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### Keywords

Tandem repeats – Amyotrophic lateral sclerosis – Frontotemporal lobe degeneration – C9ORF72 – TDP43 – *Drosophila* – *Danio*

### Science

#### C9ORF72

In the early nineties three unrelated neurological disorders were found to be associated with tandem repeat (TR) expansions. In the last years this list grew up to more than 25 disorders. Most recently, ALS-FTLD was added to this list due to the discovery of hexanucleotide expansions within the C9ORF72 non-coding region. Moreover, these C9ORF72 expansions are the most important mutation underlying familial ALS and familial FTLD, respectively 50% and 25%. However, the exact pathogenic mechanism(s) remains unresolved.

To tackle this problem we recently developed several C9ORF72 models. These include fruitfly and zebrafish models. This strategy allows us to take advantage of each model organism and compensate for its disadvantages. We also take a more multidisciplinary approach in this project with the extensive use of bioinformatics and techniques from structural biology.

#### TDP43

Neuronal protein inclusions positive for TDP43 constitute a hallmark of ALS pathogenesis. In recent years, several murine models have been developed, but all largely fail to replicate pathogenesis as observed in humans. Most currently available models rely on ubiquitous expression in all tissues or restricted to the central nervous system. We on the other hand make use of cell type specific expression of human TDP43 to restrict this to motor neurons or different glia cells. Herewith we aim to: first, create a more 'subtle' overexpression model circumventing the problems with high ubiquitous overexpression of TDP43, and second, we can elucidate the role of the different glial populations in ALS pathogenesis as these cells may constitute new targets for therapy.

### Bibliography

R. Gemayel, J. Cho, **S. Boeynaems** and K.J. Verstrepen (2012). Beyond Junk - Variable Tandem Repeats as Facilitators of Rapid Evolution of Regulatory and Coding Sequences. *Genes* 2012, vol. 3(3), p. 461-480.