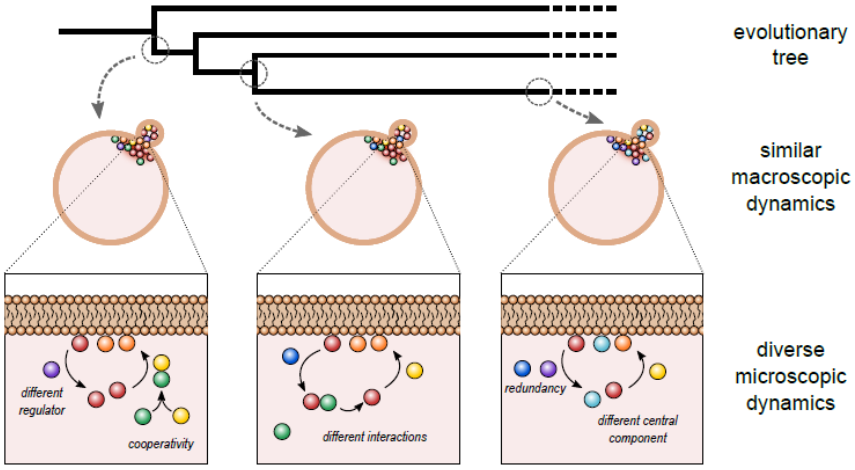
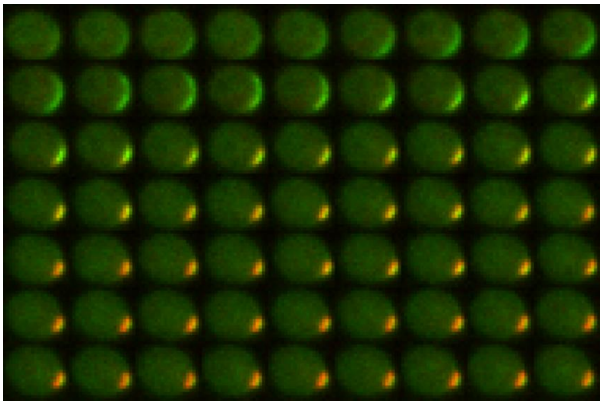
Research in biology makes extensive use of model organisms: certain species that have become default subjects due to their ease of handling and genetic manipulation. For eukaryotic cells, the group to which our own human cells belong, the most simple unicellular model is *Saccharomyces cerevisiae*, or baker's yeast. After decades of intensive study, we can describe many processes inside yeast cells down to a molecular level, from gene regulation to metabolism. From this we can build mechanistic models that try to explain which particular protein interacts with which and how these interactions precisely support cellular function.

Our lab is mainly interested in cell polarization, or the process by which a cell distinguishes between different sides of itself. In the case of budding yeast, the cell polarizes to indicate its next division site. Cell polarization in budding yeast is a much studied subject, so we know quite a lot about many important polarity proteins and their interactions. However, when we extend our view to other species of yeast and fungi, it becomes clear that this is only a limited picture (Glazenburg and Laan, 2023). Close relatives of budding yeast turn out to use very different sets of proteins to polarize, their identical proteins have different functions in the cell, or sometimes they even lack certain genes that are essential in our model species (Diepeveen et al., 2018). How can we understand this variability and flexibility that we see throughout evolution on the one hand, and the robustness of polarization as a core cellular function on the other hand?



In my project, I try to better understand this question by making use of a convenient case study. From experimental evolution studies, it is known that budding yeast follows a highly reproducible trajectory of rescuing mutations upon deletion of a near-essential polarization gene, *BEM1* (Laan et al., 2015). At the end of this trajectory, the cells can divide just as fast as wild-type cells that still have *BEM1*, even though the components of their polarization machinery have changed significantly. I'm interested in the similarities and differences between these successful 'polarization solutions' and their intermediates, which I study using live cell microscopy of important polarity proteins. By tracking and quantifying the dynamics of these proteins during cell polarization, I hope to learn more about the inherent properties of polarization and how they are affected by evolutionary processes.



Live cell microscopy timelapse of central regulator Cdc42 (green) and septin Cdc10 (red) during polarization

If you're interested in doing a project with me, don't hesitate to contact me! You can check out the Positions page for specific project ideas, but if none are currently listed there, we can always think up something new. Such a project might include…

- Strain construction using CRISPR-Cas to engineer new strains with fluorescently labelled proteins
- Live cell fluorescence imaging using high resolution confocal microscopes
- Developing image analysis techniques to deal with 3D fluorescence data
- Changing or replacing protein domains *in vivo* and characterizing the effect on polarization
- Examining the role of structural components (actin, septins etc.) in polarization
- Theoretical/conceptual analysis of the relation between molecular self-organization and natural selection

Diepeveen, E. T., Gehrmann, T., Pourquié, V., Abeel, T. and Laan, L. (2018). Patterns of Conservation and Diversification in the Fungal Polarization Network. *Genome Biol. Evol.* **10**, 1765–1782.

Glazenburg, M. M. and Laan, L. (2023). Complexity and self-organization in the evolution of cell polarization. *J. Cell Sci.* **136**, jcs259639.

Laan, L., Koschwanez, J. H. and Murray, A. W. (2015). Evolutionary adaptation after crippling cell polarization follows reproducible trajectories. *eLife* **4**, e09638.