Genome-Wide Systematic Reorganization of Mitotic Exit Network in *Saccharomyces cerevisiae*

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Cell cycle progression is a highly regulated process, being subjected to the conservation of chromosome stability and cell mass. Replicated chromosomes are segregated equally to mother and daughter cells during mitosis, which is critical to maintain genome stability in cell cycle. Mitotic exit network (MEN) of budding yeast *Saccharomyces cerevisiae* plays a crucial role in mitosis to ensure the proper segregation of duplicated chromosomes to the mother and the daughter, but how MEN is triggered and regulated is not well documented. To understand the details of MEN in *S. cerevisiae*, more components and their functions in regulating mitosis should be elucidated. Here, we demonstrated the identification of novel components of MEN by Tandem affinity purification (TAP). We constructed strains in which each known component of MEN of budding yeast is chromosomal TAP-tagged in the C-terminus and purified endogenous protein complex using the tagged proteins by TAP. Co-purified proteins with each TAP-tagged MEN component were visualized in 1-D PAGE gel with silver staining and identified with LC/MS. Tens of novel components and their interactions with known MEN proteins were discovered and their functions in the control of mitotic spindle orientation and cell cycle are now under investigation. Mitotic exit network of *S. cerevisiae* is reorganized with previously known MEN components and newly found proteins, which provides an informative model on the regulation of mitotic exit as a whole network in the eukaryotic cell cycle.

Mitotic exit network (MEN), *Saccharomyces cerevisiae*, Tandem affinity purification (TAP), cell cycle, chromosome stability