

# 浙江红花油茶花叶型新品种‘叠翠流金’叶色变异的细胞学、多组学分析

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**摘要:**【目的】‘叠翠流金’是江西省林业科学院培育的浙江红花油茶新品种, 该品种同时具有正常叶片以及突变叶片, 其中突变叶片自叶脉发散黄化突变, 从而形成“花叶”, 是研究色素合成及光合作用机制的理想材料。【方法】从细胞结构、色素含量、转录水平的变化系统阐述了浙江红花油茶叶片黄化无性系‘叠翠流金’的形成机制及叶色变异对于光合作用的影响。【结果】研究表明, 黄化叶片的细胞结构、色素含量和光合作用均发生明显变化, 其中叶绿体类囊体结构不明显, 表现出退化的现象; 叶绿素 a 和类胡萝卜素含量明显低于正常叶而叶绿素 b 则相反; 光合测定发现黄化叶片的光合效率明显低于正常叶片。利用代谢组和转录组测序技术, 我们从 18 个浙江红花油茶样本的有参转录组测序共获得 123.74 G 的 Clean reads 以及 2756 种代谢物, 通过比较分析发现在 3 个时期的两种叶片中均表现出显著性差异的基因 251 个和代谢物 113 种。【结论】综合分析, 我们得出蓝绿色叶绿素 a 的降低伴随黄绿色叶绿素 b 的上升是黄化叶片形成的主要原因, 其中催化叶绿素 a 降解 (PAO,RCCR) 以及向叶绿素 b 转化的基因 (CAO) 发挥了重要作用; 同时光合作用 PSII 的 PsaB 基因、参与光合作用 PSI 中电子传递的 PsbB 以及 Cytochrome b 复合体的亚基 PetB 均在黄化部分表现出下调, 可能是黄化叶片光合作用下降的内在原因。本研究发现花叶的形成原因主要是叶绿素 a 下降伴随叶绿素 b 的上升, 并系统阐明了叶绿素 a 向叶绿素 b 转化导致色素变化并造成光合作用下降的分子机制, 本研究将为叶色变异及调控研究提供依据。

**关键词:** 土壤动物; 浙江红花油茶; 叶色变异; 多组学分析; 细胞结构; 光合色素含量

## Cytological and Multiomic Analysis of Leaf Color Variation in a *Camellia chekiangoleosa* New Variety 'Diecui Liujin'

**Abstract:** 【Objective】 'Diecui Liujin' is a new variety of *Camellia chekiangoleosa* cultivated by Jiangxi Academy of Forestry. This variety has both normal and mutant leaves, among which the mutant leaves emit yellowing mutations from the leaf veins, resulting in the formation of 'flower leaves'. It is an ideal material for studying pigment synthesis and photosynthesis mechanisms. 【Method】 The formation mechanism of *Camellia chekiangoleosa* leaf color variation clone 'Diecui Liujin' and the effect of leaf color variation on photosynthesis were systematically expounded from the changes of cell structure, pigment content and transcription level. 【Result】 The results showed that the cell structure, pigment content and photosynthesis of etiolated leaves had obvious changes, and the chloroplast thylakoid structure was not obvious, showing a degradation phenomenon; The contents of chlorophyll a and Carotenoid were significantly lower than those of normal leaves, but the opposite was true for Chlorophyll b; Photosynthetic measurements showed that the photosynthetic efficiency of yellowed leaves was significantly lower than that of normal leaves. Using metabolome and Transcriptome sequencing techniques, we obtained 123.74 G of Clean reads and 2756 kinds of metabolites from the transcriptome of 18 samples of *Camellia chekiangoleosa*. Through comparative analysis, we found 251 genes and 113 metabolites that showed significant differences.

ces in the two leaves at three stages. **【Conclusion】** Comprehensive analysis shows that the main reason for the formation of yellowing leaves is the decrease of Teal chlorophyll a accompanied by the increase of yellow green Chlorophyll b, in which the genes that catalyze the degradation of chlorophyll a (PAO, RCCR) and transform to Chlorophyll b (CAO) play an important role. Meanwhile, the PsaB gene of PSI I for photosynthesis, the PsbB involved in electron transfer in PSI for photosynthesis, and the PetB subunit of Cytochrome b complex all showed downregulation in the yellowing part, which may be the internal reason for the decrease in photosynthesis in yellowed leaves. This study found that the main reason for the formation of flowers and leaves was the decline of chlorophyll a accompanied by the rise of Chlorophyll b, and systematically clarified the molecular mechanism of the transformation of chlorophyll a to Chlorophyll b, which led to the change of pigments and the decline of photosynthesis. This study will provide a basis for the study of leaf color variation and regulation.

**Keywords:** Soil animals; *Camellia chekiangoleosa*; Leaf variation; Multiomics analysis; Cell structure; Photosynthetic pigment content

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