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Mass Spectroscopy Based Proteomics for Identification of a Novel Alpha Amylase Inhibitor

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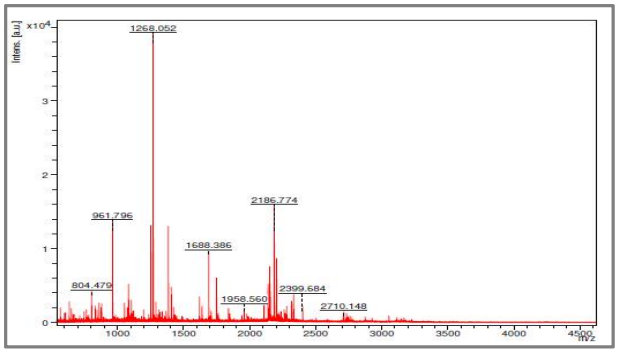
ABSTRACT

Mass Spectroscopy (MS) based Proteomics is a promising tool in macromolecular research. The wide range of protein activities, quantification of protein abundance, interactions and modifications, sequence analysis, comparative structural analysis can be probed effectively using MS. Most macromolecular research relies on the use of ESI or MALDI as an ionization source. The structural details or sequence information can be elucidated using Tandem MS. The utility of MS in protein and peptide analysis lies in its ability to provide highly accurate molecular weight information of intact molecules that is extremely useful for the characterization of newer proteins. A protein aceous alpha amylase inhibitor from a medicinal herb Oxalis corniculata has been isolated using standard protein purification techniques. The sequence analysis and structural determination was done using MS. The purified protein from the aqueous extract of Oxalis corniculata had a molecular weight of approximately 34Kda when separated on SDS PAGE which was further studied by MS analysis to get a peptide mass fingerprint (PMF). The peptide masses obtained were submitted to MASCOT search engine and the proteins similar to the putative alpha amylase inhibitor were observed. The isolated pure protein had 100% sequence similarity with PLDG3 protein of Arabidopsis thaliana. This MS based proteomic data paved way for the structural elucidation of the new protein. Further in silico analysis using Pair wise alignment and Virtual screening can help in building the structural and functional efficacy of the purified protein as an alpha amylase inhibitor.

Graphical Abstract



PMF of the purified protein

Keywords: Mass spectroscopy, Alpha amylase inhibitor, *Oxalis corniculata*, Virtual screening, Peptide Mass Fingerprint (PMF),