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Characterization of Multiple Polyadenylation Sites in One Alpha-Tubulin Transcript of *Capsicum annuum* L.

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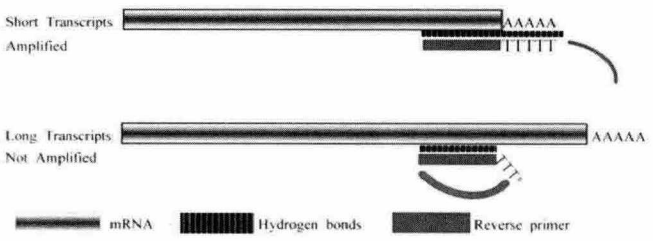
Objectives

Multi-polyadenylation sites are independently governed by three cis-acting elements, that is, FUE (Far Upstream Element), NUE (Near Upstream Element) and CS (Cleavage Site) in most 3′ untranslated region. This study was carried out to reveal the function of multi-polyadenylation sites from one α-tubulin gene in hot pepper (*Capsicuum annuum* L.).

Materials and Methods

We used hot pepper α-tubulin cDNA. Sequence specific primers form a loop and stem structure when they didn't bind to complementary template in 5′ primer region. Therefore, they could discriminate polyadenylation sites in the template.



Results and Discussion

The α-tubulin cDNA from hot pepper had four polyadenylation sites in 3′ untranslated region used as template in sequence discriminating RT-PCR. It is suggested that these four polyadenylation sites may be regulated by two sets of FUE and NUE from sequence homology analysis. Therefore, we could classify these polyadenylation sites to two functional groups that produced long transcript or short one. Interestingly, in the inter-polyadenylation site region there are putative DST (Down Stream Element) sequence that instabilize mRNA of small auxin up RNA (SAUR) in *Arabidopsis thaliana*.

To analyze the function of these mRNA instability region in multiple transcripts from one α-tubulin gene, we developed the sequence discriminating RT-PCR technique. Reverse primers with poly (T) and loop-step structure could discriminate their complementary template precisely. On the basis of these results, we could exclusively amplify some transcripts among all transcripts transcribed from one α-tubulin gene. Furthermore, we will discuss on half life of diverse transcripts that have or have not mRNA instability element.

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