Poster

From Yeast to Fly: A Study of the Evolutionary Conservation of Cohesin in Schizosaccharomyces pombe and Drosophila melanogaster

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Keywords: Cohesin Conservation, Functional genetics, Cohesinopathies

ABSTRACT

Motivation: Cohesin is a crucial protein complex composed of Psm1, Psm3 and Rad21, arranged in a like-ring conformation. This complex plays a key role in maintaining chromosome structure, facilitating accurate chromosome segregation, regulating DNA repair, and controlling gene expression by influencing chromatin architecture and transcriptional processes. Defects in cohesin can lead to severe cellular consequences, including chromosome missegregation, genomic instability, and developmental disorders. Schizosaccharomyces pombe is an wide-spread eukaryotic model organism for genetic studies due to its simplicity, ease of genetic manipulation, and well-characterized genetic structure, making it an ideal tool for research in fundamental cellular processes. The evolutionary gap between Schizosaccaromyces pombe and Drosophila melanogaster (approximately 1.2 billion years) and between D. melanogaster and humans (around 600 million years) provides a unique opportunity to investigate the conservation and divergence [3] of cohesin function across a broad evolutionary spectrum. This study aims to explore the conservation and functional roles of cohesin in these species, providing valuable insights into its molecular mechanisms and the potential impact of its dysfunction across different eukaryotic organisms.

Methods: Each of the three S. pombe cohesin subunits, Psm1, Psm3 and Rad21, were replaced by their D. melanogaster orthologues. This was achieved by transforming a diploid strain with a linear fragment containing the Drosophila gene, a selection marker and homology sequences with the upstream and downstream regions of the gene to be replaced. The correct insertion of the fragment was verified by PCR. Viability of the transgenic yeast in haploidy was studied by sporulating the heterozygous mutants and segregating their four spores using a micromanipulator.

Results: Psm1 and Psm3 genes were replaced by their fly orthologues, SMC1 and SMC3, in a diploid strain resulting in a double heterozygous transgenic mutant. Upon tetrad segregation, it was observed that drosophila´s version can not substitute yeast´s natives genes.

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