Molecular Cloning and Characterization of Eukaryotic Translation Initiation Factor 5A (eIF-5A) from Potato (Solanum tuberosum L.)

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Many physiological changes occur in potato plant upon tuberization. The molecular mechanisms of tuberization remain to be clarified. Differential display based on PCR was employed to identify genes expressed during tuber-developing stage of potato (Solanum tuberosum L. cv. Irish Cobbler). An eukaryotic initiation factor 5A (eIF-5A) clone isolated from a lamda ZAP cDNA library constructed from developing micro-tuber using a probe of PCR fragment. The northern blot analysis of eIF5A has shown abundant expression, mainly in flower organs (stamen, ovary, petal, sepal), fruit and stolon. This clone revealed high sequence similarity to tomato eIF 5A cDNA. At the DNA level, there is 94.8 \% identity with the tomato eIF-5A4, whereas at the protein level there was a high identity with 97.5 %. The potato eIF 5A clone is 716 bp in length and contains a single open reading frame from 57 to 539 bp, a 56 bp 5 $^{\prime}$ untranslated region and a 177 bp 3 '-untranslated region. The deduced protein composed of 160 amino acid residues, with a predicted molecular mass of 17.4 kD and an estimated pI of 5.5. The sequence of 12 (STSKTGKHGHAK) amino acids among eIF-5A proteins is perfectly conserved from yeast to human. That sequence in potato eIF-5A protein is also conserved at position 46 to 57 amino acid. This region embeds the post-translational modification site of the lysine residue (at the seventh K) to hypusine that is crucial to eIF-5A activity.