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LARGE-SCALE APPROACHES TO DISSECT MOLECULAR MECHANISMS AND NETWORKS DISRUPTED IN MENTAL RETARDATION

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Massive efforts are undertaken to understand the genetics of Mental Retardation (MR). More than 420 MR genes have been identified to date, and we are now at the point where functional studies have to catch up with gene identification. This is a big challenge, but very worthwhile for two reasons. First, functional studies into Fragile X Syndrome and a few other MR disorders have identified first therapeutic strategies. Second, there is accumulating evidence that MR genes/proteins form molecular networks. MR research can therefore identify molecular key pathways that control brain development and cognition. To identify novel connections between MR genes and to analyse their function in high throughput, we use the fruitfly *Drosophila melanogaster* as a model organism. I will present the principle approach of our research that systematically investigates MR gene function *in vivo* and aims to provide conceptual advance in our understanding of brain development in health and disease. With our pilot projects, we have already uncovered highly specialized functions of uncharacterised MR genes, unravelled unanticipated common molecular mechanisms between MR genes causing clinically overlapping phenotypes and identified novel MR candidate genes. We are also setting out for the first targeted drug projects to alleviate relevant fly phenotypes. Our goal is to significantly contribute to the development of novel diagnostic and therapeutic strategies for the large and still growing group of MR disorders.

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