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论文

中棉所12及其选系配制的4个杂交棉幼苗期基因差异表达

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摘要:

以中棉所12及其2个选系为亲本组配的4个杂交棉中棉所28、中棉所29、湘杂棉2号和冀棉18苗期的根和顶端叶为研究材料, 采用cDNA-AFLP技术分析苗期杂交棉与亲本的根和叶基因差异表达, 并用Quantitative Real-Time技术加以验证。结果表明: (1)在4个杂交组合中, 中棉所12选系是营养生长杂种优势高值亲本; (2)杂交种和亲本间存在显著的基因表达差异, 可分为杂交种上调、单亲显性、单亲沉默、杂交种下调4种表达型。4个杂交组合在三叶期根和叶中差异表达基因的4种类型比例趋势基本一致, 单亲差异表达型(包括显性和沉默表达)在根和叶中所占比例较高, 杂种下调表达型所占比例较低, 反映出苗期单亲差异表达型在杂种优势形成中起主要作用; 叶部差异表达基因数目和比例(29.20%~46.09%)比根(15.65%~22.49%)高的多, 说明叶中基因差异表达可能比根中基因差异表达对杂种优势形成作用更大; (3)高值亲本中棉所12选系与杂交棉共同表达的基因多于低值亲本与杂交棉共同表达的基因, 从分子水平上证明中棉所12选系在杂交棉冀棉18、中棉所29和中棉所28的苗期营养生长杂种优势产生中起优势亲本的作用; (4)4种杂交组合差异表达基因(包含叶和根)占总表达基因的27.00%~34.56%, 分析差异表达基因类型和4个杂交组合的关系发现, 超显性效应占3.30%~7.17%, 超低亲效应占2.62%~4.14%, 低亲效应占5.65%~13.03%, 显性效应和加性效应是主要的杂种优势效应, 占79.52%~83.79%。多种杂种优势效应的并存说明杂种优势可能是多基因共同作用产生多种效应的结果; (5)超亲优势组合中棉所28的超显性效应占7.17%, 明显高于其他3个表现中亲优势组合, 说明杂交种上调表达型可能对苗期杂种优势产生起重要作用。

关键词: 中棉所12 杂交棉 基因差异表达

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Gene Differential Expression at Seedling Stage in Four Cotton Combination Hybridized by CRI-12 and Its Pedigree-Derived Lines

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Abstract:

CRI-12, an Upland cotton variety with high yield, elite fiber quality and disease resistance, is characterized by its high heritability, combining ability and genetic stability. CRI-12 and its pedigree-derived lines were used to develop high heterosis cotton hybrids such as Zhongmiansuo 28, CRI-29, XZM2, and Jimian 18. The roots and leaves at seedling stage of these hybrids and their corresponding parents were sampled for cDNA-AFLP analysis and validation by Quantitative Real-Time PCR. The results were as follows: (1) CIR-12 played a predominant role in the heterosis of vegetative growth in CRI-28, CRI-29, and Jimian18 at seedling stage. (2) Four differential expression types were detected between the hybrid and its parents: I. Up expression only showed in hybrid but not in both parents; II. Dominant expression showed in one of the parents but not in F₁ and another parent, including the expression pattern in female parent and hybrid not in male parent, and the expression pattern in male parent and hybrid not in female parent; III. The gene silenced in one of the parents, including the expression pattern in male parent not in hybrid and female parent and the expression pattern in female parent not in hybrid and male parent, IV. Down expression showed in both parents but not in F₁. The tendency of proportion in four types was consistent and showed a high ratio in dominant expression and silencing in single parent, but a low ratio in down expression in roots and leaves of hybrids. The type expressed only in one parent and F1 or only in one parent played main role in heterosis. Differential expression genes in leaves and roots accounted for 29.20–46.09% and 15.65–22.49%, respectively. The differential expression genes in leaves were more than those in roots, indicating that some genes play larger roles for heterosis than these in roots. (3) Genes co-expressed between hybrids and high value parent CRI-12 and/or its derived lines were much more than those between hybrids and the relative low value parents, indicating that CIR-12 plays a predominant role in the expression of genes responsible for heterosis in CRI-28, CRI-29, and Jimian18 at seedling stage. (4) Differentially expressed genes in the four hybrids accounted for 27.00–34.56% of total genes detected. Further analysis revealed that the main modes of gene action involved in hybrids were additive and dominant effects accounting for 79.52–83.79%, and the effect of over-dominance accounting for 3.30–7.17%, under-dominance effects accounting for 2.62–4.14% and low-parent dominance effects accounting for 5.65–13.03%. All possible modes of gene action co-existed supported the hypothesis of multiple gene mechanisms contributed to heterosis. (5) Over-dominance effect in CRI-28 which express high

parent heterotic is 7.17%, higher than that in three other middle heterotic crosses at three earlier growing stages, which suggesting the differential expression type expressed only in F_1 play an important role in heterosis of vegetative growth.

Keywords: CRI-12 Hybrid Cotton Differential Expression gene

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