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RESEARCH AREA

Organelles of eukaryotic cells represent an intricate network the members of which are connected with each other either via vesicular transport processes or permanent physical contacts. Significance of the latter type of organellar communication (the so-called membrane contact sites) has only been recognized in the last decade. The complex, dynamic endomembrane system plays a pivotal role in normal cell physiology and its proper function requires the concerted action of several proteins. Main research focus of our group is the investigation of genes and proteins involved in vesicular trafficking routes chanelling to the lysosomes, the central degradative organelles of cells. Members of the Sorting nexin (Snx) protein family play important roles in numerous points of the endolysosomal system. All Snx proteins contain the lipid-binding PX-domain that enables them to associate with organellar membranes where they utilize other protein domains to take part in versatile molecular events. However, exact cellular functions of many Snx proteins are currently unknown, and importantly, some of these proteins are involved in the pathogenesis of human diseases. Most of the Sorting nexins are evolutionarily conserved, offering the possibility to investigate their functions in model organisms. We use various fruitfly tissues to study the molecular functions of the less well-characterized Snx proteins in the endolysosomal system. Our current focus is on the investigation of the function of Snx25, a known membrane contact site protein, which is involved in a human hereditary neurodegenerative disease. Our results show that the mutation of the fruitfly counterpart of this gene leads to severe defects in the endosomal maturation process of the highly endocytic larval nephrocytes. However, the exact mechanism of this phenomenon is currently not known.

TECHNIQUES AVAILABLE IN THE LAB

To explore Sorting nexin functions in the endolysosomal system, we primarily use light-microscopy techniques (fluorescent immunohistochemistry and other labeling methods). In our research we exploit the genetic and cell biology toolkit of the fruitfly (*Drosophila melanogaster*), the model organism with a history of more than a hundred years. Beside larval nephrocytes, we use other fruitfly tissues (e.g. larval fat body and salivary gland) as well to analyze the endolysosomal network. Routine molecular biology approaches (cloning and protein detection methodsbetc.) are also used mainly in order to generate new genetic tools (mutant and transgenic animals).

SELECTED PUBLICATIONS

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Lőrincz, P., Lakatos, Z., **Maruzs, T.**, Szatmári, Z., Kis, V., & Sass, M. (2014). Atg6/UVRAG/Vps34-containing lipid kinase complex is required for receptor downregulation through endolysosomal degradation and epithelial polarity during Drosophila wing development. **BioMed Res Int 2014:** 851349