

«METABOTYPING OF ALS PATIENTS: *SOD1* AND *TARDBP* MUTATED FIBROBLASTS DISPLAY AN ENHANCED METABOLIC ACTIVITY AND GLYCOLYTIC STATE



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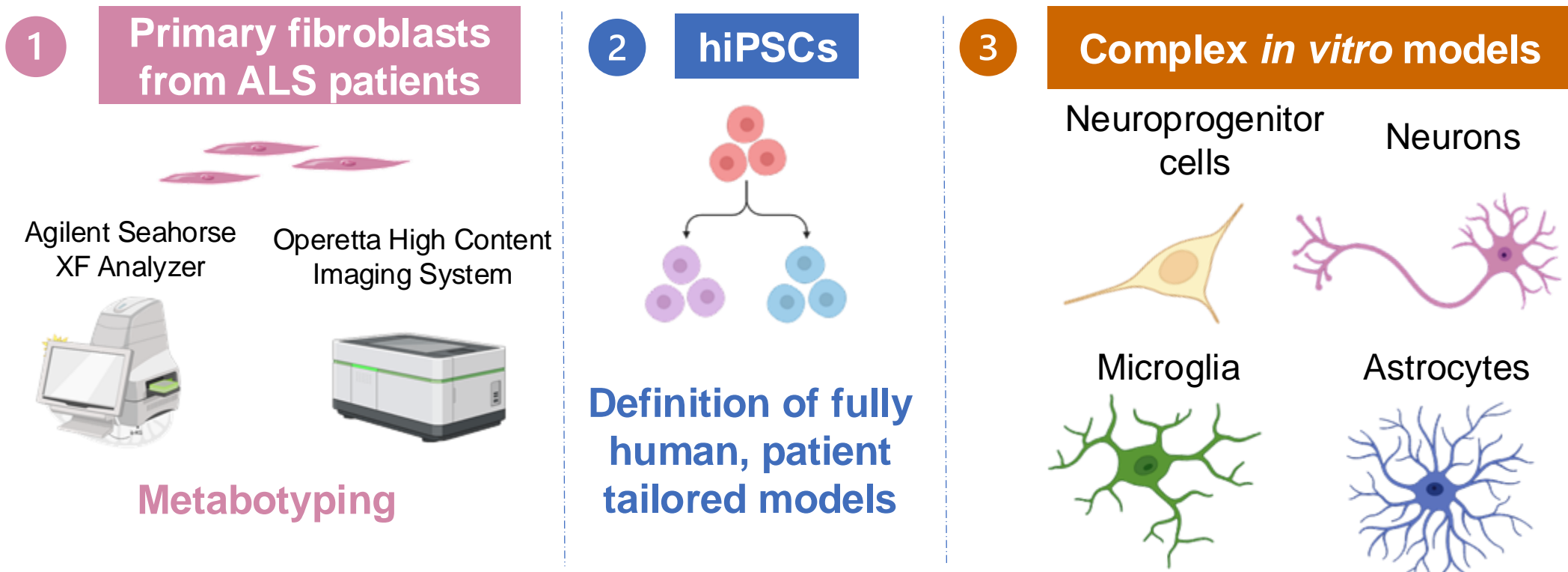
CONTACTS



Background

Among the 150 genes associated with ALS, *TARDBP* and *SOD1* play an important role. Mutant *SOD1* protein induce toxicity through a gain-of-function mediated by the adoption of misfolded conformations and formation of protein aggregates. While mutant TDP-43 protein is mis-localized from the nucleus and aggregates in the cytoplasm, thus losing its RNA metabolism-related activity. Interplay between oxidative stress and metabolic dysfunctions has been associated with ALS. Indeed, *SOD1* and TDP-43 mutations affect the electron transport chain complexes activity, thus initiating a “vicious-cycle” that sustain metabolic stress¹.

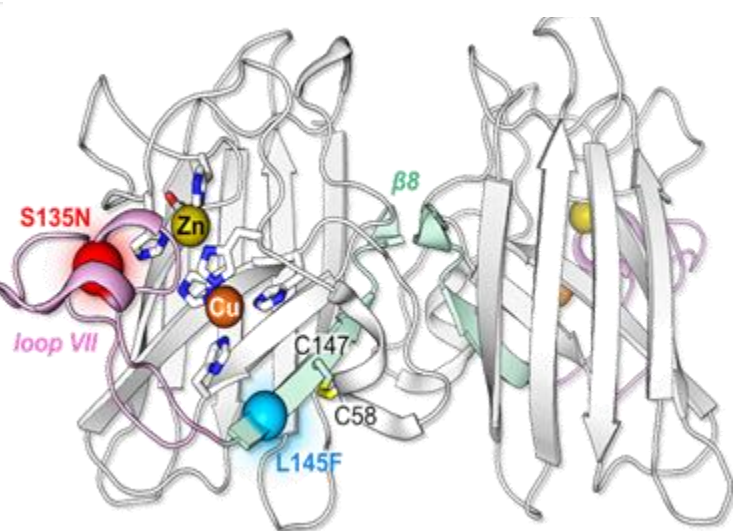
Experimental approach



Finding a link between **genetic background and metabolic manifestations** and correlation with disease features (susceptibility, age of onset and progression rate/survival).

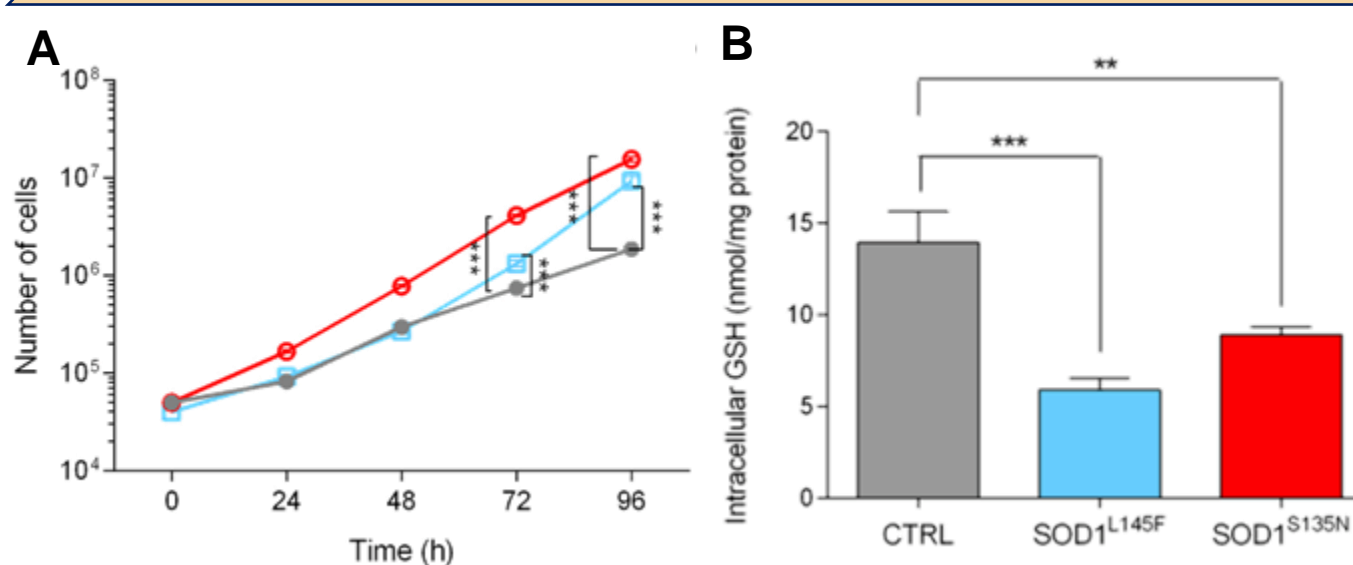
Results

SOD1



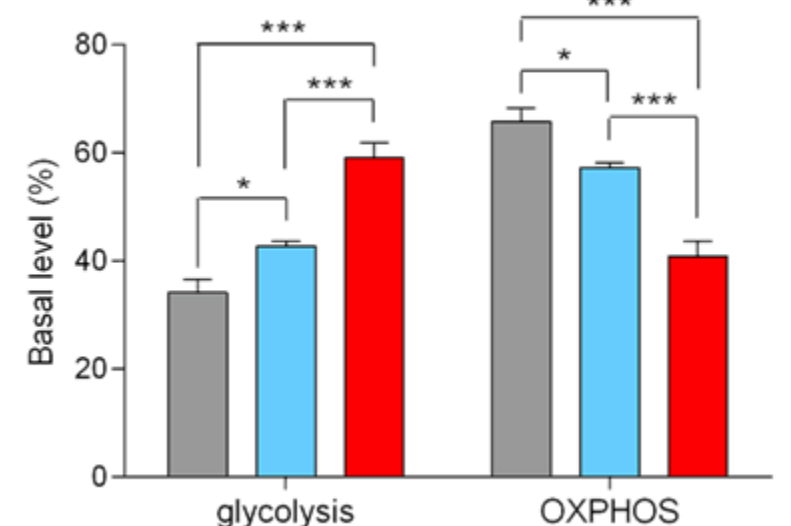
Bioinformatic analysis revealed that p.S135N results in greater destabilization as compared to p.L145F

Oxidative stress



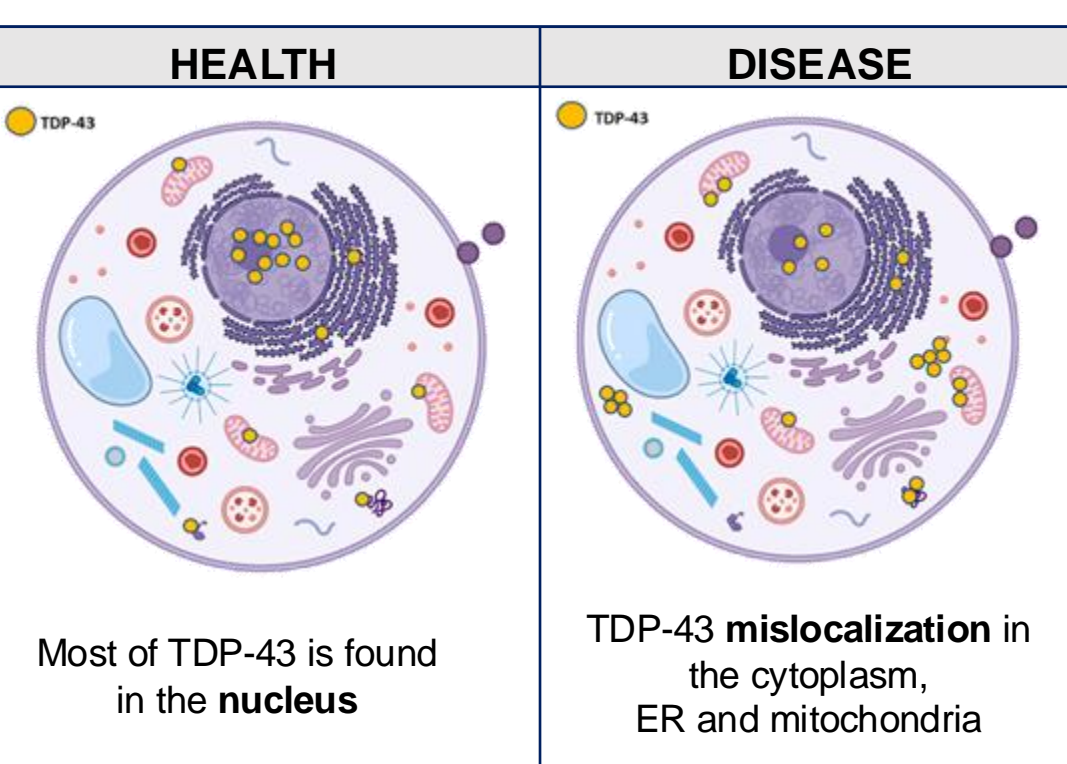
ALS-fibroblasts showed an increased proliferation rate (A) and significantly lower total intracellular glutathione levels compared to healthy control cells. These findings suggest that affected individuals may lack GSH protective activity (B).

Metabolic reframing

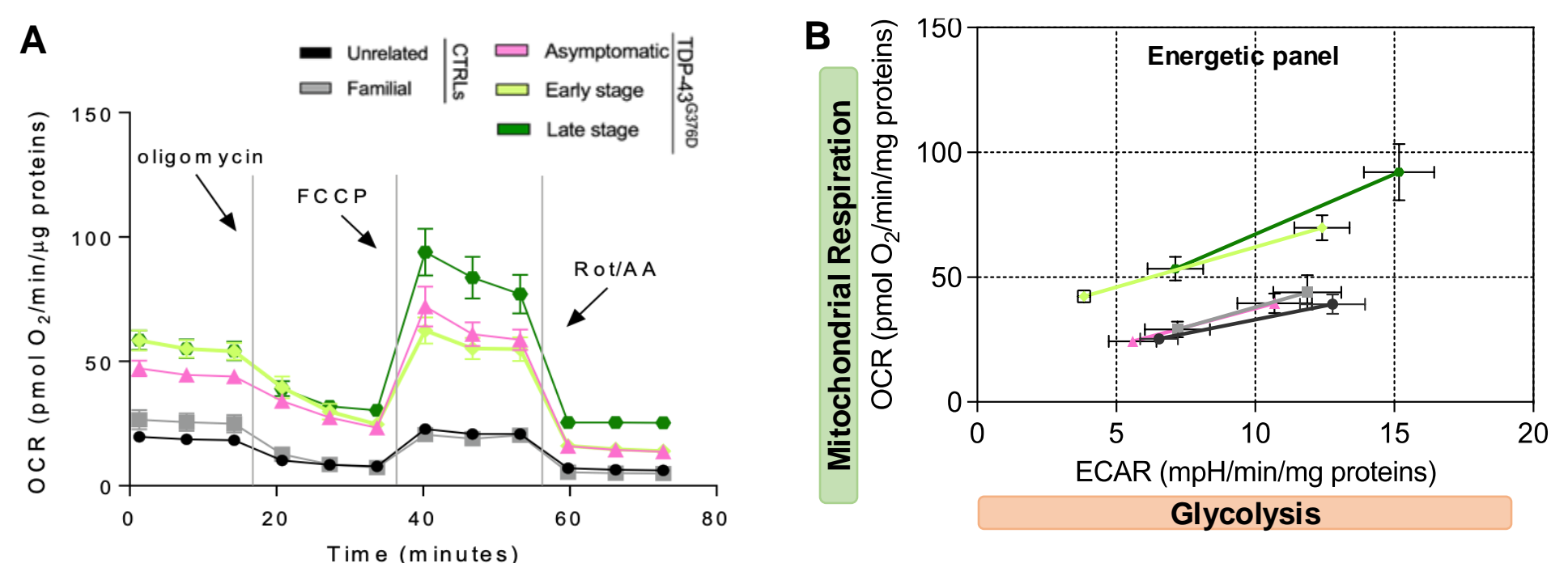


SOD1^{S135N} fibroblasts produced the majority of ATP through glycolysis, showing a shift towards Warburg effect.

TDP-43



Hypermetabolism



TDP-43^{G376D} fibroblasts possess a higher basal and maximal mitochondrial activity compared to controls (A). No differences in their ability to upregulate the mitochondrial respiration to meet changing energy demand; yet, the *TDP-43*^{G376D} patient's fibroblasts increased the glycolytic activity significantly more (B).

Conclusions

Both *SOD1* and *TARDBP* mutant fibroblasts display metabolic rearrangements («**hypermetabolism**»² and progressive reliance in **glycolysis**³). This bioenergetic rearrangement might be hampered in neural cells that have a reduced ability to switch to glycolysis upon OXPHOS limitations. So, our following step is the development of “complex” in vitro models to study the interactions among neural, and non-neural cells.

Future perspectives



References

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