A versatile, integrated workflow for interaction proteomics

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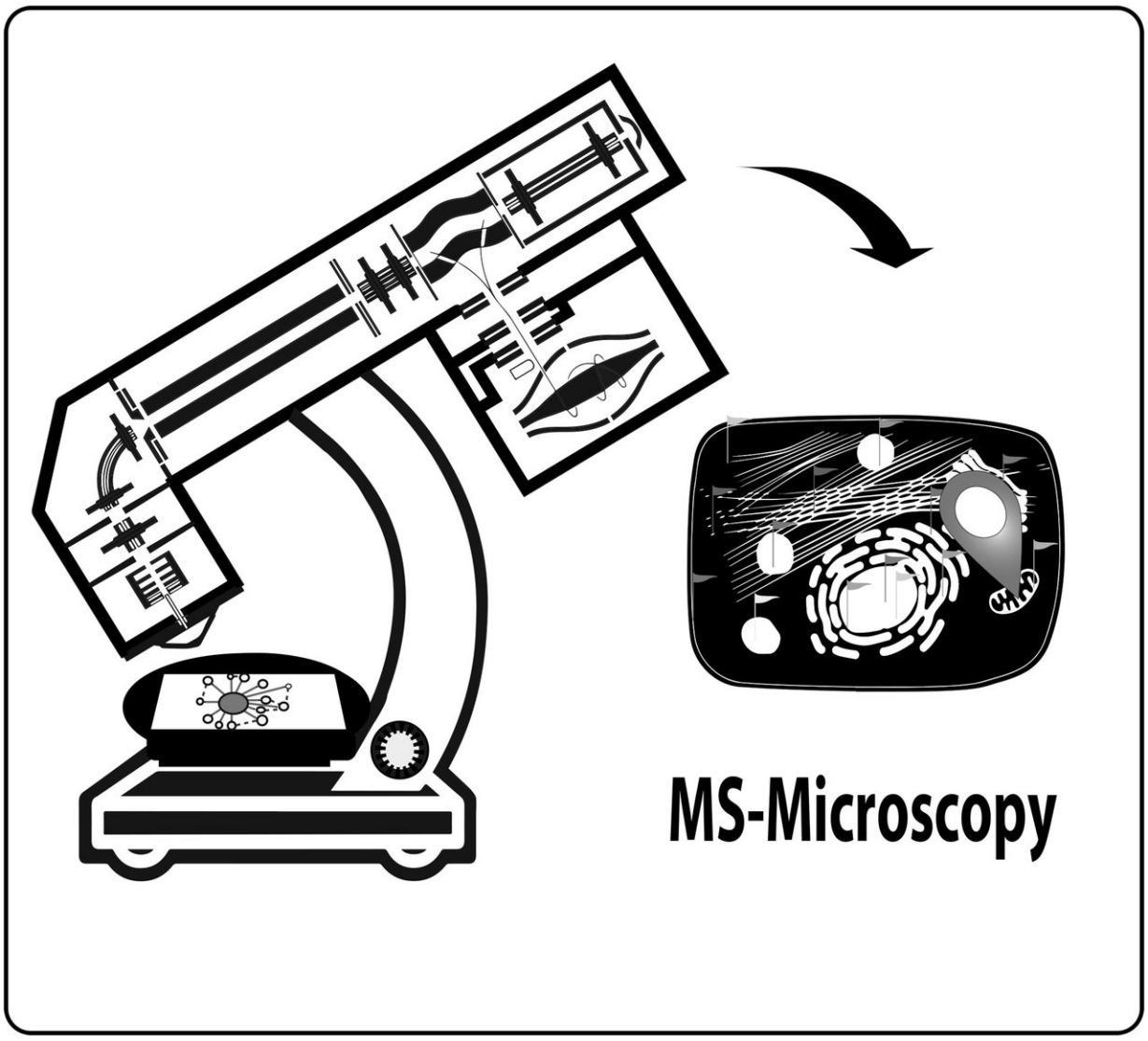

Researchers developed an integrated workflow for interaction proteomics, which proves almost as versatile as the Swiss Army Knife. Credit: Varjosalo Lab

Proteins do not function in isolation, and their interactions with other proteins define their cellular functions. Therefore, detailed understanding of protein-protein interactions (PPIs) is the key for deciphering regulation of cellular networks and pathways. These complex networks of stable and transient associations can be studied by affinity purification mass spectrometry (AP-MS) and complementary proximity-based labeling methods such as BioID.

In a study published in *Nature Communications*, a research team led by Dr. Markku Varjosalo at the University of Helsinki developed an optimized and integrated approach combining AP-MS and BioID in a single workflow. In addition to exploiting the advantages of both strategies, the authors show that their approach allows identification and quantification of protein-protein interactions and protein complex stoichiometries, identification of transient or close-proximity interactions with BioID, visualization of the bait protein and the proximal interactors with immunofluorescence microscopy, and defining the molecular context with MS microscopy utilizing the reference dataset obtained by identifying proximal interactors for bona fide subcellular localization markers.

The authors show that MS microscopy makes it possible to assign the studied protein to its correct cellular or even subcellular location in even higher resolution than with confocal microscopy. "This study is a continuum of our rigorous efforts in developing new systems biology tools for studying the molecular interactions formed by proteins. We have previously proven that AP-MS is highly reproducible method, which is also suitable for large-scale and inter-laboratory studies", Dr. Varjosalo says. "Our newly developed integrated workflow and the reference molecular context proteome map, allows an easy way to probe the molecular localization of (m)any protein(s). The developed MAC-tag

and the integrated approach should empower, not only the interaction proteomics community, but also cell, molecular and structural biologists, with an experimentally proven integrated workflow for mapping in detail the physical and functional interactions and the molecular context of proteins in human cells."

More information: Xiaonan Liu, Kari Salokas, Fitsum Tamene, Yaming Jiu, Rigbe G. Weldatsadik, Tiina Öhman and Markku Varjosalo. An AP- MS- and BioID-compatible MAC-tag enables comprehensive mapping of protein interactions and subcellular localizations, *Nature Communications* March 22, 2018, DOI: 10.1038/s41467-018-03523-2

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