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摘要: 我国大豆种质资源中存在着丰富的主要贮藏蛋白亚基变异类型,它们是大豆品质改良和育种重要的种质基础,因而研究其变异
发生的机制有着积极的指导作用。以7个A₅A₄B₃亚基缺失体、2个A₃B₄亚基缺失体和正常品种为材料,在采用SDS-PAGE验证亚基缺
失表现稳定的前提下,克隆得到缺失亚基所对应的基因序列和cDNA序列,然后通过与NCBI上已公布的正常序列进行比较,发现
7个材料编码A₅A₄B₃亚基的DNA序列和cDNA序列的起始密码子都由ATG突变成了ATA,形成一个严重错误的翻译阅读框,引起缺
失;2个材料编码A₃B₄亚基的DNA序列并无明显差异,但cDNA序列的终止密码子都由TAA突变成了CAA,可能会导致翻译出来的亚
基前体额外多出17个氨基酸的尾巴,引起缺失。

Abstract: There is great genetic diversity in the relative content of seed storage protein subunits in Chinese soybean
germplasm, which is the foundation of soybean protein quality improvement. Therefore, it will be helpful for
soybean high-quality protein breeding to understand the molecular mechanism of the subunit mutations. Based on
the validation of their subunit deficiency by sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-
PAGE), seven landraces without A₅A₄B₃ and two without A₃B₄subunit were used as experimental materials and their
subunit mutant gene sequences and cDNA sequences were obtained. Compared with normal sequences on NCBI, the
start codon ATG of the genes and cDNAs encoding the A₅A₄B₃subunits of seven mutant landraces was found to
mutate to ATA, which produced a fire-new reading frame of translation and resulted in subunit lacking. While
the stop codon TAA of cDNAs encoding A₃B₄subunit of two mutant landraces were found to mutate to CAA, which may
resulted in an additional tail in pro-glycinin and caused subunit lacking.

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