ROS conditional proteomics (2): identification of H_2O_2-rich subcellular compartments

([1]*Graduate School of Engineering, Kyoto University*, [2]*JST-ERATO*) ○Hao Zhu,[1] Itaru Hamachi[1,2]

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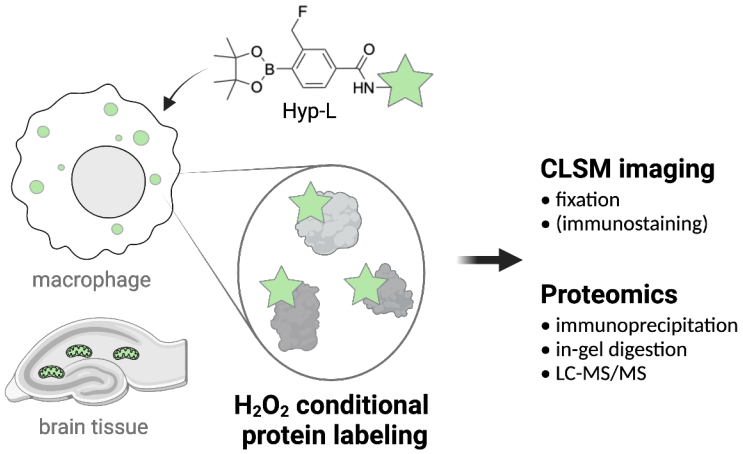
We have developed a ROS conditional proteomics approach that relies on designer chemical probes of H_2O_2-responsive protein labeling reagents (Hyp-L). In this presentation, I will introduce its application to characterize H_2O_2-rich subcellular compartments in cultured cells and mouse brain tissues.

Macrophages produce diverse ROS-rich intracellular vesicles during immune response; however, the exact identity of such vesicles has not yet been determined. In this study, the Hyp-L-based proteomics provided invaluable clues for the vesicle identification. We found, for the first time, that autophagosomes contained a high level of H_2O_2 in the activated macrophages.

Hyp-L was further applied to mouse brain tissues. It is able to detect the ROS production upon the inhibition of mitochondrial complex II. However, unlike that in cultured cells, confocal microscopy imaging in the complex-structured tissues could not clearly identify the ROS production site in the subcellular resolution. By contrast, the Hyp-L-based proteomics clearly revealed the significant enrichment of labeled proteins in mitochondria.



1) H. Zhu et al., *J. Am. Chem. Soc.*, **2020**, 142, 15711.