

### **Partial amino acid sequence of minor acid proteinase from *Nepenthes distillatoria* L**

Isolation, purification procedure and some of the enzymatic properties of minor acid proteinase of *Nepenthes* juice were reported previously. Because of its potential applications in medicine, and biology. Therefore, it is very important to investigate the primary structure of the enzyme to clarify its structure - function relationship. In this study the extended NH<sub>2</sub> - terminal amino acid sequence of the purified enzyme has been determined.

*Nepenthes* minor acid proteinase was purified to homogenous form. The NH<sub>2</sub> - terminal amino acid sequence was determined using an automated sequencer. To determine the partial internal sequence of the enzyme, reduced and carboxymethylated (RCM) protein was digested

with endoproteinases and aliquots were subjected to HPLC. An aliquot of each peptide fraction was submitted to the amino acid sequencer.

The extended NH<sub>2</sub>-terminal amino acid sequence was determined up to the 20<sup>th</sup> residue as given below.

QTVQVEPPYYAGDEYLMNV

This sequence has very little homology with the NH<sub>2</sub>-terminal amino acid sequences of other known plant aspartic proteinases (barley, rice and cardon flower). Computer homology search of the partial sequence with the protein data bank also indicates that this enzyme has much less homology with other known aspartic proteinases. These results suggest that this enzyme is a novel member of the peoteinase world. This unique amino acid sequence may reflect the probable relationship to the remarkable properties of this enzyme. Primers will be designed based on the determined partial sequence and RT-PCR cloning will be used to isolate the cDNA clone and to deduce the primary structure.