Increased Myotonic Dystrophy type 1 (DM1) Disease Severity is Associated with a Dysregulated Immune System

Nieuwenhuis S^{1,2}, Widomska J², Blom P³, 't Hoen PAC¹, van Engelen B⁴ and Glennon JC^{2,5}

¹Dept. CMBI, RadboudUMC, Nijmegen, The Netherlands, ²Dept. Cognitive Neuroscience, RadboudUMC, Nijmegen, The Netherlands, ³VDL Enabling Technologies Group B.V., The Netherlands, ⁴Dept. of Neurology, Donders Institute for Brain Cognition and Behaviour, RadboudUMC, Nijmegen, ⁵Conway Institute of Biomolecular and Biomedical Research, School of Medicine, University College Dublin, Ireland. E-mail: sylvia.nieuwenhuis@radboudumc.nl

INTRODUCTION

- Myotonic dystrophy type 1 (DM1)
- Multisystemic disorder
- Symptoms not limited to muscle¹
- Accelerated aging disease linked to immune

APPROACH

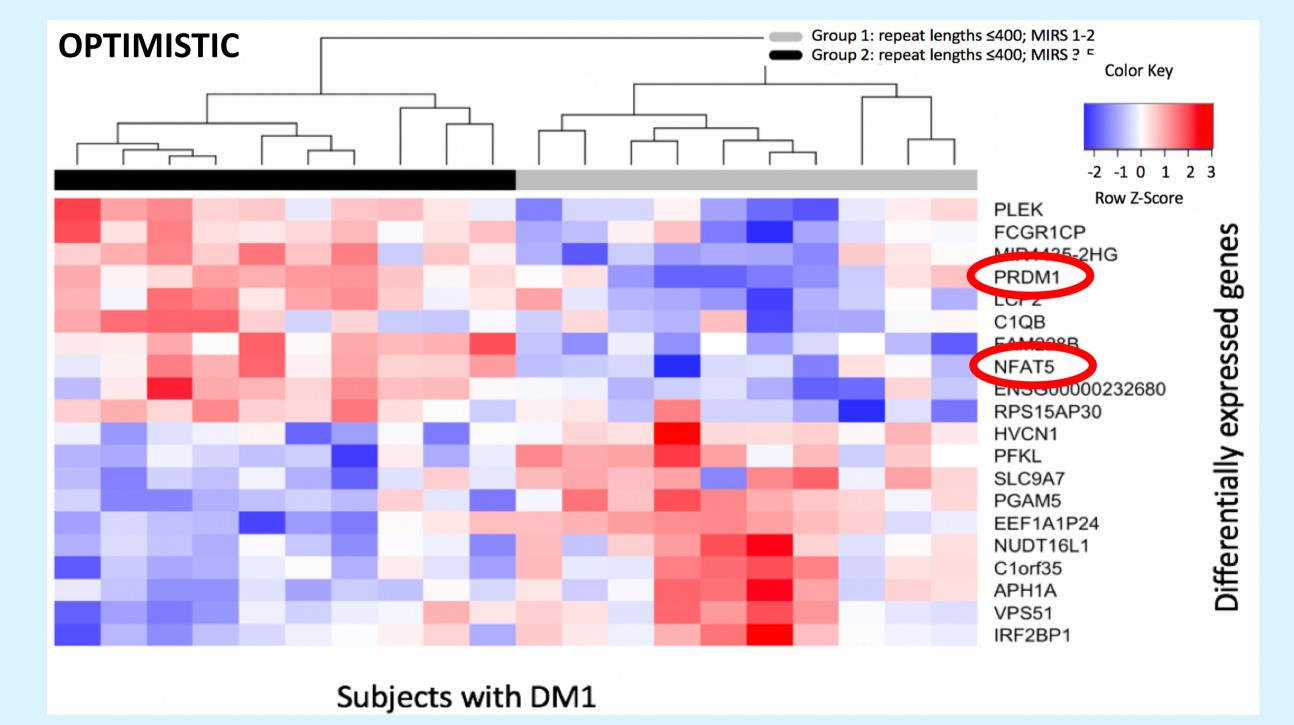
- Stratify DM1 blood samples based on MIRS severity ratings (G1 MIRS 1-2, G2 MIRS 3-5) with the same CTG repeat expansion size (CTG<400)
- Transcriptomic data from DM1 blood samples from 2 independent cohorts at baseline (without intervention) (EU OPTIMISTIC study (n=10 per group) and Marigold foundation DMBDI study (n=6 per group)

dysfunction and muscle loss¹

- CTG repeat length in DMPK gene → accumulation of RNA transcripts and splice variants
- Severity of symptoms measured by Muscle Impairment Rating Scale (MIRS) is associated with Low Quality of Life (QoL) for which biomarkers are needed as surrogate clinical outcomes
- Be aware skeletal muscles are antigen presenting cells (APCs)

RESULTS

GENE EXPRESSION



DATA ANALYSIS

 OPTIMISTIC RNAseq + differential gene expression (DGE) analysis and DMBDI - microarray gene expression³

PATHWAY ANALYSIS

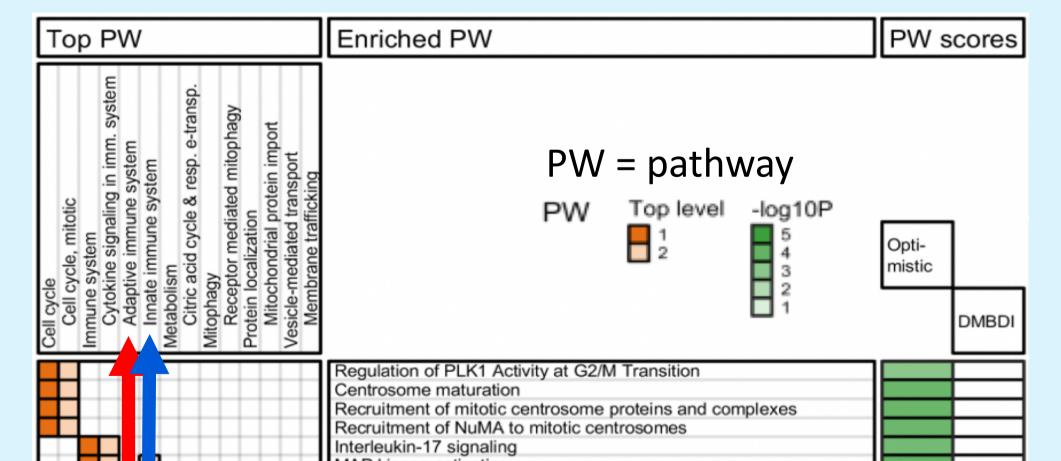
- Ingenuity Pathway Analysis (IPA), Diseases and Functions
- Reactome Pathway Analysis, Gene Ontology terms Master Regulators; causal network analysis in IPA
 Splicing

RESULTS

MASTER REGULATORS

Many master regulators, e.g., FOXD1, PAX5, CIITA, QKI, VEGFA, VIM, IL4, MLX are implicated in muscle differentiation and/or repair processes. These two processes are essential for muscle wasting observed in DM1.

PATHWAY ANALYSIS

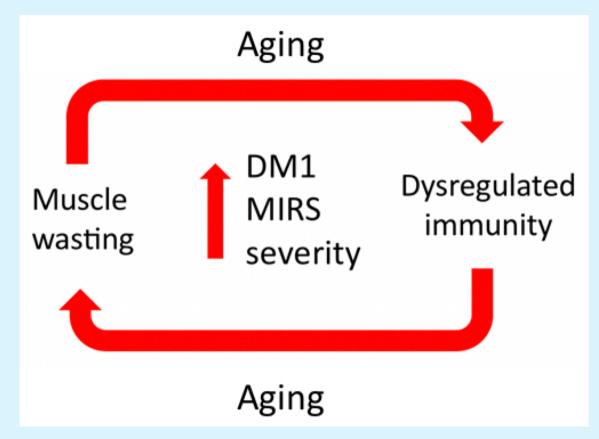


SPLICING

This study demonstrates no significant splicing changes.

CONCLUSION

The current study demonstrates that muscle wasting together with aging deteriorate immunity leading to increasing DM1 severity.



PRDM1 and NFAT5 which both play a role in immunity are among the top 20 DE genes in OPTIMISTIC.

Pathway analysis (Reactome) demonstrates that adaptive immunity plays a key role in both OPTIMISTIC and DMBDI datasets (red box in pathway analysis figure).

MAP kinase activation
TCR signaling
Downstream TCR signaling
Phosphorylation of CD3 and TCR zeta chains
Translocation of ZAP-70 to Immunological synapse
MHC class II antigen presentation
Costimulation by the CD28 family
MyD88-independent TLR4 cascade
TRIF(TICAM1)-mediated TLR4 signaling
MyD88 dependent cascade initiated on endosome
TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8
Toll Like Receptor 10 (TLR10) Cascade
MyD88 cascade initiated on plasma membrane
Toll Like Receptor 3 (TLR3) Cascade
Toll Like Receptor 5 (TLR5) Cascade
Toll Like Receptor 7/8 (TLR7/8) Cascade
Complex I biogenesis
Receptor Mediated Mitophagy
Mitochondrial protein import

Furthermore, these analysis also demonstrates a role for innate immunity which is the first line of immunity is seen in several TLR cascades (blue box).Both activated and inhibited Master Regulators also support a role for inflammatory and immune signaling.

The research leading to these results has received funding from the European Community's Seventh Framework Programme (FP7/2007–2013) under grant agreement no. 305697 (OPTIMISTIC). In addition, funding has been received under the European Community's E-RARE programme under grant agreement no. 18-038 (ReCognitiOn).

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Institute for Molecular Life Sciences Radboudume (1)