MAPPIT and Co: analytical and high-throughput protein-protein interaction mapping in human cells.

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Abstract

MAPPIT (Mammalian Protein-Protein Interaction Trap) is a cytokine receptor-based two-hybrid method that operates in intact mammalian cells (www.mappit.be, 1). This MAPPIT approach was over the years advanced into a technology suite for detailed mapping analysis of selected protein-protein and protein-small molecule interactions (reviewed in 2) in a close-to-normal physiological context. MAPPIT can also be applied as a validation tool for large-scale protein interactomics of yeast (3), C. elegans (4) and man (5). I will illustrate these opportunities and also the limitations of MAPPIT using specific examples.
More recently, the MAPPIT platform was miniaturized allowing large-scale interactomics in human cells. In its current setup, a collection of 17.000 human ORF preys can be interrogated against a selected bait using a highly-automated reverse transfection assay (6). With KISS (Kinase-Substrate Sensor), an alternative strategy was recently devised that accommodates analysis of full-size transmembrane and nuclear proteins, but uses the same read-out as the MAPPIT system (7). We expect that a combination of both methods will allow comprehensive analysis of a wide range of protein-protein interactions in intact human cells.

(1) Eyckerman et al., Nat Cell Biol 3, 1114-1119 (2001)
(2) Lievens et al., Cytokine Growth Factor Rev 22, 321-329 (2011)
(3) Yu et al., Science 322, 104-110 (2008)
(4) Simonis et al., Nat Meth 6, 47-53 (2009)
(5) Rolland et al., Cell 159, 1212-1226 (2014)
(6) Lievens et al., Mol Cell Proteomics 15, 3642-3639 (2016)
(7) Lievens et al., Mol Cell Proteomics 13, 3332-3342 (2014)