

**P047** Genome wide synthetic lethal screens reveal potential novel candidates for the abscission pathway in *S. cerevisiae*

**Harald Rauter and Yves Barral**

*Institute of Biochemistry, HPM D14.1, ETH Hönggerberg, 8093 Zürich, Switzerland*

During Anaphase, spindle elongation pulls sister chromatids apart until each pair is fully segregated between mother and bud. In turn, the cytokinetic machinery cleaves the cell perpendicular to the mother bud axis. Myo1p, the main component of the contractile actomyosin ring (CAR), is recruited to the future bud site shortly before bud emergence in a septin dependent manner. The Myo1p ring remains at the mother-bud neck until the end of anaphase and contracts upon mitotic exit. *myo1Δ* cells are able to complete cytokinesis by an abnormal process where no CAR contraction takes place and where a thick septum is finally deposited over the wide bud neck.

Hof1p is also recruited to the bud neck in a septin dependant manner during anaphase and is functionally implicated in orchestrating CAR contraction and primary septum deposition. *hof1Δ* cells are also able to finish cytokinesis in an aberrant manner. It is proposed that Myo1p and Hof1p dependent pathways act in parallel.

Cyk3p, has previously been implicated in cytokinesis and there is evidence that Cyk3p acts downstream of Myo1p and Hof1p, potentially in abscission, the final step of cytokinesis, where one continuous plasma membrane is pinched into two distinct plasma of mother and daughter cell. In *cyk3Δ* cells CAR contraction functions comparable to wild type and these cells cannot be separated by zymolyase treatment ruling out defects in cell separation. Interestingly, neither Myo1p, Hof1p nor Cyk3p are essential but every double deletion is synthetic lethal proposing that optimal cytokinesis requires the interplay of several pathways defined by Myo1p, Hof1p and Cyk3p, consisting of known and unknown genes.

Applying genome wide synthetic lethal screens for *myo1Δ*, *hof1Δ* and *cyk3Δ* we were able to identify a number of new genes potentially involved in the abscission pathway. Their mode of action and regulation of these genes is currently characterized by several cytological methods developed in the lab and will be discussed on the poster.