

基于重测序的文冠果遗传多样性、群体遗传结构及生态位模拟分析

刘莉¹, 赵永军², 王磊², 薄文浩¹, 鲁仪增², 吴丹², 陆璐², 刘鷗², 解孝满^{2*}, 庞晓明^{1*}

(1.北京林业大学 北京 100083; 2.山东省林草种质资源中心 济南 250102)

摘要:文冠果耐旱、耐贫瘠、适应性强,是我国黄土高原主要种植的优良木本油料树种。由于交叉引种历史悠久,基于核基因组分析目前栽培种群与野生种群共存地区山梨属资源的遗传多样性、遗传结构及其迁移途径存在重大技术瓶颈。【目的】为了了解目前栽培种群和野生种群共存模式下文冠花的遗传多样性和引种迁移的变化。【方法】采用基因组重测序方法,基于核基因组对我国17个种群215个文冠花基因组的遗传多样性进行了分析,并基于重测序数据对文冠花叶绿体基因组序列进行了比较,分析了172个成功组装的文冠花叶绿体基因组SNPs和叶绿体单倍型的基因多样性和遗传结构。利用PSMC有效种群规模,我们重建了分布的历史动态,并使用物种分布模型重建了末次间冰期、末次冰川、全新世中期、现在和未来(2050年代)气候情景下的潜在分布。【结果】基因组研究表明,17个群体的平均多态性信息含量(PIC)为0.277,平均香浓指数(H)为0.515,平均多样性指数(Nei)为0.371,平均观测杂合度(Ho)为0.349,期望杂合度(He)为0.339,表明遗传多样性水平处于中等状态文冠果遗传多样性处于中等水平,野生种群遗传多样性较高,栽培种群遗传多样性普遍较低。河南省三门峡资源遗传多样性丰富,其次是宁夏、甘肃南部和陕西西部。结构和NJ系统发育树将文冠花种群分为三组;叶绿体基因组分为四组。根据叶绿体基因组和单倍型推测,在山西、山西、宁夏南部等地有文冠花避难所。SDM生态位模拟和等位基因频率及环境因子相关分析结果表明,受到末次间冰期温度降低的影响,文冠果有效种群大小降低,直至全新世中期气候回温,文冠果发生种群扩张。MaxEnt模型显示该物种从长江以南区域生长,后来逐渐适应寒冷条件,向我国西北地区大范围生长,才形成现有分布文冠果适宜生长范围从末次盛冰期到现在逐渐向东北移动。【结论】根据研究结果,我们得出结论,文冠果野生资源具有丰富的多样性,黄河和子午岭在文冠果进化过程中影响了其遗传分布,其未来分布有扩大的趋势。

关键词: 文冠果, 重测序, 遗传多样性, 遗传结构, 生态位分析

Analysis of the genetic diversity, genetic structure and ecological niche of Chinese *Xanthoceras sorbifolium* based on resequencing

Li Liu¹, Yongjun Zhao², Lei Wang², Wenhao Bo¹, Yizeng Lu², Dan Wu², Lu Lu², Kun Liu², Xiaoman Xie^{2*}, Xiaoming Pang^{1,*}

(1. Beijing Forestry University, Beijing 100083; 2. Shandong Provincial Center of Forest and Grass Germplasm Resources, Jinan 250102)

Abstract: *Xanthoceras sorbifolium* is drought tolerant, barren tolerant and adaptable, and is an excellent woody oilseed tree that is mainly grown on the Loess Plateau of China. Due to the long history of cross-introduction, there are major technical bottlenecks in analyzing the genetic diversity and genetic structure of *X. sorbifolium* resources and their migration routes in the current area of coexistence between cultivated and wild populations based on the nuclear genome. 【Objective】 In order to understand the genetic diversity and the changes of introduction and migration of *X. sorbifolium* in the current coexistence pattern of cultivated and wild populations. 【Method】 The genetic diversity of 215 *X. sorbifolium* genomes from 17 populations in China is analyzed based

on nuclear genome by using genome re sequencing method, and the chloroplast genome sequence of *X. sorbifolium* was compared based on re sequencing data, the genetic diversity and genetic structure of 172 successfully assembled chloroplast genome SNPs and chloroplast Haplotype of *X. sorbifolium* were analyzed. Using the PSMC effective population size, we reconstructed the historical dynamics of the distribution and used a species distribution model to reconstruct the potential distribution under the last interglacial, last glacial, mid-Holocene, present and future (2050s) climate scenarios. **【Result】** The results of genomic research indicate that the average polymorphic information content (*PIC*) of 17 populations is 0.277, the average aroma index (*H*) is 0.515, the average diversity index (*Nei*) is 0.371, the average observed heterozygosity (*Ho*) is 0.349, and the expected heterozygosity (*He*) is 0.339, the genetic diversity of *X. sorbifolium* is at a medium level, the genetic diversity of wild populations is high, and the genetic diversity of cultivated populations is generally low. Sanmenxia in Henan Province is rich in genetic diversity of resources, followed by Ningxia, southern Gansu and western Shaanxi. Structure and NJ phylogenetic trees divide *X. sorbifolium* population into three groups; The chloroplast genome was divided into four groups. According to the chloroplast genome and Haplotype, it is speculated that there are *X. sorbifolium* shelters in Linfen, Shanxi and southern Ningxia. The results of SDM Ecological niche simulation and Allele frequency and environmental factor correlation analysis showed that temperature affected the distribution of *X. sorbifolium*, and the suitable growth range of *X. sorbifolium* gradually moved to the northeast from the last glacial maximum to now. The MaxEnt model shows that this species grew from the southern region of the Yangtze River and gradually adapted to cold conditions, growing on a large scale in the northwest region of China, forming the suitable growth range for the current distribution of *X. sorbifolium*, which gradually moved towards the northeast from the last glacial period to the present. **【Conclusion】** Based on the results of the study, we conclude that there is a rich diversity in the wild resources of *X. sorbifolium*, and the Yellow River and Meridian Ridge have influenced its genetic distribution during the evolution of *X. sorbifolium*, and its future distribution has a tendency to expand.

Key words: *Xanthocera sorbifolium* Bunge, Resequencing, Genetic diversity, Genetic Structure, Distribution modeling