

A novel neuronal cell model for the study of Ataxia Telangiectasia

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BACKGROUND

Ataxia telangiectasia (AT) is a rare multi-systemic neurodegenerative disease linked to the malfunction of the Ataxia Telangiectasia Mutated (ATM), which is a 350 KDa serine/threonine kinase. In response to DNA double-strand breaks (DBSs), ATM protein regulates cell cycle leading ultimately to the DNA repair.

AIM

Current treatments are not able to improve the patients' life expectancy \rightarrow it has become crucial to improve personalized cellular models to both deepen our knowledge in the pathophysiology of this rare disorder and to elaborate new therapies.

METHODS and RESULTS

Urine stem cells (USCs) were partly differentiated in neurons (USC-iNs)

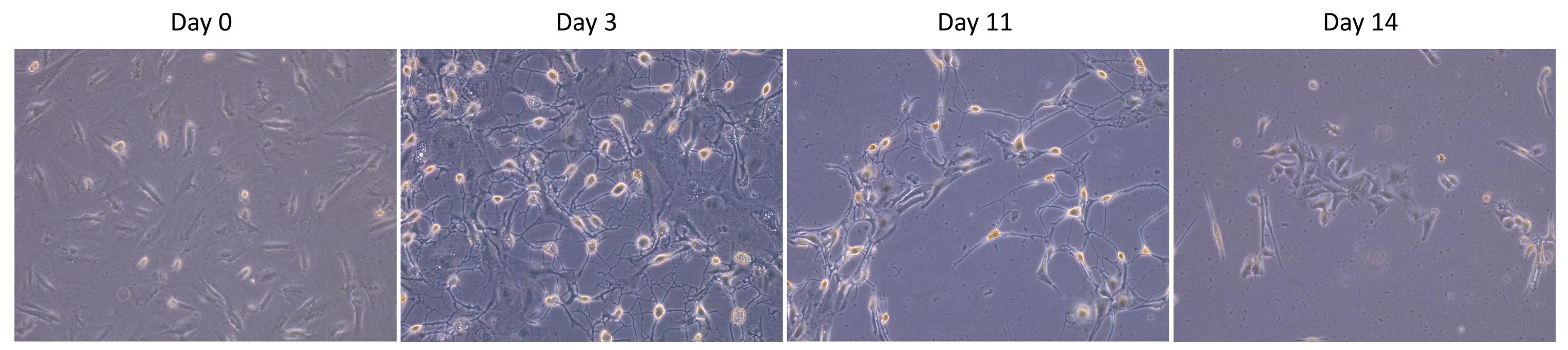


Fig 1. Neuronal differentiation of USCs. Evocative phase-contrast microscopy images of USCs at day 0, day 3, day 11 and day 14, respectively, of the neuronal differentiation based on small molecules. Magnification: 200x.

USC-iNs expressed typical neuronal markers

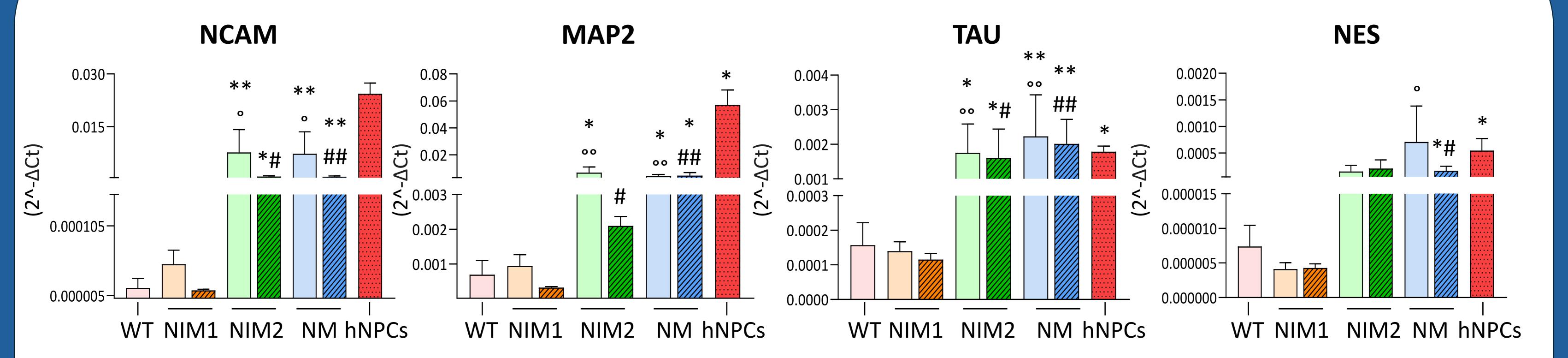


Fig 2. Characterization of USC-iNs. Gene expression analysis by qRT-PCR of USCs, USCs-iN and hNPCs of the indicated genes. Data are presented as histograms of the mean \pm SEM of 2^{- Δ Ct} values (n= at least 5 independent experiments).

NO NAM

LIMITATIONS

The **limited viability period** of USCs is one major issue common to all our experiments and RT-qPCR demonstrated that **USC-iNs don't achieve a complete neuronal development**, but rather a neural progenitor-like state.



The objective of our research is **the generation of patientspecific and autologous cellular models** to deepen our knowledge of ATM pathogenetic pathways. At the moment the protocol based on the use of small molecules has only led to a partial neuronal model.

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