Extended Abstract Journal of Molecular and Cellular Biochemistry 2021
Vol.5 No.1

Metabolic labeling with an alkyne probe reveals similarities and differences in the prenylomes of several brain-derived cell lines and primary cells

Mark D Distefano
Departments of Chemistry and Medicinal Chemistry, USA

Abstract
Protein prenylation involves the attachment of one or two isoprenoid group(s) onto cysteine residues positioned near the C-terminus. This modification is essential for many signal transduction processes. In this work, the use of the probe C15AlkOPP for metabolic labeling and identification of prenylated proteins in a variety of cell lines and primary cells is explored. Using a single isoprenoid analogue, 78 prenylated protein groups from the three classes of prenylation substrates were identified including three novel prenylation substrates in a single experiment. Applying this method to three brain-related cell lines including neurons, microglia, and astrocytes showed substantial overlap (25%) in the prenylated proteins identified. In addition, some unique prenylated proteins were identified in each type. Eight proteins were observed exclusively in neurons, five were observed exclusively in astrocytes and three were observed exclusively in microglia, suggesting their unique roles in these cells. Furthermore, inhibition of farnesylation in primary astrocytes revealed the differential responses of farnesylated proteins to an FTI. Importantly, these results provide a list of 19 prenylated proteins common to all the cell lines studied here that can be monitored using the C15AlkOPP probe as well as a number of proteins that were observed in only certain cell lines. Taken together, these results suggest that this chemical proteomic approach should be useful in monitoring the levels and exploring the underlying role(s) of prenylated proteins in various diseases.

This work is partly presented Journal of Molecular and Cellular Biochemistry on march 08-09, 2021 as webinar