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Identification of novel peroxisome functions in yeast

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**Identification
of novel peroxisome
functions in yeast**

Ritika Singh



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The studies presented in this thesis were performed in the research unit Molecular Cell Biology of the Groningen Biomolecular Sciences and Biotechnology Institute (GBB) of the University of Groningen, The Netherlands.

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and in accordance with
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Friday 01 November 2019 at 09:00 hours

by

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To Ma and Papa

for their love, support and prayers

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Ritika

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Aim and Outline



Peroxisomes are organelles occurring in most eukaryotic cells. They are involved in wide range of metabolic and non-metabolic functions. Despite the extensive research since their discovery in the fifties of the previous century, our knowledge on peroxisomal functions is incomplete. The research described in this thesis aimed to identify and characterize novel peroxisome proteins and functions in yeast.

Chapter 1 gives an overview on our current knowledge on peroxisomes focussing on peroxisome function, redox-regulation, and proliferation in yeast.

Using an organelle proteomic approach using peroxisomal fractions isolated from *Hansenula polymorpha* cells exposed to ethanol stress, we identified 6 putative peroxisomal peroxiredoxins (**Chapter 2**). Two of them, named C8BNF3 and C8BNF4, contain a putative peroxisomal targeting signal 1 (PTS1). Although C8BNF3 contains a PTS1, it is localized to the mitochondria, whereas C8BNF4 partially localizes to the peroxisomes in glucose-grown cells, but not when cells were grown on methanol. That absence of C8BNF4 did not result in a growth defect or enhanced sensitivity to any of the stress conditions tested.

Both Pnc1 (nicotinamidase) and Gpd1 (glycerol-3-phosphate dehydrogenase) are stress-related peroxisomal proteins. Gpd1 was previously reported to relocalize to the cytosol upon exposure of cells to osmotic stress. In **Chapter 3** we show that Pnc1 is transported to peroxisomes by piggy-backing on Gpd1. We show that the levels of both peroxisomal and cytosolic Gpd1 and Pnc1 increased when the cells were exposed to stress. Our quantitative analysis of the distribution of Gpd1 and Pnc1 over the cytosol and peroxisomes revealed that both proteins are predominantly localized to peroxisomes. The non-stress related peroxisomal protein thiolase, when produced under the control of *GPD1* promoter, displayed a similar behaviour indicating that the presence of peroxisomal matrix proteins in the cytosol of cells exposed to stress is a result of reduced matrix protein import efficiency and not relocalization.

Mammalian PXMP2 has been indicated to function as a non-selective pore in the peroxisomal membrane. A homologous protein in *Neurospora crassa*, Wsc, is involved in the formation of Woronin bodies from peroxisomes. In **Chapter 4** we analysed all four Pxmp2 proteins of *H. polymorpha*. One of these proteins, designated Pex37, localizes to peroxisomes. Deletion of *PEX37* resulted in a reduction in peroxisome numbers and a defect in peroxisome segregation in cells grown at peroxisome repressing conditions (glucose). This phenotype could be partially complemented by human PXMP2, suggesting that PXMP2 is a functional homologue of Pex37.

Saccharomyces cerevisiae Vac8 plays among others a role in vacuole inheritance and fusion. In addition it is a component of nucleus-vacuole junctions (NVJ). Organelle proteomics revealed that Vac8 also occurs in peroxisomal fractions isolated from *S. cerevisiae* or *H. polymorpha* (Chapter 2). In **Chapter 5** we show that HpVac8 is also required for NVJ formation and vacuole inheritance, but not for vacuole fusion. The absence of HpVac8 had no effect on peroxisome function, number and distribution indicating that a role of Vac8 in peroxisome biology is very unlikely.

