝胶电泳和NanoDrop2000 (美国赛默飞世尔科技有限公司)评价基因组DNA的质量及浓度, 检验合格的基因组DNA用于文库构建。

1.2 叶绿体基因组测序、组装与基因注释

由于广西火桐与丹霞梧桐采样和测序时间不一致, 并考虑到成本及技术的因素, 利用Illumina HiSeq测序平台(上海美吉生物医药科技有限公司)对广西火桐叶绿体进行浅层基因组测序, 而丹霞梧桐叶绿体则利用Illumina NovaSeq平台(南京集思慧远生物科技有限公司)进行浅层基因组测序。两个物种的建库插入长度均为350 bp左右, 测序读长为PE150。

为提高叶绿体基因组后续组装及分析的可靠性, 使用fastp软件(Chen et al, 2018)对测序下机后的原始数据进行过滤, 包括截除reads中的测序接头及引物序列, 并去除低质量reads (平均质量值 $Q < 5$, 未识别碱基 $N > 5$)。得到高质量叶绿体基因组测序数据(clean data)后, 用Bowtie2 v2.2.4软件(Langmead et al, 2012)进行比对, 选中比对上的测序序列作为叶绿体基因组的测序序列。随后, 以瑟伯氏棉(*Gossypium thurberi*)叶绿体全基因组(NCBI登录号: GU907100)为参考序列, 通过SPAdes v3.10.1 (Bankevich et al, 2012)组装广西火桐和丹霞梧桐的叶绿体全基因组。

为提高叶绿体基因组注释的准确性, 我们通过以下两种方法对广西火桐和丹霞梧桐的叶绿体基

因组进行注释: (1)使用prodigal v2.6.3 (Hyatt et al, 2010)、hmmer v3.1b2 (Wu et al, 2011)和aragorn v1.2.38软件(Laslett & Canbäck, 2004)分别对叶绿体基因组的蛋白编码区(coding sequences, CDS)、核糖体RNA (rRNA)和转运RNA (tRNA)进行注释。(2)提取参考基因组的基因序列, 使用NCBI的blast v2.6软件比对组装序列, 获得第二种注释结果。然后对两种注释结果进行对比, 去除错误及冗余的注释, 确定多外显子的边界, 从而获得最终的叶绿体基因注释。利用OGDRAW工具绘制叶绿体基因组结构图(Lohse et al, 2013)。

1.3 重复序列与SSR分析

利用REPuter (Kurtz et al, 2001)软件预测叶绿体基因组内的散在重复序列, 其参数设置为: 最小重复序列为30 bp, 汉明距离(Hamming distance)设置为3 (Liang et al, 2019)。串联重复序列通过在线Tandem Repeats Finder工具进行分析(Benson, 1999)。利用MISA软件(Beier et al, 2017)预测叶绿体基因组的简单重复序列(simple sequence repeats, SSR)的分布, 参数设置如下: 大于或等于10个单核苷酸重复序列; 大于或等于5个二核苷酸重复序列; 大于或等于4个三核苷酸重复序列; 大于或等于3个四核苷酸及以上核苷酸重复序列(Zhao et al, 2019)。

1.4 系统发生分析

从NCBI下载12个锦葵目植物的叶绿体全基因组序列, 包括梧桐属的云南梧桐(NC 037242)、美丽火桐(NC 036395)、火桐(BK 010724), 银叶树属(*Heritiera*)的长柄银叶树(*H. angustata*, NC 037784)、*H. fomes* (NC 043924)、银叶树(*H. littoralis*, NC 043923)、蝴蝶树(*H. parvifolia*, NC 038057), 翅子树属(*Pterospermum*)的景东翅子树(*P. kingtungense*, NC 042885), 椴树属(*Tilia*)的紫椴(*T. amurensis*, MH 169579)和少脉椴(*T. paucicostata*, KT 894775), 棉属(*Gossypium*)的*G. harknessii* (NC 033333)和克劳茨基棉(*G. klotzschianum*, NC 033394), 并将本研究中广西火桐和丹霞梧桐的叶绿体基因组纳入分析, 以十字花科的*Braya humilis* (NC 035515)为外类群。利用RAxML (Stamatakis, 2014)构建最大似然法(maximum likelihood, ML)的系统发生树, 碱基替换模型选择GTR+G, 其他参数选择默认设置, 进化树分支的可信度基于bootstrap抽样重复1,000次。

2 结果

2.1 叶绿体基因组组装与基本特征

对测序原始数据的接头序列和低质量测序数据过滤后, 获得广西火桐和丹霞梧桐的clean data分别约为5.16 G和5.91 G。随后对叶绿体基因组进行组装, 分别获得了广西火桐和丹霞梧桐的叶绿体全基因组 (NCBI 登录号分别为 MN786867、MN480318)。与典型被子植物叶绿体基因组相似, 广西火桐和丹霞梧桐的叶绿体基因组均为闭合环状四分体结构, 包含LSC、SSC及两个IR区(图1), 序列全长分别为160,836 bp和161,253 bp, 其中LSC区长度分别为89,700 bp和90,142 bp, SSC区长度分别为19,970 bp和20,067 bp, IR区长度分别为25,583 bp和25,522 bp。广西火桐与丹霞梧桐的叶绿体基因组GC含量分别为37.04%、36.87%, 且两者的IR区GC含量(42.93%、42.97%)均高于LSC (34.92%、34.68%)和SSC区(31.46%、31.24%) (表1)。

本研究中, 广西火桐与丹霞梧桐的叶绿体基因组注释到的基因总数均为131个, 包括86个蛋白编码序列、37个tRNA基因和8个rRNA基因。其中有17个基因存在两个拷贝, 包括6个蛋白编码序列(*rps7*、

rpl2、*rpl23*、*ndhB*、*ycf2*、*ycf15*)、7个tRNA基因(*trnA-UGC*、*trnI-CAU*、*trnI-GAU*、*trnL-CAA*、*trnN-GUU*、*trnR-ACG*、*trnV-GAC*)和4个rRNA基因(*rrn16*、*rrn23*、*rrn4.5*、*rrn5*) (附录1)。在广西火桐和丹霞梧桐的叶绿体基因组中均发现17个基因含有内含子, 其中14个基因含有1个内含子, 包括8个蛋白编码基因(*rps16*、*atpF*、*rpoCl*、*petB*、*petD*、*rpl2*、*ndhB*、*ndhA*)和6个tRNA基因(*trnK-UUU*、*trnG-UCC*、*trnL-UAA*、*trnV-UAC*、*trnI-GAU*、*trnA-UGC*); 有3个基因含有2个内含子(*rps12*、*ycf3*、*clpP*)。 *matK* 基因位于 *trnK-UUU* 的内含子上。另外, *rps12* 为反式剪接基因, 其5'端位于LSC区, 而3'端位于IR区。

2.2 SSR分析

利用MISA软件对广西火桐的叶绿体基因组筛选得到98个SSR位点, 包括56个单核苷酸重复类型(主要以A或T碱基重复为主, 只有3个为C碱基重复), 7个双核苷酸、2个三核苷酸、11个四核苷酸、5个五核苷酸和17个复合核苷酸类型; 而在丹霞梧桐叶绿体基因组筛选得到107个SSR位点, 其中64个为A或T组成的单核苷酸重复类型, 11个双核苷酸、1个三核苷酸、9个四核苷酸、9个五核苷酸和13个复合核苷酸类型(图2A)。广西火桐和丹霞梧桐的叶绿体基因组SSR位点主要分布于LSC区(分别为70和82个), 其次为SSC区(分别为18和15个), IR区最少(各10个) (图2B); 另外, SSR位点大部分分布于叶绿体基因组的非编码区上, 且基因间隔区(IGS)分布最多(分别有65和74个), 其次为基因内含子区(19和17个), 而在基因编码区分布较少(14和16个) (图2C, 附录2)。

2.3 重复序列分析

利用REPuter软件对广西火桐和丹霞梧桐的叶绿体基因组进行重复序列分析。在广西火桐的叶绿体基因组共鉴定出49个重复序列, 包括26个正向重复(forward repeats)、2个反向重复(reverse repeats)和21个回文重复(palindromic repeats); 在丹霞梧桐的基因组中也鉴定出49个散在重复序列, 包括23个正向重复、5个反向重复和21个回文重复(图3A)。广西火桐和丹霞梧桐叶绿体基因组重复序列长度范围分别在30–65 bp和30–60 bp之间, 且主要分布于30–45 bp之间(图3C, 附录3)。在两个物种的*ycf2*、*psaB*和*ycf1*编码区上均有重复序列的分布, 且*ycf2*

表1 广西火桐和丹霞梧桐的叶绿体基因组特征比较
Table 1 Comparison of chloroplast genome characteristics of *Firmiana kwangsiensis* and *F. danxiaensis*

基因组特征 Genome characteristics	广西火桐 <i>F. kwangsiensis</i>	丹霞梧桐 <i>F. danxiaensis</i>
序列全长 Genome size (bp)	160,836	161,253
LSC区长度 LSC length (bp)	89,700	90,142
SSC区长度 SSC length (bp)	19,970	20,067
IR区长度 IR length (bp)	25,583	25,522
GC含量 GC content (%)	37.04	36.87
LSC区GC含量 GC content of LSC (%)	34.92	34.68
SSC区GC含量 GC content of SSC (%)	31.46	31.24
IR区GC含量 GC content of IR (%)	42.93	42.97
A碱基占比 A base content (%)	30.98	31.13
T碱基占比 T base content (%)	31.98	31.99
C碱基占比 C base content (%)	18.87	18.61
G碱基占比 G base content (%)	18.17	18.26
基因总数 Total genes	131	131
编码蛋白基因数 No. of protein coding sequences	86	86
tRNA	37	37
rRNA	8	8

图1 广西火桐和丹霞梧桐叶绿体基因组的基因图谱
Fig. 1 Gene map of the *Firmiana kwangsiensis* and *F. danxiaensis* chloroplast genome

图2 广西火桐和丹霞梧桐的叶绿体基因组SSR分析。(A)不同SSR类型的数量;(B)大单拷贝区(LSC)、反向重复区(IR)和小单拷贝区(SSC)的SSR数量;(C)基因间隔区(IGS)、基因编码区(CDS)及内含子(intron)的SSR数量。
Fig. 2 SSR analysis of the chloroplast genomes of *Firmiana kwangsiensis* and *F. danxiaensis*. (A) Number of SSRs in different types; (B) Number of SSRs in the LSC (large single copy), SSC (small single copy), and IR (inverted repeat region); (C) Number of SSRs in the intergenic regions (IGS), protein-coding gene (CDS) and introns.

图3 广西火桐和丹霞梧桐的叶绿体基因组重复序列分析。(A)不同重复序列类型的分布数量;(B)串联重复序列长度的分布范围;(C)正向、反向和回文重复序列长度的分布范围。
Fig. 3 Repeat sequences analysis of *Firmiana kwangsiensis* and *F. danxiaensis* chloroplast genome. (A) Number of different types of repeats; (B) Size of tandem repeats in specific range; (C) Size of forward, reverse and palindromic repeats in specific range.

编码区分布数量最多(均有17个); *tRNA-GCU*基因上各分布有1个重复序列;在*ycf3*、*clpP*和*ndhA*的内含子上也发现有重复序列分布。此外,在丹霞梧桐的叶绿体*rrn4.5*基因上发现有4个重复序列,而广西火桐的*rRNA*基因则无重复序列(附录3)。

通过Tandem Repeats Finder软件(<https://tandem.bu.edu/>)鉴定出广西火桐和丹霞梧桐的叶绿体基因

组的串联重复序列分别有21个和30个(图3A),长度在10-32 bp之间(图3B,附录4)。这些串联重复序列的重复次数基本为2次,但在丹霞梧桐叶绿体基因组发现1个重复次数为3的串联重复序列。两个物种的叶绿体基因组均有3个串联重复序列分布于*clpP*

图4 基于叶绿体全基因组序列最大似然法构建的15个物种的系统发生树

Fig. 4 Phylogenetic tree of 15 species based on chloroplast genome using maximum likelihood (ML) method

和 $rpl2$ 的内含子上, 其余均分布于基因间隔区(IGS) (附录4)。

2.4 系统发生分析

基于15个物种的叶绿体全基因组序列构建的系统树显示(图4): 棉属(*Gossypium*)、银叶树属(*Heritiera*)、梧桐属(*Firmiana*)和椴树属(*Tilia*)的单系性得到强烈支持(支持率均为100%), 景东翅子树(*P. kingtungense*)与椴树属形成姐妹群, 并得到100%支持, 共同构成银叶树属和梧桐属分支的姐妹群, 支持率为97%。在梧桐属内部, 丹霞梧桐和云南梧桐构成一支, 其余3种(广西火桐、美丽火桐和火桐)构成一支, 其中广西火桐和美丽火桐为姐妹群关系。

3 讨论

本研究利用二代高通量测序技术对梧桐属内濒危极小种群植物广西火桐和丹霞梧桐的叶绿体全基因组进行组装与注释。两个物种叶绿体基因组与大多数被子植物的叶绿体基因组结构相似, 均为典型的四分体式结构(Cheng et al, 2020; Tan et al, 2020), 其长度分别为160,836和161,253 bp。二者的叶绿体基因组均编码131个基因, 包括86个蛋白编码序列, 37个tRNA和8个rRNA基因。此外, 广西火桐和丹霞梧桐的叶绿体基因组结构、基因数量和类型、GC含量等与已公布的梧桐属植物(Ya et al, 2018)、美丽火桐(Wang et al, 2018)和火桐(Abdullah et al, 2019)的叶绿体基因组相似, 表明梧桐属内相

关物种的叶绿体基因组结构相对保守。

有研究发现叶绿体基因组的重排决定了重复序列的数量(Haberle et al, 2008; Gao et al, 2009; Somaratne et al, 2019)。因此, 重复序列为基因组重排的研究提供了有效信息。本研究中, 虽然在广西火桐和丹霞梧桐的叶绿体基因组中均鉴定出49个重复序列, 但在正向重复和反向重复的数量上有一定的差异, 在其他梧桐属植物如云南梧桐、美丽火桐和火桐也发现类似现象(Abdullah et al, 2019)。这些重复序列为梧桐属系统进化的进一步深入研究提供了重要依据。此外, 我们还发现串联重复序列的数量及长度在两个物种中也存在差异, 丹霞梧桐叶绿体基因组大于15 bp以上的串联重复序列数量要多于广西火桐, 目前关于串联重复序列的起源机制尚不清楚, 可能与DNA重排、变异和基因复制相关(Chen et al, 2019)。

叶绿体基因组的SSRs是一种被应用于群体遗传结构和谱系地理学等研究的高效标记工具(Du et al, 2012; Chmielewski et al, 2015)。本研究中, 在广西火桐和丹霞梧桐的叶绿体基因组中分别获得98个和107个SSR位点, 这些SSR位点可以为濒危梧桐属植物的遗传多样性和保护遗传学等研究提供候选分子标记。与大多数被子植物的叶绿体基因组SSR位点分布相似(Abdullah et al, 2019; 乔永刚等, 2019; 张明英等, 2020), 本文两个物种的叶绿体基因组SSR位点主要分布于LSC区, 且主要以A/T碱

基组成。此外,非编码区(IGS和内含子)的SSR位点出现的数量远多于编码区(CDS),这可能与编码区的保守性高于非编码区有关(乔永刚等,2019)。

植物叶绿体基因组序列(如*matK*、*psbA-trnH*、*trnL-trnF*、*ndhF*和*ycf1*等)常被用于物种的系统发生关系研究(蒋明等,2020)。但对于梧桐亚科等一些复杂类群,有限的DNA片段信息并不能充分揭示其系统发生关系(Wilkie et al, 2006),需要更多的分子信息。本研究基于叶绿体全基因组构建系统发生关系,将14个锦葵科物种明确划分为5个分支(支持率100%),其中锦葵科棉属与梧桐亚科构成姐妹群;梧桐亚科的梧桐属与银叶树属互为姐妹群,表明这两个属的亲缘关系较近,印证了Wilkie等(2006)的结论。此外,梧桐属内部分为两个分支,其中广西火桐、火桐和美丽火桐聚为一支,丹霞梧桐和云南梧桐构成一支,与凡强等(2011)基于ITS片段的梧桐属内系统发育关系研究结论一致。但目前受限于梧桐亚科内其他物种的叶绿体基因组尚未测序公布,尚未能整体重构其系统发生关系。本研究报道的广西火桐和丹霞梧桐的叶绿体基因组特征为梧桐属乃至梧桐亚科物种系统发生、进化和保护遗传学等研究提供了重要的遗传信息。

参考文献

- Abdullah, Shahzadi I, Mehmood F, Ali Z, Malik MS, Waseem S, Mirza B, Ahmed I, Waheed MT (2019) Comparative analyses of chloroplast genomes among three *Firmiana* species: Identification of mutational hotspots and phylogenetic relationship with other species of Malvaceae. *Plant Gene*, 19, 100199.
- Ajaib M, Wahla SQ, Khan KM (2014) *Firmiana simplex*: A potential source of antimicrobials. *Journal of the Chemical Society of Pakistan*, 36, 744–753.
- 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. *Journal of Computational Biology*, 19, 455–477.
- Beier S, Thiel T, Münch T, Scholz U, Mascher M (2017) MISA-web: A web server for microsatellite prediction. *Bioinformatics*, 33, 2583–2585.
- Benson G (1999) Tandem repeats finder: A program to analyze DNA sequences. *Nucleic Acids Research*, 27, 573–580.
- Birky CW (1995) Uniparental inheritance of mitochondrial and chloroplast genes: Mechanisms and evolution. *Proceedings of the National Academy of Sciences, USA*, 92, 11331–11338.
- Chen L, Zhou H, Wang MQ, Wu XT, Lin XY, Zhang Y, Wen YF (2018) Community characteristics comparison of *Firmiana danxiaensis* species. *Chinese Wild Plant Resources*, 37(2), 46–49. (in Chinese with English abstract) [陈璐, 周宏, 王敏求, 武星彤, 林雪莹, 张原, 文亚峰 (2018) 丹霞梧桐群落特征比较研究. *中国野生植物资源*, 37(2), 46–49.]
- Chen Q, Wu XB, Zhang DQ (2019) Phylogenetic analysis of *Fritillaria cirrhosa* D. Don and its closely related species based on complete chloroplast genomes. *PeerJ*, 7, e7480.
- Chen SF, Li MW, Hou RF, Liao WB, Zhou RC, Fan Q (2014) Low genetic diversity and weak population differentiation in *Firmiana danxiaensis*, a tree species endemic to Danxia landform in northern Guangdong, China. *Biochemical Systematics and Ecology*, 55, 66–72.
- Chen SF, Zhou YQ, Chen YR, Gu J (2018) Fastp: An ultra-fast all-in-one FASTQ preprocessor. *Bioinformatics*, 34, i884–i890.
- Chen SF, Li MW, Jing HJ, Zhou RC, Yang GL, Wu W, Fan Q, Liao WB (2015) De novo transcriptome assembly in *Firmiana danxiaensis*, a tree species endemic to the Danxia landform. *PLoS ONE*, 10, e0139373.
- Cheng Y, Zhang LM, Qi JM, Zhang LW (2020) Complete chloroplast genome sequence of *Hibiscus cannabinus* and comparative analysis of the Malvaceae family. *Frontiers in Genetics*, 11, 227.
- Chmielewski M, Meyza K, Chybicki IJ, Dzialuk A, Litkowiec M, Burczyk J (2015) Chloroplast microsatellites as a tool for phylogeographic studies: The case of white oaks in Poland. *iForest*, 8, 765–771.
- Daniell H, Lin CS, Yu M, Chang WJ (2016) Chloroplast genomes: Diversity, evolution, and applications in genetic engineering. *Genome Biology*, 17, 134.
- Doyle JJ (1987) A rapid DNA isolation procedure for small quantities of fresh leaf tissue. *Phytochemical Bulletin*, 19, 11–15.
- Du QZ, Wang BW, Wei ZZ, Zhang DQ, Li BL (2012) Genetic diversity and population structure of Chinese white poplar (*Populus tomentosa*) revealed by SSR markers. *Journal of Heredity*, 103, 853–862.
- Fan Q, Guo W, Chen SF, Liao WB (2011) Phylogeny of *Firmiana* (Sterculiaceae) based on nrDNA ITS analysis. In: *The 10th Youth Academic Seminar of National System and Evolutionary Botany* (ed. Botanic Society of Yunnan), p. 68. Kunming. (in Chinese with English abstract) [凡强, 郭微, 陈素芳, 廖文波 (2011) 基于nrDNA ITS序列探讨梧桐属的系统发育. 见: 2011年全国系统与进化植物学暨第十届青年学术研讨会论文集(云南植物学会编), 68页. 昆明.]
- Gao L, Yi X, Yang YX, Su YJ, Wang T (2009) Complete chloroplast genome sequence of a tree fern *Alsophila*

spinulosa: Insights into evolutionary changes in fern chloroplast genomes. BMC Evolutionary Biology, 9, 130.

- Haberle RC, Fourcade HM, Boore JL, Jansen RK (2008) Extensive rearrangements in the chloroplast genome of *Trachelium caeruleum* are associated with repeats and tRNA genes. Journal of Molecular Evolution, 66, 350–361.
- Hyatt D, Chen GL, Locascio PF, Land ML, Larimer FW, Hauser LJ (2010) Prodigal: Prokaryotic gene recognition and translation initiation site identification. BMC Bioinformatics, 11, 119.
- Ivanova Z, Sablok G, Daskalova E, Zahmanova G, Apostolova E, Yahubyan G, Baev V (2017) Chloroplast genome analysis of resurrection tertiary relict *Haberlea rhodopensis* highlights genes important for desiccation stress response. Frontiers in Plant Science, 8, 204.
- Jiang M, Wang JF, Ying MH, Yang RM, Ma JY (2020) Assembly and sequence analysis of *Tetrastigma hemsleyanum* chloroplast genome. Chinese Traditional and Herbal Drugs, 51, 461–468. (in Chinese with English abstract) [蒋明, 王军峰, 应梦豪, 杨如棉, 马佳莹 (2020) 三叶崖爬藤叶绿体基因组的组装与序列分析. 中草药, 51, 461–468.]
- Kim JW, Yang H, Cho N, Kim B, Kim YC, Sung SH (2015) Hepatoprotective constituents of *Firmiana simplex* stem bark against ethanol insult to primary rat hepatocytes. Pharmacognosy Magazine, 11(41), 55–60.
- Kurtz S, Choudhuri JV, Ohlebusch E, Schleiermacher C, Stoye J, Giegerich R (2001) REPuter: The manifold applications of repeat analysis on a genomic scale. Nucleic Acids Research, 29, 4633–4642.
- Langmead B, Salzberg SL (2012) Fast gapped-read alignment with Bowtie 2. Nature Methods, 9, 357–359.
- Laslett D, Canback B (2004) ARAGORN, a program to detect tRNA genes and tmRNA genes in nucleotide sequences. Nucleic Acids Research, 32, 11–16.
- Li Q, Guo QQ, Gao C, Li HE (2020) Characterization of complete chloroplast genome of *Camellia weiningensis* in Weining, Guizhou Province. Acta Horticulturae Sinica, 47, 779–787. (in Chinese with English abstract) [李倩, 郭其强, 高超, 李慧娥 (2020) 贵州威宁红花油茶叶绿体基因组特征分析. 园艺学报, 47, 779–787.]
- Liang CL, Wang L, Lei J, Duan BZ, Ma WS, Xiao SM, Qi HJ, Wang Z, Liu YQ, Shen XF, Guo S, Hu HY, Xu J, Chen SL (2019) A comparative analysis of the chloroplast genomes of four *Salvia* medicinal plants. Engineering, 5, 907–915.
- Lim SY, Subedi L, Shin D, Kim CS, Lee KR, Kim SY (2017) A new neolignan derivative, balanophonin isolated from *Firmiana simplex* delays the progress of neuronal cell death by inhibiting microglial activation. Biomolecules & Therapeutics, 25, 519–527.
- Luo WH, Mao SZ, Ding L, Huang YS, Deng T (2010) Study on community characteristics of endangered species *Erythropsis kwangsiensis*. Journal of Fujian Forestry Science and Technology, 37(4), 6–10. (in Chinese with English abstract) [骆文华, 毛世忠, 丁莉, 黄俞淞, 邓涛 (2010) 濒危植物广西火桐群落特征研究. 福建林业科技, 37(4), 6–10.]
- Luo WH, Dai WJ, Liu J, Hu XH, Li XJ, Huang SX (2015) Comparison of genetic diversity of natural and *ex-situ* conservation populations of *Erythropsis kwangsiensis*. Journal of Central South University of Forestry & Technology, 35(2), 66–71. (in Chinese with English abstract) [骆文华, 代文娟, 刘建, 胡兴华, 李祥军, 黄仕训 (2015) 广西火桐自然种群和迁地保护种群的遗传多样性比较. 中南林业科技大学学报, 35(2), 66–71.]
- Lohse M, Drechsel O, Kahlau S, Bock R (2013) OrganellarGenomeDRAW—A suite of tools for generating physical maps of plastid and mitochondrial genomes and visualizing expression data sets. Nucleic Acids Research, 41, W575–W581.
- National Forestry Administration, Ministry of Agriculture (1999) List of Key State Protected Wild Plants (The first batch). Plant Journal, (5), 4–11. [国家林业局, 农业部 (1999) 国家重点保护野生植物名录(第一批). 植物杂志, (5), 4–11.]
- Nie XJ, Lü SZ, Zhang YX, Du XH, Wang L, Biradar SS, Tan XF, Wan FH, Song WN (2012) Complete chloroplast genome sequence of a major invasive species, crofton weed (*Ageratina adenophora*). PLoS ONE, 7, e36869.
- Qiao YG, He JX, Wang YF, Cao YP, Jia MJ, Zhang XR, Liang JP, Song Y (2019) Analysis of chloroplast genome and its characteristics of medicinal plant *Sophora flavescens*. Acta Pharmaceutica Sinica, 54, 2106–2112. (in Chinese with English abstract) [乔永刚, 贺嘉欣, 王勇飞, 曹亚萍, 贾孟君, 张鑫瑞, 梁建萍, 宋芸 (2019) 药用植物苦参的叶绿体基因组及其特征分析. 药学报, 54, 2106–2112.]
- Somaratne Y, Guan DL, Wang WQ, Zhao L, Xu SQ (2019) Complete chloroplast genome sequence of *Xanthium sibiricum* provides useful DNA barcodes for future species identification and phylogeny. Plant Systematics and Evolution, 305, 949–960.
- Stamatakis A (2014) RAxML version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics, 30, 1312–1313.
- Tan W, Gao H, Zhang HY, Yu XL, Tian XX, Jiang WL, Zhou K (2020) The complete chloroplast genome of Chinese medicine (*Psoralea corylifolia*): Molecular structures, barcoding and phylogenetic analysis. Plant Gene, 21, 100216.
- Wang JH, Cai YC, Zhao KK, Zhu ZX, Zhou RC, Wang HF (2018) Characterization of the complete chloroplast genome sequence of *Firmiana pulcherrima* (Malvaceae). Conservation Genetics Resources, 10, 445–448.
- Wang S, Xie Y (2004) China Species Red List (Vol. 1). Higher Education Press, Beijing. (in Chinese) [汪松, 解焱 (2004) 中国物种红色名录(第一卷). 高等教育出版社, 北京.]
- Wilkie P, Clark A, Pennington RT, Cheek M, Bayer C, Wilcock CC (2006) Phylogenetic relationships within the

- subfamily Sterculioideae (Malvaceae/Sterculiaceae-Sterculieae) using the chloroplast gene *ndhF*. *Systematic Botany*, 31, 160–170.
- Woo KW, Choi SU, Kim KH, Lee KR (2015) Ursane saponins from the stems of *Firmiana simplex* and their cytotoxic activity. *Journal of the Brazilian Chemical Society*, 26, 1450–1456.
- Wu ST, Zhu ZW, Fu LM, Niu BF, Li WZ (2011) WebMGA: A customizable web server for fast metagenomic sequence analysis. *BMC Genomics*, 12, 444.
- Wu XT, Chen L, Wang MQ, Zhang Y, Lin XY, Li XY, Zhou H, Wen YF (2018) Population structure and genetic divergence in *Firmiana danxiaensis*. *Biodiversity Science*, 26, 1168–1179. (in Chinese with English abstract) [武星彤, 陈璐, 王敏求, 张原, 林雪莹, 李鑫玉, 周宏, 文亚峰 (2018) 丹霞梧桐群体遗传结构及其遗传分化. 生物多样性, 26, 1168–1179.]
- Ya JD, Yu ZX, Yang YQ, Zhang SD, Zhang ZR, Cai J, Yang JB, Yu WB (2018) Complete chloroplast genome of *Firmiana major* (Malvaceae), a critically endangered species endemic to southwest China. *Conservation Genetics Resources*, 10, 713–715.
- Yu T, Zhang YY, Gao J, Ke L, Ma WB, Li JQ (2019) Complete chloroplast genome sequence of *Betula halophila*, a plant species with extremely small populations. *Scientia Silvae Sinicae*, 55(2), 41–49. (in Chinese with English abstract) [于涛, 张宇阳, 高健, 柯蕾, 马文宝, 李俊清 (2019) 极小种群濒危植物盐桦叶绿体基因组特征分析. 林业科学, 55(2), 41–49.]
- Zhang MY, Wang XF, Gao J, Liu AP, Yan YG, Yang XJ, Zhang G (2020) Complete chloroplast genome of *Paeonia mairei* H. Lév.: Characterization and phylogeny. *Acta Pharmaceutica Sinica*, 55, 168–176. (in Chinese with English abstract) [张明英, 王西芳, 高静, 刘阿萍, 颜永刚, 杨新杰, 张岗 (2020) 美丽芍药叶绿体全基因组解析及系统发育分析. 药学报, 55, 168–176.]
- Zhao XQ, Yan M, Ding Y, Huo Y, Yuan ZH (2019) Characterization and comparative analysis of the complete chloroplast genome sequence from *Prunus avium* ‘Summit’. *PeerJ*, 7, e8210.

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附录 Supplementary Material

附录1 广西火桐和丹霞梧桐的叶绿体基因组注释基因

Appendix 1 List of the annotated genes in chloroplast genome of *Firmiana kwangsiensis* and *F. danxiaensis*
<https://www.biodiversity-science.net/fileup/PDF/2020263-1.pdf>

附录2 广西火桐和丹霞梧桐的叶绿体基因组SSR位点信息

Appendix 2 SSR sequences identified in *Firmiana kwangsiensis* and *F. danxiaensis* chloroplast genome
<https://www.biodiversity-science.net/fileup/PDF/2020263-2.pdf>

附录3 广西火桐和丹霞梧桐的叶绿体基因组重复序列

Appendix 3 The repeat sequences identified in *Firmiana kwangsiensis* and *F. danxiaensis* chloroplast genome
<https://www.biodiversity-science.net/fileup/PDF/2020263-3.pdf>

附录4 广西火桐和丹霞梧桐的串联重复序列

Appendix 4 The tandem repeat sequences identified in *Firmiana kwangsiensis* and *F. danxiaensis* chloroplast genome
<https://www.biodiversity-science.net/fileup/PDF/2020263-4.pdf>

附录 1 广西火桐和丹霞梧桐的叶绿体基因组注释基因

Appendix 1 List of the annotated genes in chloroplast genome of *Firmiana kwangsiensis* and *F. danxiaensis*

基因分类 Category	基因分组 Group of gene	基因名称 Name of genes
表达相关基因 Self-replication	核糖体 RNA 基因 Ribosomal RNAs	<i>rrn16</i> (×2), <i>rrn23</i> (×2), <i>rrn4.5</i> (×2), <i>rrn5</i> (×2)
	转运 RNA 基因 Transfer RNAs	<i>trnA-UGC</i> (×2), <i>trnC-GCA</i> , <i>trnD-GUC</i> , <i>trnE-UUC</i> , <i>trnF-GAA</i> , <i>trnI-M-CAU</i> , <i>trnG-GCC</i> , <i>trnG-UCC</i> , <i>trnH-GUG</i> , <i>trnI-CAU</i> (×2), <i>trnI-GAU</i> (×2), <i>trnK-UUU</i> , <i>trnL-CAA</i> (×2), <i>trnL-UAA</i> , <i>trnL-UAG</i> , <i>trnM-CAU</i> , <i>trnN-GUU</i> (×2), <i>trnP-UGG</i> , <i>trnQ-UUG</i> , <i>trnR-ACG</i> (×2), <i>trnR-UCU</i> , <i>trnS-GCU</i> , <i>trnS-GGA</i> , <i>trnS-UGA</i> , <i>trnT-GGU</i> , <i>trnT-UGU</i> , <i>trnV-GAC</i> (×2), <i>trnV-UAC</i> , <i>trnW-CCA</i> , <i>trnY-GUA</i> ,
	核糖体小亚基基因 Small subunit of ribosome	<i>rps2</i> , <i>rps3</i> , <i>rps4</i> , <i>rps7</i> (×2), <i>rps8</i> , <i>rps11</i> , <i>rps12</i> , <i>rps14</i> , <i>rps15</i> , <i>rps16</i> , <i>rps18</i> , <i>rps19</i> , <i>rpoA</i> , <i>rpoB</i> , <i>rpoC1</i> , <i>rpoC2</i>
	核糖体大亚基基因 Large subunit of ribosome	<i>rpl2</i> (×2), <i>rpl14</i> , <i>rpl16</i> , <i>rpl20</i> , <i>rpl22</i> , <i>rpl23</i> (×2), <i>rpl32</i> , <i>rpl33</i> , <i>rpl36</i>
光合作用相关基因 Photosynthesis	ATP 酶合成基因 ATP synthase gene	<i>atpA</i> , <i>atpB</i> , <i>atpE</i> , <i>atpF</i> , <i>atpH</i> , <i>atpI</i>
	装配/稳定光系统 I 基因 Assembly/stability of photosystem I	<i>ycf3</i> , <i>ycf4</i>
	细胞色素复合体基因 Cytochrome b/f complex	<i>petA</i> , <i>petB</i> , <i>petD</i> , <i>petG</i> , <i>petL</i> , <i>petN</i>
	c 型细胞色素合成基因 c-type cytochrome synthesis	<i>ccsA</i>
	ccsA 基因	
	NADH 脱氢酶基因 NADPH dehydrogenase	<i>ndhA</i> , <i>ndhB</i> (×2), <i>ndhC</i> , <i>ndhD</i> , <i>ndhE</i> , <i>ndhF</i> , <i>ndhG</i> , <i>ndhH</i> , <i>ndhI</i> , <i>ndhJ</i> , <i>ndhK</i>
	光合系统 I 基因 Photosystem I	<i>psaA</i> , <i>psaB</i> , <i>psaC</i> , <i>psaI</i> , <i>psaJ</i>
	光合系统 II 基因 Photosystem II	<i>psbA</i> , <i>psbB</i> , <i>psbC</i> , <i>psbD</i> , <i>psbE</i> , <i>psbF</i> , <i>psbH</i> , <i>psbI</i> , <i>psbJ</i> , <i>psbK</i> , <i>psbL</i> , <i>psbM</i> , <i>psbN</i> , <i>psbT</i> , <i>psbZ</i>
	二磷酸核酮糖羧化酶大亚基基因 RubisCO large subunit	<i>rbcL</i>
	蛋白水解作用基因 Proteolysis	<i>clpP</i>
	成熟酶基因 Maturase	<i>matK</i>
	包裹膜蛋白基因 Envelop membrane protein	<i>cemA</i>
	乙酰辅酶 A 羧化酶亚基基因 Subunit of acetyl-CoA-carboxylase	<i>accD</i>
	转录起始因子基因 Transcription initiation factor IF-1	<i>InfA</i>
其他基因 Other genes	TIC 复合体组成基因 Component of TIC complex	<i>ycf1</i>
	假定叶绿体阅读框 Hypothetical chloroplast reading frames	<i>ycf2</i> (×2), <i>ycf15</i> (×2)

附录 2 广西火桐和丹霞梧桐的叶绿体基因组 SSR 信息。p1 为单核苷酸重复类型；p2 为双核苷酸重复类型；p3 为三核苷酸重复类型；p4 为四核苷酸重复类型；p5 为五核苷酸重复类型；c 为复合核苷酸类型。

Appendix 2 SSR sequences identified in *Firmiana kwangsiensis* and *F. danxiaensis* chloroplast genome. p1, mononucleotide; p2, dinucleotide; p3, trinucleotide; p4, tetranucleotide; p5, pentanucleotide; c, composite nucleotide.

序号 Code	重复类型 SSR type	简单重复序列 SSR sequence	大小 Size	起始 Start	终止 End	分布位置 Location	分布区域 Region
广西火桐 <i>Firmiana kwangsiensis</i>							
1	p1	(T)11	11	1537	1547	IGS	LSC
2	p1	(A)11	11	3742	3752	<i>tRNA-Lys</i> (intron)	LSC
3	p1	(A)12	12	4264	4275	IGS	LSC
4	p1	(C)10	10	5403	5412	<i>rps16</i> (intron)	LSC
5	c	(A)12...(A)10	78	5567	5644	<i>rps16</i> (intron)	LSC
6	p1	(A)12	12	6785	6796	IGS	LSC
7	p1	(A)10	10	7486	7495	IGS	LSC
8	c	(A)10(G)10	20	7965	7984	<i>psbI</i> -IGS	LSC
9	p4	(TTAT)3	12	8223	8234	IGS	LSC
10	p1	(A)12	12	8436	8447	IGS	LSC
11	p1	(A)10	10	8756	8765	IGS	LSC
12	p1	(T)12	12	9357	9368	<i>tRNA-Gly</i> (intron)	LSC
13	p1	(T)11	11	9664	9674	<i>tRNA-Gly</i> (intron)	LSC
14	p4	(TCTA)3	12	9830	9841	IGS	LSC
15	p1	(T)11	11	12282	12292	<i>atpF</i> (intron)	LSC
16	p1	(C)11	11	14616	14626	IGS	LSC
17	p4	(ATAA)3	12	15037	15048	IGS	LSC
18	p1	(A)10	10	16047	16056	IGS	LSC
19	c	(T)12...(A)10	25	16966	16990	IGS	LSC
20	p1	(T)10	10	17325	17334	<i>rpoC2</i>	LSC
21	p1	(T)10	10	19236	19245	<i>rpoC2</i>	LSC
22	p1	(T)11	11	21663	21673	<i>rpoC1</i>	LSC
23	c	(C)11(A)11	22	23298	23319	<i>rpoC1</i> (intron)	LSC
24	p1	(T)12	12	26974	26985	<i>rpoB</i>	LSC
25	p1	(A)10	10	27909	27918	IGS	LSC
26	p1	(A)11	11	28533	28543	IGS	LSC
27	c	(A)11...(T)10	37	30246	30282	IGS	LSC
28	p2	(AT)5	10	30616	30625	IGS	LSC
29	p2	(TA)5	10	32371	32380	IGS	LSC
30	c	(A)10...(T)11	77	32557	32633	IGS	LSC
31	p2	(TA)5	10	32918	32927	IGS	LSC
32	c	(TGAAA)3...(AT)5	103	33909	34011	IGS	LSC
33	p1	(T)14	14	34331	34344	IGS	LSC
34	p1	(A)10	10	38021	38030	IGS	LSC

序号 Code	重复类型 SSR type	简单重复序列 SSR sequence	大小 Size	起始 Start	终止 End	分布位置 Location	分布区域 Region
广西火桐 <i>Firmiana kwangsiensis</i>							
35	p4	(ATCT)3	12	44132	44143	IGS	LSC
36	c	(T)10...(A)12	95	46737	46831	<i>ycf3</i> (intron)	LSC
37	p2	(AT)8	16	47104	47119	IGS	LSC
38	p1	(A)10	10	50346	50355	IGS	LSC
39	p4	(AAAT)3	12	50618	50629	IGS	LSC
40	p2	(AT)5	10	51486	51495	IGS	LSC
41	c	(T)10...(TAT)4	65	51888	51952	IGS	LSC
42	c	(TATT)3...(TA)5	110	54619	54728	IGS	LSC
43	p1	(T)10	10	55001	55010	IGS	LSC
44	p1	(T)11	11	58571	58581	IGS	LSC
45	p1	(T)10	10	58921	58930	IGS	LSC
46	p4	(TAGT)3	12	63084	63095	IGS	LSC
47	p2	(AT)5	10	65694	65703	IGS	LSC
48	p2	(TC)5	10	65996	66005	<i>cemA</i>	LSC
49	p4	(AGGA)3	12	68124	68135	IGS	LSC
50	p1	(A)16	16	68576	68591	IGS	LSC
51	p1	(T)11	11	69157	69167	IGS	LSC
52	p1	(A)15	15	70244	70258	IGS	LSC
53	p1	(T)12	12	71046	71057	IGS	LSC
54	p4	(TATT)3	12	72353	72364	IGS	LSC
55	c	(TAT)4...(TAT)4	33	72855	72887	IGS	LSC
56	p4	(AAAT)3	12	73525	73536	IGS	LSC
57	c	(T)13...(T)10	103	75608	75710	<i>clpP</i> (intron)	LSC
58	p1	(A)10	10	75834	75843	<i>clpP</i> (intron)	LSC
59	p1	(T)10	10	76541	76550	<i>clpP</i> (intron)	LSC
60	p1	(A)12	12	76879	76890	<i>clpP</i> (intron)	LSC
61	p3	(ATT)4	12	79680	79691	<i>psbN</i>	LSC
62	p1	(A)10	10	80328	80337	<i>petB</i> (intron)	LSC
63	p1	(A)11	11	81702	81712	IGS	LSC
64	p1	(T)11	11	82061	82071	<i>petD</i> (intron)	LSC
65	p1	(A)10	10	83043	83052	IGS	LSC
66	p1	(T)14	14	83175	83188	IGS	LSC
67	p1	(T)11	11	85400	85410	IGS	LSC
68	p1	(A)10	10	86443	86452	IGS	LSC
69	p4	(TTTA)3	12	87529	87540	<i>rpl16</i> (intron)	LSC
70	p1	(T)11	11	88001	88011	<i>rpl16</i> (intron)	LSC
71	c	(T)13...(TA)5	115	89706	89820	IGS	IRb
72	p1	(T)11	11	104784	104794	IGS	IRb

丹霞梧桐 *Firmiana danxiaensis*

序号 Code	重复类型 SSR type	简单重复序列 SSR sequence	大小 Size	起始 Start	终止 End	分布位置 Location	分布区域 Region
12	p4	(TCTA)3	12	9756	9767	IGS	LSC
13	p1	(T)11	11	12320	12330	<i>atpF</i> (intron)	LSC
14	p1	(T)10	10	12437	12446	<i>atpF</i> (intron)	LSC
15	p1	(T)10	10	12696	12705	<i>atpF</i> (intron)	LSC
16	p1	(T)10	10	13534	13543	IGS	LSC
17	p1	(C)14	14	14646	14659	IGS	LSC
18	c	(ATAA)4(A)10	24	15062	15085	IGS	LSC
19	p1	(A)11	11	16079	16089	IGS	LSC
20	p1	(A)13	13	17011	17023	IGS	LSC
21	p1	(T)10	10	17358	17367	<i>rpoC2</i>	LSC
22	p1	(T)11	11	19268	19278	<i>rpoC2</i>	LSC
23	p2	(AT)5	10	20647	20656	<i>rpoC2</i>	LSC
24	p1	(T)11	11	21696	21706	<i>rpoC1</i>	LSC
25	p1	(T)12	12	27009	27020	<i>rpoB</i>	LSC
26	p1	(A)11	11	27944	27954	IGS	LSC
27	p1	(T)10	10	30335	30344	IGS	LSC
28	p2	(AT)5	10	30672	30681	IGS	LSC
29	p1	(T)10	10	30921	30930	IGS	LSC
30	p1	(A)16	16	31947	31962	IGS	LSC
31	p2	(TA)6	12	32426	32437	IGS	LSC
32	p1	(T)17	17	32673	32689	IGS	LSC
33	p2	(TA)5	10	32974	32983	IGS	LSC
34	c	(TGAAA)3...(AT)5	112	33975	34086	IGS	LSC
35	p1	(T)12	12	34406	34417	IGS	LSC
36	p1	(T)10	10	37119	37128	IGS	LSC
37	p1	(A)10	10	37983	37992	IGS	LSC
38	p4	(ATCT)3	12	44185	44196	IGS	LSC
39	p2	(AT)5	10	44590	44599	IGS	LSC
40	p1	(A)10	10	46268	46277	<i>ycf3</i> (intron)	LSC
41	c	(T)14...(A)11	81	46804	46884	<i>ycf3</i> (intron)	LSC
42	p1	(T)17	17	47147	47163	IGS	LSC
43	p1	(A)10	10	47671	47680	IGS	LSC
44	p1	(T)10	10	49240	49249	IGS	LSC
45	p1	(T)11	11	50447	50457	IGS	LSC
46	p1	(A)10	10	50807	50816	IGS	LSC
47	p4	(AAAT)3	12	51079	51090	IGS	LSC
48	p1	(T)11	11	51510	51520	<i>tRNA-Leu</i> (intron)	LSC
49	p2	(AT)5	10	51953	51962	IGS	LSC
50	c	(T)15...(TAT)4	68	52355	52422	IGS	LSC

序号 Code	重复类型 SSR type	简单重复序列 SSR sequence	大小 Size	起始 Start	终止 End	分布位置 Location	分布区域 Region
51	p4	(TATT)3	12	55063	55074	IGS	LSC
52	p2	(TA)5	10	55222	55231	IGS	LSC
53	p1	(T)10	10	55446	55455	IGS	LSC
54	p1	(T)13	13	59379	59391	IGS	LSC
55	c	(TAGT)3...(T)10	115	63557	63671	IGS	LSC
56	p1	(T)10	10	64443	64452	IGS	LSC
57	p1	(T)12	12	65531	65542	IGS	LSC
58	p2	(AT)5	10	66134	66143	IGS	LSC
59	p2	(TC)5	10	66436	66445	<i>cemA</i>	LSC
60	p1	(T)10	10	67186	67195	IGS	LSC
61	p1	(A)11	11	69013	69023	IGS	LSC
62	p1	(T)20	20	71482	71501	IGS	LSC
63	p1	(T)10	10	72467	72476	IGS	LSC
64	p4	(TATT)3	12	72801	72812	IGS	LSC
65	c	(TAT)4...(TA)6	80	73261	73340	IGS	LSC
66	p4	(AAAT)3	12	73909	73920	IGS	LSC
67	p1	(A)12	12	75762	75773	<i>clpP</i> (intron)	LSC
68	p1	(T)10	10	75916	75925	<i>clpP</i> (intron)	LSC
69	p1	(A)11	11	76031	76041	<i>clpP</i> (intron)	LSC
70	c	(A)10...(A)10	25	76213	76237	<i>clpP</i> (intron)	LSC
71	p1	(A)11	11	77258	77268	<i>clpP</i> (intron)	LSC
72	p3	(ATT)4	12	80059	80070	<i>psbN</i>	LSC
73	p1	(A)11	11	80707	80717	IGS	LSC
74	p1	(A)10	10	82077	82086	IGS	LSC
75	p1	(A)14	14	83424	83437	IGS	LSC
76	p1	(T)14	14	83560	83573	IGS	LSC
77	p1	(T)11	11	85806	85816	IGS	LSC
78	p1	(T)10	10	86315	86324	IGS	LSC
79	p1	(A)10	10	86851	86860	IGS	LSC
80	p5	(AAAAT)3	15	87990	88004	IGS	LSC
81	p1	(T)10	10	88423	88432	IGS	LSC
82	p2	(TA)7	14	90205	90218	IGS	LSC
83	p1	(T)12	12	105151	105162	IGS	IRb
84	p5	(TATTA)3	15	105719	105733	IGS	IRb
85	p5	(TAAAG)3	15	110818	110832	IGS	IRb
86	p1	(A)19	19	114289	114307	<i>rm5</i>	IRb
87	p5	(AGAAA)3	15	115599	115613	IGS	IRb
88	c	(A)10...(T)18	34	118309	118342	IGS	SSC
89	p5	(TAGAA)3	15	118721	118735	IGS	SSC

序号 Code	重复类型 SSR type	简单重复序列 SSR sequence	大小 Size	起始 Start	终止 End	分布位置 Location	分布区域 Region
90	c	(AT)6(T)10	21	119151	119171	IGS	SSC
91	c	(T)10...(T)15	60	121528	121587	IGS	SSC
92	p4	(TTGA)3	12	123799	123810	<i>ndhE</i>	SSC
93	p5	(TAGAA)3	15	124164	124178	IGS	SSC
94	c	(AATA)(A)10	21	126610	126630	<i>ndhA</i> (intron)	SSC
95	c	(A)10...(A)10	95	126759	126853	<i>ndhA</i> (intron)	SSC
96	p1	(T)10	10	131719	131728	<i>ycfI</i>	SSC
97	p4	(CATT)3	12	131893	131904	<i>ycfI</i>	SSC
98	p1	(T)11	11	132884	132894	<i>ycfI</i>	SSC
99	p1	(T)11	11	134161	134171	<i>ycfI</i>	SSC
100	p1	(T)10	10	134691	134700	<i>ycfI</i>	SSC
101	p1	(T)13	13	134810	134822	<i>ycfI</i>	SSC
102	p5	(TTTTTC)3	15	135782	135796	IGS	SSC
103	p1	(T)19	19	137089	137107	<i>rrn5</i>	IRa
104	p5	(ACTTT)3	15	140563	140577	IGS	IRa
105	p5	(TAATA)3	15	145663	145677	IGS	IRa
106	p1	(A)12	12	146234	146245	IGS	IRa
107	p2	(AT)7	14	161177	161190	IGS	IRa

附录 3 广西火桐和丹霞梧桐的叶绿体基因组重复序列。注：F 为正向重复序列；R 为反向重复序列；P 为回文重复序列。

Appendix 3 The repeat sequences identified in *Firmiana kwangsiensis* and *F. danxiaensis* chloroplast genome.

The F means forward sequence, R means reverse sequence and P means palindromic sequence.

序列长度 Length (bp)	重复类型 Repeat type	重复 1 起始位点 Repeat 1 start position	重复 1 位置 Repeat 1 location	重复 2 起始位点 Repeat 2 start position	重复 2 位置 Repeat 2 location	E 值 E value
广西火桐 <i>Firmiana kwangsiensis</i>						
45	P	4362	IGS	4362	IGS	7.93E-16
65	F	4752	IGS	4779	IGS	6.30E-24
38	F	4752	IGS	4806	IGS	2.19E-08
30	P	8048	<i>tRNA-GCU</i>	48024	<i>trnS-GGA</i>	5.68E-07
35	P	16961	IGS	16961	IGS	1.09E-06
49	F	40893	<i>psaB</i>	43117	<i>psaA</i>	2.43E-16
41	F	40901	<i>psaB</i>	43125	<i>psaA</i>	1.85E-13
30	R	44132	IGS	44132	IGS	2.47E-05
30	P	44521	IGS	44521	IGS	2.47E-05
41	F	46143	<i>ycf3</i> intron	125994	<i>ndhA</i> intron	4.33E-10
36	F	46148	<i>ycf3</i> intron	104382	IGS	1.66E-10
36	P	46148	<i>ycf3</i> intron	146118	IGS	1.66E-10
30	F	46157	<i>ycf3</i> intron	104391	IGS	5.68E-07
30	P	46157	<i>ycf3</i> intron	146115	IGS	5.68E-07
30	F	49729	IGS	49771	IGS	2.47E-05
31	F	63398	IGS	63430	IGS	1.58E-09
49	F	72823	IGS	72844	IGS	3.37E-18
32	F	72823	IGS	72865	IGS	1.76E-06
32	F	72844	IGS	72865	IGS	3.79E-08
34	R	76828	<i>clpP</i> intron	76828	<i>clpP</i> intron	1.24E-07
48	P	79503	IGS	79503	IGS	9.18E-20
31	F	94543	<i>ycf2</i>	94564	<i>ycf2</i>	1.47E-07
31	P	94543	<i>ycf2</i>	155941	<i>ycf2</i>	1.47E-07
31	P	94564	<i>ycf2</i>	155962	<i>ycf2</i>	1.47E-07
47	F	96989	<i>ycf2</i>	97007	<i>ycf2</i>	1.61E-13
47	P	96989	<i>ycf2</i>	153482	<i>ycf2</i>	1.61E-13
35	F	97001	<i>ycf2</i>	97019	<i>ycf2</i>	3.30E-08
35	P	97001	<i>ycf2</i>	153482	<i>ycf2</i>	3.30E-08
33	F	97002	<i>ycf2</i>	97038	<i>ycf2</i>	1.45E-05
33	P	97002	<i>ycf2</i>	153465	<i>ycf2</i>	1.45E-05
47	P	97007	<i>ycf2</i>	153500	<i>ycf2</i>	1.61E-13
35	P	97019	<i>ycf2</i>	153500	<i>ycf2</i>	3.30E-08
33	P	97038	<i>ycf2</i>	153501	<i>ycf2</i>	1.45E-05
38	F	104382	IGS	125999	<i>ndhA</i> intron	6.09E-10
30	F	105325	IGS	105352	IGS	2.47E-05

序列长度 Length (bp)	重复类型 Repeat type	重复 1 起始位点 Repeat 1 start position	重复 1 位置 Repeat 1 location	重复 2 起始位点 Repeat 2 start position	重复 2 位置 Repeat 2 location	E 值 E value
广西火桐 <i>Firmiana kwangsiensis</i>						
30	P	105325	IGS	145154	IGS	2.47E-05
34	F	113544	IGS	113576	IGS	1.24E-07
34	P	113544	IGS	136926	IGS	1.24E-07
34	P	113576	IGS	136958	IGS	1.24E-07
43	P	122739	IGS	122739	IGS	3.13E-11
38	P	125999	<i>ndhA</i> intron	146116	IGS	6.09E-10
35	P	126392	<i>ndhA</i> intron	126392	<i>ndhA</i> intron	1.09E-06
31	F	130542	<i>ycf1</i>	130563	<i>ycf1</i>	6.60E-06
34	F	136926	IGS	136958	IGS	1.24E-07
33	F	153465	<i>ycf2</i>	153501	<i>ycf2</i>	1.45E-05
47	F	153482	<i>ycf2</i>	153500	<i>ycf2</i>	1.61E-13
38	F	153491	<i>ycf2</i>	153509	<i>ycf2</i>	6.09E-10
30	F	153499	<i>ycf2</i>	153517	<i>ycf2</i>	5.68E-07
31	F	155941	<i>ycf2</i>	155962	<i>ycf2</i>	1.47E-07
丹霞梧桐 <i>Firmiana danxiaensis</i>						
45	P	4372	IGS	4372	IGS	7.98E-16
30	P	8000	<i>tRNA-GCU</i>	48084	<i>trnS-GGA</i>	5.71E-07
47	P	9796	IGS	9796	IGS	5.21E-17
30	P	10078	IGS	10078	IGS	2.48E-05
35	P	10189	IGS	10200	IGS	3.32E-08
39	F	29987	IGS	30006	IGS	2.42E-14
30	R	38301	IGS	38301	IGS	6.34E-09
49	F	40946	<i>psaB</i>	43170	<i>psaA</i>	2.44E-16
41	F	40954	<i>psaB</i>	43178	<i>psaA</i>	1.86E-13
30	R	44185	IGS	44185	IGS	2.48E-05
32	P	44575	IGS	44575	IGS	1.77E-06
41	F	46192	<i>ycf3</i> intron	126437	<i>ndhA</i> intron	4.35E-10
36	F	46197	<i>ycf3</i> intron	104749	IGS	1.67E-10
36	P	46197	<i>ycf3</i> intron	146610	IGS	1.67E-10
30	F	46206	<i>ycf3</i> intron	104758	IGS	5.71E-07
30	P	46206	<i>ycf3</i> intron	146607	IGS	5.71E-07
31	F	73203	IGS	73223	IGS	6.64E-06
34	R	77207	<i>clpP</i> intron	77207	<i>clpP</i> intron	1.25E-07
48	P	79882	IGS	79882	IGS	9.23E-20
30	F	87921	IGS	87951	IGS	6.34E-09
31	F	94910	<i>ycf2</i>	94931	<i>ycf2</i>	1.47E-07
31	P	94910	<i>ycf2</i>	156433	<i>ycf2</i>	1.47E-07
31	P	94931	<i>ycf2</i>	156454	<i>ycf2</i>	1.47E-07
47	F	97356	<i>ycf2</i>	97374	<i>ycf2</i>	1.62E-13

序列长度 Length (bp)	重复类型 Repeat type	重复 1 起始位点 Repeat 1 start position	重复 1 位置 Repeat 1 location	重复 2 起始位点 Repeat 2 start position	重复 2 位置 Repeat 2 location	E 值 E value
丹霞梧桐 <i>Firmiana danxiaensis</i>						
47	P	97356	<i>ycf2</i>	153974	<i>ycf2</i>	1.62E-13
35	F	97368	<i>ycf2</i>	97386	<i>ycf2</i>	3.32E-08
35	P	97368	<i>ycf2</i>	153974	<i>ycf2</i>	3.32E-08
33	F	97369	<i>ycf2</i>	97405	<i>ycf2</i>	1.46E-05
33	P	97369	<i>ycf2</i>	153957	<i>ycf2</i>	1.46E-05
47	P	97374	<i>ycf2</i>	153992	<i>ycf2</i>	1.62E-13
35	P	97386	<i>ycf2</i>	153992	<i>ycf2</i>	3.32E-08
33	P	97405	<i>ycf2</i>	153993	<i>ycf2</i>	1.46E-05
38	F	104749	IGS	126442	<i>ndhA</i> intron	6.12E-10
34	F	113911	<i>rrn4.5</i>	113943	<i>rrn4.5</i>	1.25E-07
34	P	113911	<i>rrn4.5</i>	137418	<i>rrn4.5</i>	1.25E-07
34	P	113943	<i>rrn4.5</i>	137450	<i>rrn4.5</i>	1.25E-07
33	R	115673	IGS	115673	IGS	4.71E-07
60	F	115688	IGS	115708	IGS	9.90E-25
40	F	115688	IGS	115728	IGS	4.25E-11
30	R	115857	IGS	115858	IGS	5.71E-07
38	P	126442	<i>ndhA</i> intron	146608	IGS	6.12E-10
34	P	126836	<i>ndhA</i> intron	126836	<i>ndhA</i> intron	1.25E-07
31	F	134006	<i>ycf1</i>	134033	<i>ycf1</i>	6.64E-06
34	F	137418	<i>rrn4.5</i>	137450	<i>rrn4.5</i>	1.25E-07
33	F	153957	<i>ycf2</i>	153993	<i>ycf2</i>	1.46E-05
47	F	153974	<i>ycf2</i>	153992	<i>ycf2</i>	1.62E-13
38	F	153983	<i>ycf2</i>	154001	<i>ycf2</i>	6.12E-10
30	F	153991	<i>ycf2</i>	154009	<i>ycf2</i>	5.71E-07
31	F	156433	<i>ycf2</i>	156454	<i>ycf2</i>	1.47E-07

附录 4 广西火桐和丹霞梧桐的串联重复序列

Appendix 4 The tandem repeat sequences identified in *Firmiana kwangsiensis* and *F. danxiaensis* chloroplast genome

起始点	终止点	重复单 元长度	重复单 元数量	比对得分	重复单元序列	串联重复序列	串联重复序 列所在位置
Start	End	Size of repeat unit	Copy of Repeat Units	Alignment score	Sequence of the repeat unit	Sequence of the entire repeat	Region
广西火桐 <i>Firmiana kwangsiensis</i>							
155	184	15	2.0	60	TAAAGAAAAAACAAA	TAAAGAAAAAACAAATAAAGAAAAAACAAA	IGS
8305	8345	21	2.0	82	TATAGATATATACAACCTTTTC	TATAGATATATACAACCTTTTCTATAGATATATACAACCTTTT	IGS
28976	29003	14	2.0	56	AGCAAAAAACAAGTG	AGCAAAAAACAAGTGAGCAAAAAACAAGTG	IGS
38039	38065	13	2.1	54	TAATTATTCTAAT	TAATTATTCTAATTAATTATTCTAATT	IGS
38757	38784	14	2.0	56	ATAGTTGACTGTAA	ATAGTTGACTGTAAATAGTTGACTGTAA	IGS
44135	44165	15	2.1	62	TATCTATCTATTTTT	TATCTATCTATTTTTTATCTATCTATTTTT	IGS
44720	44755	18	2.0	72	ATTAAATTAATATTTTTT	ATTAAATTAATATTTTTTATTAAATTAATATTTTTT	IGS
44806	44845	20	2.0	80	TAAGGTAATTTATTTAATTA	TAAGGTAATTTATTTAATTATAAGGTAATTTATTTAATTA	IGS
49642	49668	12	2.3	54	ATTCAATCTAAT	ATTCAATCTAATATTCAATCTAATATT	IGS
49672	49700	15	1.9	58	AGAATATAATAATTA	AGAATATAATAATTAAGAATATAATAATTA	IGS
50030	50063	15	2.3	68	AATAGAAATGAATGG	AATAGAAATGAATGGAATAGAAATGAATGGAATA	IGS
54424	54475	26	2.0	104	TCGATATAGTACTAATTTGTATA	TCGATATAGTACTAATTTGTATAGTATCGATATAGTACTAATTTGTATAGT	IGS
					GTA	A	
63302	63334	16	2.1	66	AATTTTATCTTCCTCT	AATTTTATCTTCCTCTAATTTTATCTTCCTCTA	IGS
63399	63461	32	2.0	126	ATCTCCCGAGAATTCTATTTTGA	ATCTCCCGAGAATTCTATTTTGACTAAAAATCATCTCCCGAGAATTCTATT	IGS
					CTAAAAATC	TTGACTAAAAAT	

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<http://www.biodiversity-science.net/CN/10.17520/biods.2020263>

起始点	终止点	重复单 元长度	重复单 元数量	比对得分 Alignment score	重复单元序列 Sequence of the repeat unit	串联重复序列 Sequence of the entire repeat	串联重复序 列所在位置 Region
Start	End	Size of repeat unit	Copy of Repeat Units				
广西火桐 <i>Firmiana kwangsiensis</i>							
63733	63766	17	2.0	68	TTAGATATACTTAGTAT	TTAGATATACTTAGTATTTAGATATACTTAGTAT	IGS
68340	68378	18	2.2	78	TATTAAGTATAAAATAAG	TATTAAGTATAAAATAAGTATTAAGTATAAAATAAGTAT	IGS
76830	76867	17	2.2	76	ATTTATATATATTTATA	ATTTATATATATTTATAATTTATATATATTTATAATTT	<i>ClpP</i> intron
90443	90473	14	2.2	62	TATCGTATAATTCT	TATCGTATAATTCTTATCGTATAATTCTTAT	<i>rpl2</i> intron
105310	105337	14	2.0	56	TTTTCTATTCTATT	TTTTCTATTCTATTTTCTATTCTATT	IGS
145200	145227	14	2.0	56	AATAGAATAGAAAA	AATAGAATAGAAAAAATAGAATAGAAAA	IGS
160064	160094	14	2.2	62	ATAAGAATTATACG	ATAAGAATTATACGATAAGAATTATACGATA	<i>rpl2</i> intron
丹霞梧桐 <i>Firmiana danxiaensis</i>							
155	184	15	2.0	60	TAAAGAAAAACAAA	TAAAGAAAAACAAATAAAGAAAAACAAA	IGS
6494	6530	19	1.9	74	CTTTTCTATTCTAATTAAG	CTTTTCTATTCTAATTAAGCTTTTCTATTCTAATTAA	IGS
9781	9813	16	2.1	66	TAATTCAATTCAATGA	TAATTCAATTCAATGATAATTCAATTCAATGAT	IGS
10141	10165	12	2.1	50	TAATTAGATAAT	TAATTAGATAATTAATTAGATAATT	IGS
29988	30045	19	3.1	116	ACTGTTCAAAGAGAAAAAA	ACTGTTCAAAGAGAAAAAACTGTTCAAAGAGAAAAAACTGTTCAAAG AGAAAAAA	IGS
38112	38138	13	2.1	54	TAATTATTCTAAT	TAATTATTCTAATTAATTATTCTAAT T	IGS
38248	38274	13	2.1	54	ATATTAGAATATT	ATATTAGAATATTATATTAGAATATT A	IGS
38271	38306	17	2.1	72	ATTAGAATAATAATATA	ATTAGAATAATAATATAATTAGAATAATAATATAAT	IGS
44188	44218	15	2.1	62	TATCTATCTATTTTT	TATCTATCTATTTTTTATCTATCTATTTTTT	IGS

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<http://www.biodiversity-science.net/CN/10.17520/biods.2020263>

起始点	终止点	重复单 元长度	重复单 元数量	比对得分 Alignment score	重复单元序列 Sequence of the repeat unit	串联重复序列 Sequence of the entire repeat	串联重复序 列所在位置 Region
Start	End	Size of repeat unit	Copy of Repeat Units				
丹霞梧桐 <i>Firmiana danxiaensis</i>							
44776	44813	18	2.1	76	ATTAAATTAATATTTTTT	ATTAAATTAATATTTTTTATTAAATTAATATTTTTTAT	IGS
44855	44894	20	2.0	80	TAAGGTAATTTATTTAATTA	TAAGGTAATTTATTTAATTATAAGGTAATTTATTTAATTA	IGS
49665	49702	18	2.1	76	TACTTAATATAACATATT	TACTTAATATAACATATTTACTTAATATAACATATTTA	IGS
49869	49894	13	2.0	52	TTAGATTTAAATC	TTAGATTTAAATCCTTAGATTTAAATC	IGS
50491	50524	15	2.3	68	AATAGAAATGAATGG	AATAGAAATGAATGGAATAGAAATGAATGGAATA	IGS
50673	50714	20	2.1	84	AATAAAATGAAATTAAAGA	AATAAAATGAAATTAAAGAAATAAAATGAAATTAAAGAAA	IGS
55132	55160	13	2.2	58	TATTTTATATCGA	TATTTTATATCGATATTTTATATCGATAT	IGS
55184	55223	20	2.0	80	ATGTTATTTCTATATATTTA	ATGTTATTTCTATATATTTAATGTTATTTCTATATATTTA	IGS
63776	63808	16	2.1	66	AATTTTATCTTCCTCT	AATTTTATCTTCCTCTAATTTTATCTTCCTCT A	IGS
64164	64197	17	2.0	68	TTAGATATACTTAGTAT	TTAGATATACTTAGTATTTAGATATACTTAGTAT	IGS
68777	68815	18	2.2	78	TATTAAGTATAAAATAAG	TATTAAGTATAAAATAAGTATTAAGTATAAAATAAGTAT	IGS
77209	77246	17	2.2	76	ATTTATATATATTTATA	ATTTATATATATTTATAATTTATATATATTTATAATTT	<i>ClpP</i> intron
83587	83618	15	2.1	64	AAATGAAATAAATCC	AAATGAAATAAATCCAAATGAAATAAATCCAA	IGS
87922	87981	30	2.0	120	CTTAATTTAATATTTATTTAATA ATTTAAT	CTTAATTTAATATTTATTTAATAATTTAATCTTAATTTAATATTTATTTAAT AATTTAAT	IGS
89825	89866	21	2.0	84	TCTTTATTATATTAATATTAA	TCTTTATTATATTAATATTAATCTTTATTATATTAATATTAA	IGS
90810	90840	14	2.2	62	TATCGTATAATTCT	TATCGTATAATTCTTATCGTATAATTCTTAT	<i>rpl2</i> intron
105678	105705	14	2.0	56	TTTTCTATTCTATT	TTTTCTATTCTATTTTTTCTATTCTATT	IGS

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<http://www.biodiversity-science.net/CN/10.17520/biods.2020263>

起始点	终止点	重复单	重复单	比对得分	重复单元序列	串联重复序列	串联重复序
Start	End	元长度	元数量	Alignment	Sequence of the repeat unit	Sequence of the entire repeat	列所在位置
		Size of	Copy of	score			Region
		repeat	Repeat				
		unit	Units				
丹霞梧桐 <i>Firmiana danxiaensis</i>							
118358	118399	21	2.0	84	AATATTATCAATTATTATTTA	AATATTATCAATTATTATTTAAATATTATCAATTATTATTTA	IGS
118834	118878	22	2.0	90	ATAGATAAATAATGACATAAAG	ATAGATAAATAATGACATAAAGATAGATAAATAATGACATAAAG	IGS
145691	145718	14	2.0	56	AATAGAATAGAAAA	AATAGAATAGAAAAAATAGAATAGAAAA	IGS
160556	160586	14	2.2	62	ATAAGAATTATACG	ATAAGAATTATACGATAAGAATTATACGATA	<i>rpl2</i> intron