

全基因组关联分析鉴定出促进文冠果种子油积累的候选基因

张杰，班卓，毕泉鑫，王利兵*

(国家林木遗传育种重点实验室，中国林业科学研究院林业研究所，北京 100091)

摘要：种子油不仅为种子萌发后发育提供能量，还为人类产品提供必需的营养素和原材料。然而，控制种子油积累的转录调控机制在很大程度上仍然未知。文冠果 (*Xanthoceras sorbifolium* Bunge) 是一种木本油料树种，其种子油富含不饱和脂肪酸和罕见的神经酸，可用作高级食用油或生物柴油生产的原料。然而，文冠果中与种子油相关的遗传机制尚未得到很好的阐明。为了鉴定控制文冠果种子油的基因，本研究基于 164 个文冠果品种的全基因组重测序数据，确定了 2,909,151 个有效的单核苷酸多态性 (SNP) 位点。我们对影响种子油的三个核心性状 (种子干重、种仁重和种仁含油率) 进行了 2023 年和 2022 年的全基因组关联研究 (GWAS) 分析，并确定了 490 个显著的 SNP 位点。在这些位点中，Chr2_28304074 和 Chr2_26335997 位点引起了我们的关注，因为它们在多次分析中均表现出一致的关联性。通过 Sanger 测序，我们验证了这两个位点在 16 个种质资源中的基因型，证实了它们与 GWAS 分析结果的一致性。在这两个显著位点的下游，我们鉴定了两个候选基因，分别编码一个 MYB 转录因子蛋白和一个关键酶基因，我们将其命名为 *XsMYB58* 和 *XsLACS8*。RT-qPCR 分析显示 *XsMYB58* 和 *XsLACS8* 基因在种子中高表达，并且其表达水平与种子干重、种仁重和种仁含油量之间存在显著正相关，表明其在正常种子发育过程中可能发挥重要作用。与野生型大豆 (*Glycine max*) 相比，过表达 *XsMYB58* 和 *XsLACS8* 基因的转基因大豆品系表现出不同程度的种子大小增加、每株荚果种子数增加、每株植物荚果数增加、油细胞大小增加、油脂组分的增加以及含油率的增加。综合这些结果，我们假设 *XsMYB58* 和 *XsLACS8* 基因可能对文冠果种子油具有正向调控作用。这些研究结果为文冠果高油分子的育种提供了参考。

Genome-wide association analysis identifies a candidate gene promotes seed oil accumulation in *Xanthoceras sorbifolium* Bunge

Jie Zhang, Zhuo Ban, Quanxin Bi, and Libing Wang*

(State Key Laboratory of Tree Genetics and Breeding, Research Institute of Forestry Chinese Academy of Forestry, Beijing 100091, China)

Abstract: Seed oil not only provides energy for seed postgermination development but also provides essential nutrients and raw materials for human products. However, the transcriptional regulatory mechanism controlling seed oil accumulation remains largely unknown. Yellow horn (*Xanthoceras sorbifolium* Bunge) is a woody oilseed tree species whose seed oil is rich in unsaturated fatty acids and rare neuronics acids, and can be used as a high-grade edible oil or as a feedstock for biodiesel production. However, the genetic mechanisms related to seed oil in yellow horn are not well elucidated. To identify the genes controlling *Xanthoceras sorbifolia* seed oil, this study based on the whole-genome resequencing data of 164 *Cotinus coggygria* varieties identified 2,909,151 effective single nucleotide polymorphism (SNP) loci. We conducted genome-wide association study (GWAS) analysis on three core traits (seed dry weight, seed kernel weight, and kernel oil content) that influence seed oil for the years 2023

and 2022, and identified 490 significant SNP loci. Among these loci, the Chr2_28304074 and Chr2_26335997 loci caught our attention due to their consistent associations across multiple analyses. Through Sanger sequencing, we validated the genotypes of these two loci across 16 germplasms, confirming their consistency with the GWAS analysis results. Downstream of these two significant loci, we identified two candidate genes encoding an MYB transcription factor protein and encoding an key enzyme gene, which we named *XsMYB58* and *XsLACS8*. RT-qPCR analysis revealed high expression of the *XsMYB58* and *XsLACS8* genes in seeds, and a significant positive correlation between its expression levels and seed dry weight, seed kernel weight, and kernel oil content, suggesting its potential role in the normal seed development process. Transgenic Glycine max lines with the overexpressed *XsMYB58* and *XsLACS8* genes exhibited varying degrees of increase in seed size, number of seeds per silique, and number of siliques per plant compared with wild-type Glycine max. Combining these results, we hypothesize that the *XsMYB58* and *XsLACS8* genes may have a positive regulatory effect on seed oil of yellow horn. These results provide a reference for the molecular breeding of high-oil yellow horn.