

[本期目录](#) | [下期目录](#) | [过刊浏览](#) | [高级检索](#)[\[打印本页\]](#) [\[关闭\]](#)**论文****玉米S-腺苷甲硫氨酸合成酶基因家族成员在盐胁迫条件下的差异表达**朱晶莹<sup>1</sup>, 王寒玉<sup>1</sup>, 张晏萌<sup>2</sup>, 余爱丽<sup>1</sup>

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**摘要:**

S-腺苷甲硫氨酸合成酶(SAMS)是植物代谢过程中的一个关键酶,催化甲基供体和化合物前体S-腺苷甲硫氨酸的合成。为研究S-腺苷甲硫氨酸合成酶基因在盐胁迫条件下的响应和功能,以玉米甘油醛-3-磷酸脱氢酶(GAPDH)基因为内参基因,通过半定量RT-PCR法分析玉米SAMS基因在盐胁迫条件下的表达模式。结果表明,玉米SAMS基因家族4个成员(SAMS1、SAMS2、SAMS3和SAMS4)在正常生长(对照)和盐胁迫条件下都表达,对照根茎中的表达量大于叶中。SAMS1受盐胁迫后,茎中表达量降低,而叶中表达量略有增加,根中无明显变化。SAMS2和SAMS4受盐胁迫明显诱导,而SAMS3似乎不受盐胁迫诱导,处理植株与对照株相比均无差异。说明玉米SAMS基因家族的4个基因在表达模式上存在差异,推测在功能上存在分工的不同。

**关键词:** 玉米 S- 腺苷甲硫氨酸合成酶(SAMS) 盐胁迫 表达分析 半定量RT-PCR

### DI FFERENTIAL EXPRESSION OF MAI ZE S-ADENOSYLMETHIONINE SYNTHETASE GENE FAMILY MEMBERS DURING SALT STRESS

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**Abstract:**

S-adenosylmethionine synthetase SAMS is a key enzyme in plant metabolism, catalyzing the biosynthesis of SAM, which is a donor for methyl groups and the precursor of many compounds. To study the response and functions of SAMS under salt stress in maize, the semi-quantitative RT-PCR was used to investigate the expression patterns of SAMS gene, using maize glyceraldehyde-3-phosphate dehydrogenase gene as a control. The results showed that all of the four maize SAMS genes family members were expressed both under normal and salt conditions. In the control seedlings, the mRNA levels of the four genes were higher in roots and stems than those in leaves. Under the salt stress the expression of SAMS1 was down-regulated in stems, up-regulated in leaves, but no change in roots. The transcript levels of SAMS2 and SAMS4 also increased significantly under salt stress. However, SAMS3 had no response to NaCl in any organs. In maize, the four genes of SAMS family were differentially expressed under salt stress condition, suggesting the possibility of functional differences between their proteins.

**Keywords:** maize S-adenosyl methionine synthetase salt stress expression analysis semi-quantitative RT-PCR

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