

光氮互作对于两种玉簪光合生长特性和表皮蜡质沉积的影响

赵舒怡¹, 许玉凤²

(1 沈阳农业大学林学院, 沈阳 110866; 2 沈阳农业大学生物科学技术学院, 沈阳 110866)

摘要:通过研究光氮互作对玉簪叶片生长光合特性以及表皮蜡质含量的影响, 为阐明阴生植物玉簪叶片表皮蜡质合成的分子调控机制提供基础, 为玉簪品种的改良与创新提供新的途径和理论支撑。以蓝叶色系(叶片表皮有白霜状蜡粉)的‘翠鸟’玉簪(*Hosta* ‘Halcyon’)和绿叶色系(叶片表皮无白霜状蜡粉)的东北玉簪(*Hosta ensata*)为材料, 通过对两种玉簪进行不同的光氮处理。5种遮荫处理分别为自然光的10%、30%、50%、70%、100%, 3种施氮处理分别为低氮(0.0 g/kg)、中氮(1.0 g/kg)和高氮(1.5 g/kg)。处理5周以后进行指标测定。研究表明, 1.两种玉簪在光强相同条件下中氮和低氮处理的叶片总面积、冠幅、株高、叶长叶宽、干重鲜重等均明显高于高氮处理, 并随着光强的增加呈现先升高后降低的趋势。2.在相同的光照条件下, 两种玉簪绿素a、b和叶绿素总含量随氮素含量增加都呈现先上升后下降的趋势, 其中高氮处理对于‘翠鸟’玉簪影响明显高于东北玉簪。3.通过对净光合速率、光合气体交换参数和叶绿素荧光参数的测定, 在中氮和透光度为50%的遮荫下最有利于提高玉簪的光合作用, 重度遮荫和高氮都会降低玉簪的光合速率。4.通过对两种玉簪蜡质含量的测定, 发现氮肥对于两种玉簪蜡质含量影响不显著。5.玉簪转录组测序数据及结果分析表明, 光强作为一种环境信号, 通过转录、信号转导等途径调节叶片不同蜡质生物合成途径中候选基因的表达量, 从而影响玉簪脂肪酸代谢, 并影响次生物质代谢, 如蜡质等的沉积。6.我们筛选得到了7个蜡质候选基因和2个转录因子, 并发现随着光强增加初级醇合成途径的脂肪酰CoA还原酶基因FAR和转录因子MYB60有明显的下调, 另外在上调了的CER1和烷羟化酶基因MAH1表达量与烷烃含量不一致变化也说明在同一蜡质合成途径中基因间存在功能冗余性。

Effects of photonitrogen interaction on photosynthetic growth characteristics and epidermal wax deposition of two hostas

Zhao Shuyi¹, Xu Yufeng²

(1 College of Forestry, Shenyang Agricultural University, Shenyang 110866, China; 2 College of Bioscience and Technology, Shenyang Agricultural University, Shenyang 110866, China)

Abstract: By studying the effects of photonitrogen interaction on the growth photosynthetic characteristics and epidermal wax content of hosta leaves, this paper provides a basis for elucidating the molecular regulation mechanism of epidermal wax synthesis in leaves of hosta pubic plants, and provides new ways and theoretical support for the improvement and innovation of hosta varieties. Hosta 'Halcyon' with blue leaf color (with hoarfrost-like wax powder on the leaf skin) and Hosta ensata (no hoarfrost-like wax powder on the leaf skin) were used as materials, and the two hostas were treated with different light nitrogen. The five shade treatments were 10%, 30%, 50%, 70% and 100% of natural light, and the three nitrogen application treatments were low nitrogen (0.0 g/kg), medium nitrogen (1.0 g/kg) and high nitrogen (1.5 g/kg). After 5 weeks of treatment, the index was measured. The results showed that: 1. The total leaf area, crown width, plant height, leaf length, leaf width, dry weight, fresh weight and so on of medium nitrogen and low nitrogen treatments were significantly higher than those of high nitrogen treatments, and showed a trend of first increasing and then decreasing with the increase of light intensity. 2. Under the same light conditions, the total contents of chlorophyll a, b and chlorophyll in the two hostas increased first and then decreased with the increase of nitrogen content, and the effect of high nitrogen treatment on 'Kingfisher' hosta was significantly higher than that of Northeast hosta. 3. Through the determination of net photosynthetic rate, photosynthetic gas exchange parameters and chlorophyll fluorescence parameters, the photosynthesis of hosta was most conducive to improving under the shade of medium nitrogen and light transmittance of 50%, and heavy shading and high nitrogen would reduce the photosynthetic rate of hosta. 4. Through the determination of the wax content of the two hostas, it was found that nitrogen fertilizer had no significant effect on the wax content of the two hostas. 5. The analysis of transcriptome sequencing data and results showed that light intensity, as an environmental signal, regulates the expression of candidate genes in different wax biosynthesis pathways in leaves through transcription and signal transduction, thereby affecting the fatty acid metabolism of hosta and the metabolism of secondary biomass, such as the deposition of wax. 6. We screened 7 wax candidate genes and 2 transcription factors, and found that the fatty acyl CoA reductase gene FAR and transcription factor MYB60 of the primary alcohol synthesis pathway were significantly down-regulated with the increase of light intensity, and the expression levels of CER1 and alkyl hydroxylase gene MAH1 were not consistent with the alkane content, which also indicated that there was functional redundancy between genes in the same wax synthesis pathway.