

7èmes Journées de la Recherche SLA/MNM

Identifying motor unit specific alterations in a FUS deletion mutant zebrafish model

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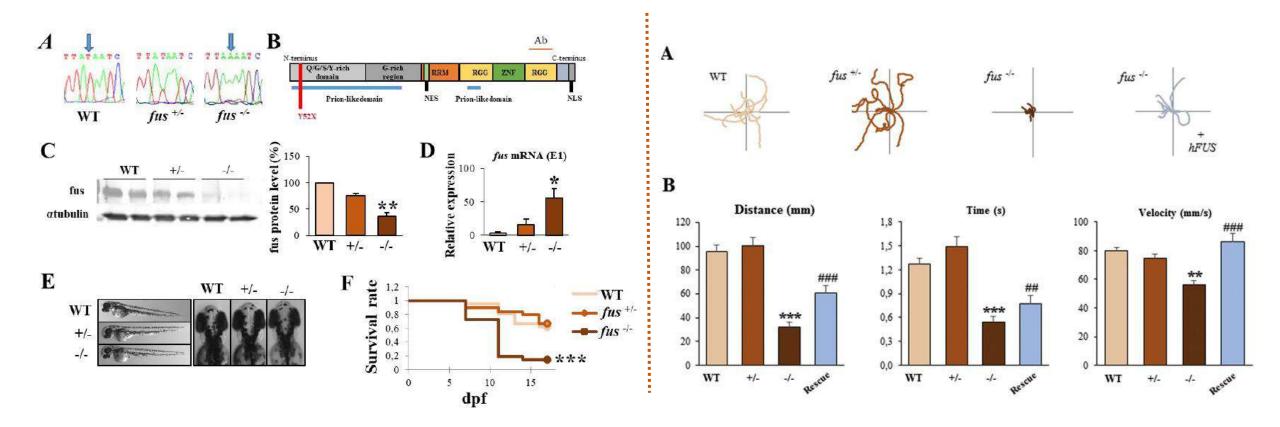






Chiara Guerrera ,**Proteomic Platform Necker** Ivan Nemazanyy, **Plateforme d'étude du métabolisme Necker**

- ☐ Characterization and phenotypic analysis of a deletion mutant of the unique FUS orthologue in zebrafish
- If the function causes zebrafish mobility defects at the touch-evoked escape response



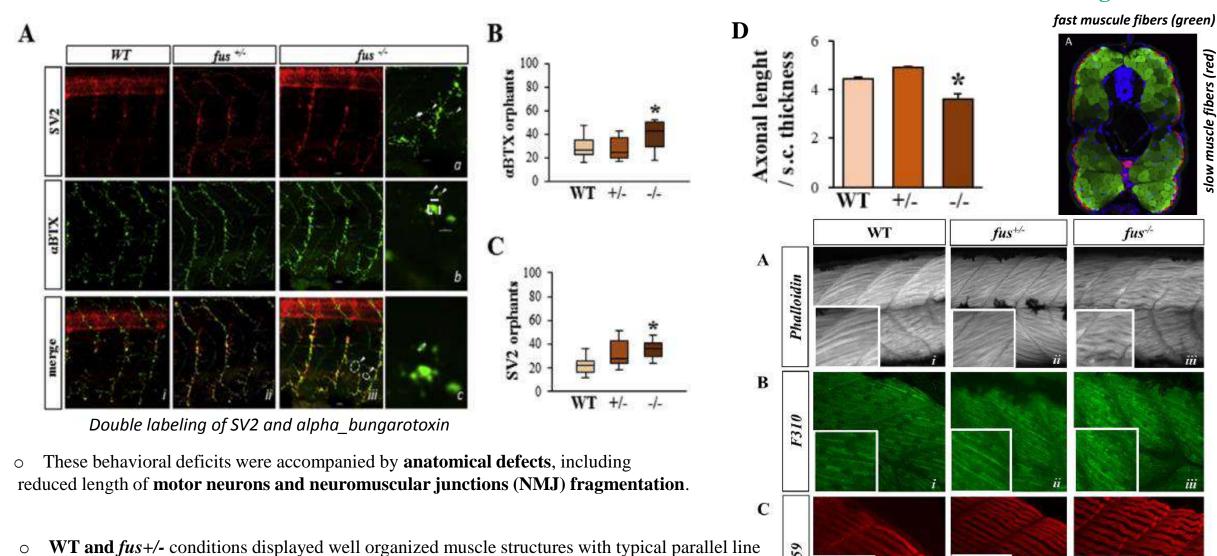
- o FUS, mutated in ALS patients, encodes for an RNA-binding protein, involved in multiple aspects of RNA metabolism
- o The majority of FUS mutations are localized in exon 15, which encodes for NLS (nuclear localization signal), causing FUS redistribution into the cytoplasm
- Our team report for the first time the generation and phenotypic characterization of a stable zebrafish line mutant for the unique FUS orthologue in zf
- o In this model, we demonstrated that the loss of its function reduces lifespan of homozygous individuals and leads to motor deficits

☐ fus LoF (loss of function) causes defects at the zebrafish NMJs

■ Motor neuron and muscle structure in FUS mutants fus KO causes slow muscle disorganization

slow muscle fibers (red)

fus-/-



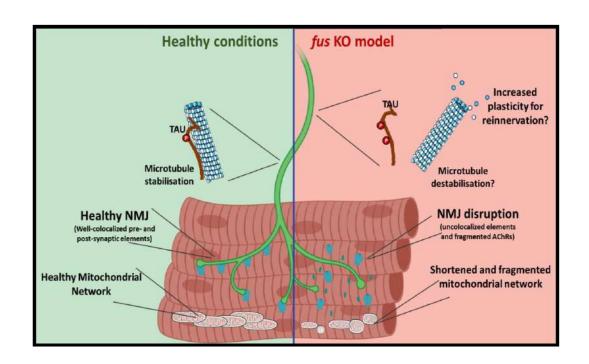
fus-/- conditions showed a disorganized structure with curvy and non-parallel fibers

pattern.

immunolabelling of fast muscle fibers with F310 antibody immunolabelling of slow muscle fibers with F59 antibody

F59

☐ Hypothesis of ALS features occurrence in our us KO zebrafish model



fus is KO in zebrafish, pre- and post-synaptic elements fail to colocalize properly to form functional synapses, with AChRs presenting pathological fragmentations

This plasticity could depend on enhanced cytoskeletal dynamics involving the microtubules and thus, modulating tau function as well as tau-related kinases to ensure tau phosphorylation.

☐ Perspective and Future Directions

o Transcriptomic and proteomic sequencing

identify biomarkers candidates and therapeutic targets in FUS-ALS patients

- Generation of a specific transgenic line harboring the *fus* non-sense mutation on a *hb9:GFP* background.
- o MNs express the GFP (green fluorescent protein) construct, as the *hb9* gene is involved in **MN differentiation**
- o Sort through **FACS** (Fluorescence activated cell sorting) the MN and perform specifically the transcriptomic/proteomic analysis
- Cross compare our omics analysis with the transcriptomic analysis from FUS knock-out and knock-in mouse models (Luc Dupuis, Strasbourg) and iPSCs and biopises from ALS patients carrying FUS mutations (Alberto Catanese, Ulm University)

