

Abstract 47

USING *DROSOPHILA* TO SYSTEMATICALLY STUDY THE ROLE OF ALL MENTAL RETARDATION GENES IN SYNAPTIC DEVELOPMENT

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Molecular mechanisms involved in synapse formation, organization and plasticity underlie normal cognitive functioning. Although some of these mechanisms have been unraveled, our understanding of synapse physiology is far from complete. Advancements in this field would not only deepen our fundamental insight, but could also at some point benefit patients suffering from cognitive disorders such as mental retardation (MR). Currently, there are over 420 genes known to cause MR. Of the vast majority of these genes their function in the nervous system has not been explored. Since cognition and synaptic functioning are so intimately related, we hypothesize that within this gene set there is a high percentage of genes involved in synaptic physiology. We aim to systematically analyze the role of MR genes in synapse development and functioning by combining tissue restricted knockdown of these genes in the nervous system with the analysis of the *Drosophila* neuromuscular junction (NMJ), an easily accessible model synapse which for decades has provided fundamental insight into synapse physiology. Studying MR genes in this system provides us with a great opportunity to identify and unravel novel molecular mechanisms involved in synapse development and functioning. I will present our methodology and rationale and highlight some of the first exciting findings we have obtained using this approach.

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