This technique could be extended to screen drugs

NCL scientists develop new tech

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Scientists at the National Chemical Laboratory (NCL) in Pune have demonstrated for the first time, a technique to screen drugs in-vivo for regulation of protein expression. This technique could be extended to screening of drugs that inhibit protein synthesis in various diseases.

Protein expression, a subcomponent of gene expression, is commonly used by proteomics researchers to denote the measurement of the presence and abundance of one or more proteins in a particular cell or tissue.

NCL scientist (mass spectrometry and proteomics) Mahesh Kulkarni along with Mala Rao, VP Vinod, PK Umasankar and Milind Patole have done this research recently. The technique involved for the first time

applications of intact cell matrix-assisted laser desorption or ionisation mass spectrometry (ICM-MS) to study the regulation of protein expression.

Kulkarni told *DNA* that the technique was important as it could study the expression of a single protein which otherwise was difficult. He said that it needed the presence of protein in abundance for which arabinose inducible promoter was used. The regulation of protein expression was studied using glucose as an alternative metabolite.

Significance

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According to Kulkarni, this technique could be extended to in-vivo screening of drugs and it had tremendous potential to discover novel drugs against specific protein expressions in different diseases. Currently, the methods available to assay protein expression are tedious and time-consuming which make it difficult to screen large numbers of combinatorial compounds.

Kulkarni said that with the development of matrix assisted laser desorption or ionization (MALDI) and electrospray ionization (ESI) as well as improvement in time-of-flight mass spectrometry (TOF-MS), it had become feasible to produce and analyse protein expression directly from an intact-cell laser desorption or ionisation, using ICM-MS. Kulkarni said that major limitation of this assay was that the protein had to be present in abundance, although, with the existing limitation, the assay had the potential for studying the regulation of proteins in some of the cell lines where the protein was over-expressed.