© 2018. Published by The Company of Biologists Ltd | Journal of Cell Science (2018) 131, jcs224006. doi:10.1242/jcs.224006

FIRST PERSON

First person – Łukasz Rymer

First Person is a series of interviews with the first authors of a selection of papers published in Journal of Cell Science, helping early-career researchers promote themselves alongside their papers. Łukasz Rymer is the first author on 'The budding yeast Pex5p receptor directs Fox2p and Cta1p into peroxisomes via its N-terminal region near the FxxxW domain', published in Journal of Cell Science. Łukasz is a PhD student in the lab of Dr Marek Skoneczny at the Department of Genetics of the Polish Academy of Sciences, Warsaw, Poland investigating the targeting of peroxisomal proteins.

Łukasz Rymer

How would you explain the main findings of your paper in lay terms?

Peroxisomes are relatively small but interesting organelles in eukaryotic cells. These compartments are isolated from the cell matrix by a single membrane and unlike mitochondria, do not contain their own DNA, so proteins that work in peroxisomes have to be somehow guided and transported after their production in the cytosol. They are relatively simple structures; in yeast, only 61 proteins reside in peroxisomes, whereas mitochondria harbor around 800 proteins. Despite this apparent simplicity, peroxisomes have diverse functions among different organisms. In yeast, their main roles are degradation of fatty acids, to provide energy, and mediating the degradation of H_2O_2. For years, it was known that peroxisomal matrix proteins have two conserved signal sequences for their import called PTS1 and PTS2. These signals are recognized by two protein receptors, Pex5p for PTS1 and Pex7p for PTS2, and after signal recognition, they translocate cargo proteins from the cytosol to the inside of peroxisomes across the membrane. In our work, we showed that there is a subgroup of matrix proteins that can also be imported by Pex5p, but without any involvement of PTS1; these are Pox1p, Cat2p, Fox2p and Cta1p, suggesting that they should have another import signal, which although not identified, has been named PTS3.

Were there any specific challenges associated with this project? If so, how did you overcome them?

The main challenges in our project were several time-consuming tasks. At the very beginning of the research, we needed to go through GFP-fusion protein localization databases and the literature to search if there were any yeast peroxisomal proteins (or proteins that could be associated with peroxisomes) that had not been thoroughly examined for their intracellular transport mechanism and could match our PTS3 hypothesis criteria. Next, were microscopy observations and fractionation experiments. For that, we transformed different yeast mutant and wild-type strains with two to three plasmids per strain. Moreover, strains also had different sets of gene markers that we could use for plasmid selection. Therefore, this resulted in a large number of combinations of possible experimental steps. We also needed to do these experiments step-by-step to consider the information obtained from observation of protein localization in one genomic background, before we proceeded to another. It took patience and regular re-evaluation of task priorities at group meetings to overcome these challenges.

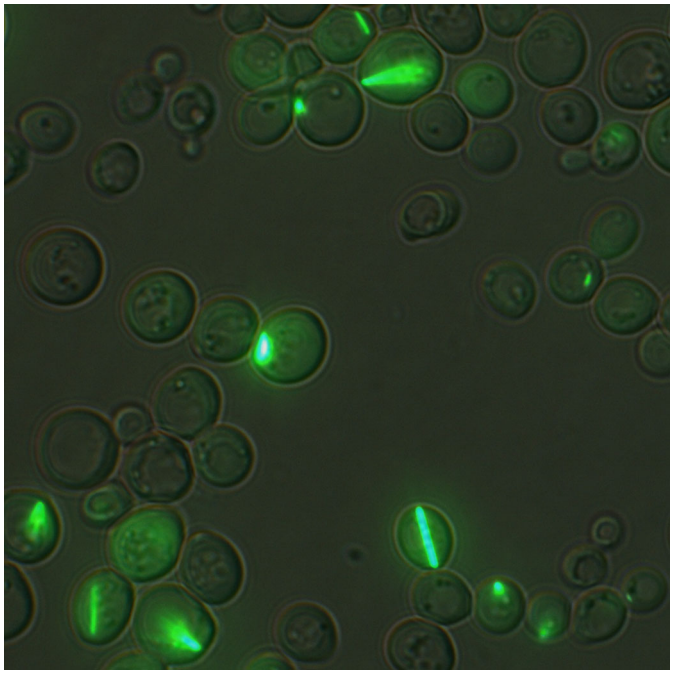
When doing the research, did you have a particular result or 'eureka' moment that has stuck with you?

Yes, we didn't have any explanation of why we could still observe residual peroxisomal localization of Cta1p and Fox2p in strains devoid of Pex5p. In 2016, two papers were published in Journal of Cell Science, one from Ralf Erdmann's lab and the other one from Maya Schuldiner's and Einat Zalckvar's labs, describing a new accessory peroxisomal receptor named Pex9p. So, I looked for a possible involvement of Pex9p in Cta1p and Fox2p transport and it turned out that this receptor could indeed substitute for the missing Pex5p in import of these proteins.

"What inspired me most was the complex nature of molecular processes […] and the fact that there are still so many things to discover."

Łukasz Rymer's contact details: Department of Genetics, Institute of Biochemistry and Biophysics, Polish Academy of Sciences, Pawińskiego 5a 02-106 Warszawa, Poland.
E-mail: lrymer@ibb.waw.pl

Journal of Cell Science (2018) 131, jcs224006. doi:10.1242/jcs.224006



Pnc1p fused to GFP gives a tantalizing bar-shaped localization and it still puzzles me what this structure is. Green fluorescence channel overlay with DIC channel.

Have you had any significant mentors who have helped you beyond supervision in the lab?

I am thankful to Dr Marek Skoneczny, my PhD supervisor who supported me all the way through this project. He is always willing to discuss results, plan new tasks and share his knowledge. Dr Anna Chełstowska often helped me with problematic experiments. Also at the beginning, when I joined the lab, my colleague Dr Urszula Natkańska taught me many of the techniques used in our field. Apart from our group, meetings with Dr Adrianna Skoneczna's group from the Laboratory of Mutagenesis and DNA Repair in our Institute provided the inspiration to take our project further.

What motivated you to pursue a career in science, and what have been the most interesting moments on the path that led you to where you are now?

I really liked chemistry and biology courses while I was in high school. During my master's studies I had the opportunity to see how satisfying scientific work could be. What inspired me most was the complex nature of molecular processes that I researched then and the fact that there are still so many things to discover.

What's next for you?

At present I am still working on my PhD; after I graduate I will see what the possible options are for me. I'm interested in cell biology research and would appreciate a project that uses a variety of microscopy techniques.

Tell us something interesting about yourself that wouldn't be on your CV

In my spare time I enjoy bike rides, hiking and nature photography. It is the best way to relax after a hard day.

Reference

Rymer, Ł., Kempiński, B., Chełstowska, A. and Skoneczny, M. (2018). The budding yeast Pex5p receptor directs Fox2p and Cta1p into peroxisomes via its N-terminal region near the FxxxW domain. *J. Cell Sci.* **131**, jcs216986.