

Speaker Abstracts

Sessions I – VII

- Session I: Exploring the function of dysferlin
- Session II: Impact of dysferlin's absence
- Session III: Animal models of dysferlinopathy
- Session IV: Genetic therapies for dysferlinopathy
- Session V: Dysferlin protein structure
- Session VI: Pursuing interventions
- Session VII: The clinical perspective

Tatiana V Cohen, PhD

Kennedy Krieger Institute, Baltimore, MD
cohenta@kennedykrieger.org



Dysferlin-Deficient Myoblasts Show an Attenuated Response to Pro-Inflammatory Macrophages Due to Upregulated TGFβ1 and IL-1β Signaling

Tatiana V Cohen^{1,3}, Bryan Fleming², Gina Many¹, Svetlana Ghimbovski¹, Shakila Ziashakeri¹, David M Mosser², Eric P Hoffman¹, Terence A Partridge¹

¹Center for Gen. Med. Research, Children's National Medical Center, 111 Michigan Avenue NW, Washington, DC; ²Dept. of Cell Biol. & Molecular Genetics, University of Maryland, College Park, MD, ³Current address: Center for Genetic Muscle Disorders, Kennedy Krieger Institute, 707 N. Broadway, Baltimore, MD

Limb-girdle muscular dystrophy 2B results from mutations in dysferlin and is characterized by inflammatory foci and macrophage infiltration. During an acute injury, classically activated (M1) and alternatively activated (M2a) macrophages are sequentially recruited to remove necrotic cells, and facilitate regeneration of muscle fibers, respectively. This process is modified in dysferlin-deficient muscle, in which there are ongoing rounds of necrosis and regeneration. The aim of these studies is to understand the interactions between macrophages and myoblasts, in order to improve the targeting of treatments that potentiate regeneration by shifting the balance away from the pro-inflammatory M1 macrophage and towards the M2a macrophage phenotype. We hypothesized that the interactions between muscle and macrophages will be perturbed in dysferlin-deficient muscle. Thus, we tested the effect of these macrophage phenotypes on muscle regeneration in dysferlin-deficiency using an *in vitro* co-culture approach. WT or A/J myoblasts were differentiated in the presence of M1 and M2 macrophages. Myogenesis was assayed by calculating the myogenic index. Gene expression profiles were obtained using Illumina gene arrays. Supernatants were assayed for secreted cytokines and chemokines. Gene arrays show that co-culture with M1 macrophages in WT myoblasts activates pro-inflammatory networks and down-regulates MyoD-activated muscle specific genes. The robust response to M1 is attenuated in A/J myotubes. In contrast, the response to M2 co-culture in WT myotubes does not activate pro-inflammatory networks. In A/J myotubes, the response to M2 co-culture includes up-regulation of muscle-specific genes. Additionally, WT and A/J cells differ in their response to IL-1β, a key mediator of macrophage activation. Upregulated pro-inflammatory networks in dysferlin-deficient myoblasts decrease their regenerative capacity and lessen their response to external signals from macrophages that promote myogenesis. Our studies suggest potential therapeutic approaches in modifying the responses to these macrophages and promoting regeneration.

Work supported by the Jain Foundation

Notes:

Joseph A Roche, PT, PhD

University of Maryland School of Medicine, Baltimore, MD
jroche@som.umaryland.edu



The Absence of Dysferlin Results in ER Stress, RyR Redistribution, and Mitochondrially-Mediated Myofiber Death

Joseph A Roche¹, Amber L Mueller¹, Mohan E Tulapurkar², Robert J Bloch¹

¹Department of Physiology, University of Maryland School of Medicine, Baltimore, MD; ²Division of Pulmonary and Critical Care, University of Maryland School of Medicine, Baltimore, MD

We hypothesized that ER/SR stress is elevated in dysferlin-null muscle, and that mitochondrially-mediated myofiber death occurs following injurious lengthening contractions. We found by immunoblots that the ER stress marker CHOP was elevated in dysferlin-null A/J muscle compared to control A/WySnJ muscle. We subjected the *tibialis anterior* muscle of A/J and A/WySnJ mice to *in vivo* dynamometry and injurious lengthening contractions, and found no difference in tetanic torque before injury or at 10 minutes and 3 hours thereafter. At 6 hours and beyond, torque declined in A/J muscle, whereas A/WySnJ muscle continued to recover. In A/J muscle, organization of RyR was altered in >75% myofibers 10 minutes after injury; disruption to DHPR and desmin increased 3 hours later. Immunolabeling of cytochrome-c and complex IV showed that the intermyofibrillar mitochondrial network in A/J muscle becomes condensed 3 hours after injury; and that at 6 hours after injury, cytochrome-c is released into the myoplasm. Between 6 hours and 12 hours after injury, TUNEL+ apoptotic nuclei increased from 72±21 nuclei/mm² to 247±48 nuclei/mm² in A/J muscle, but only from 12±7 nuclei/mm² to 77±28 nuclei/mm² in A/WySnJ muscle. Injurious lengthening-contractions cause changes in mitochondria associated with cell death in dysferlin-null myofibers, which may be linked to ER/SR stress and RyR instability.

Work supported by the Jain Foundation

Notes:

Horizontal lines for taking notes.

Isabelle Richard, PhD

Généthon, Évry, France
richard@genethon.fr



Overview of Compensation Strategies for Therapeutic Approach in Dysferlinopathies
Katrine Charton¹, Francois Monjaret¹, Marina Pryadkina¹, William Lostal¹, Carinne Roudaut¹, Nathalie Bourg¹, Joseph A Roche², Robert J Bloch², Rumaisa Bashir³, Isabelle Richard¹

¹Généthon, CNRS, 1, rue de l'Internationale, 91000 Évry, France; ²University of Maryland, School of Medicine, Department of Physiology, 655 W. Baltimore Street, Baltimore, MD; ³School of Biological and Biomedical Sciences South Road, University of Durham, DH1 3LE, United Kingdom

Mutations in the dysferlin gene are the cause of Limb-girdle Muscular Dystrophy type 2B and Miyoshi Myopathy. The dysferlin protein has been implicated in sarcolemmal resealing, leading to the idea that the pathophysiology of dysferlin deficiencies is due to a deficit in membrane repair. In addition, to test various strategies to transfer the full length dysferlin using AAV vectors (see abstract by Marina Pryadkina), we are investigating the possibility to compensate dysferlin deficiencies using different proteins. First, we generated a transgenic mouse overexpressing myoferlin, the member of the ferlin family closest to dysferlin. The myoferlin overexpressors show no skeletal muscle abnormalities, and crossing them with a dysferlin-deficient model rescues the membrane fusion defect present in dysferlin-deficient mice *in vitro*. However, myoferlin overexpression does not correct muscle histology *in vivo*. In addition, our data suggest that the pathogenicity of dysferlin deficiency is not solely related to impairment in sarcolemmal repair and highlight the care needed in selecting assays to assess potential therapies for dysferlinopathies. Second, we tested the hypothesis that the Anoctamin 5 protein (ANO5) could compensate for dysferlin absence (see abstract by Karine Charton). As for dysferlin, ANO5 when mutated can lead both to limb-girdle muscular dystrophy or Miyoshi-like myopathy and has been implicated in sarcolemmal resealing. We demonstrated that AAV-mediated transfer of human ANO5 (hANO5) was not able to compensate for dysferlin deficiency in the Dysf^{prmd} mouse model and that hANO5 overexpression does not improve the membrane repair defect seen in the absence of dysferlin. Third, we want to assess the consequences of modulating the expression level of calpain 3, another protein involved in limb-girdle muscular dystrophy, on the myopathology of dysferlin deficiencies. For this purpose, a double knock-out mutant is under generation in our laboratory. In conclusion, our attempts to compensate dysferlin deficiencies have not been successful so far. These observations, together with data generated with minidysferlins, suggest the importance of restoring the totality of dysferlin functions.

Work supported by the Jain Foundation

Notes:

Altin Sula

Institute for Structural and Molecular Biology (Birkbeck and UCL), London, United Kingdom
a.sula@mail.cryst.bbk.ac.uk



Crystal Structure of Human Dysferlin Inner DysF Domain

Altin Sula¹, Ambrose R Cole¹, Corin Yeats², Christine A Orengo², Nicholas H Keep¹

¹Institute for Structural and Molecular Biology, Department of Biological Sciences, Birkbeck College, London, United Kingdom.; ²Institute of Structural and Molecular Biology, University College London, Darwin Building, London, United Kingdom.

Dysferlin and the other type I ferlins contain a nested DysF double domain, where the inner domain is surrounded by two sections of the outer domain. Our group solved the first three dimensional structure of this family, the inner DysF domain of myoferlin, by NMR (Patel et al, 2008 J.Mol. Biol. 379, 981–990). We have now confirmed the unique nature of

this fold by solving the crystal structure of the dysferlin inner DysF domain at a resolution of 1.9 Å. The DysF forms a long two-stranded beta sheet held together by tryptophan and arginine stacks. Most of the dysferlinopathy causing mutations found in the DysF domains fall in these residues, indicating that the integrity of this domain is needed for the function of dysferlin or at least to prevent its degradation. The loop between the two strands is structurally well conserved between dysferlin and myoferlin and the combination of crystal and NMR data gives an idea of the flexibility of regions of this domain. We have also looked at the wider occurrence of the DysF domain in sequences genomes.

Notes:

R Bryan Sutton, PhD

Texas Tech University Health Sciences Center, Lubbock, TX
roger.b.sutton@ttuhsc.edu



Alternate Splicing of Dysferlin C2A Confers Ca²⁺-Dependent and Ca²⁺-Independent Binding for Membrane Repair

Kerry Fuson¹, Anne Rice³, Ryan Mahling³, Adam Snow¹, Kamakshi Nayak¹, Prajna Shanbhogue¹, Austin G Meyer¹, Greg Redpath², Anne Hinderliter³, Sandra T Cooper², Roger B Sutton¹

¹Department of Cell Physiology and Molecular Biophysics, Texas Tech University Health Sciences Center, Lubbock, TX; ²Institute for Neuroscience and Muscle Research, The Children's Hospital at Westmead, Sydney, NSW, Australia; ³Department of Chemistry and Biochemistry, University of Minnesota Duluth, Duluth, MN

Dysferlin plays a critical role in the Ca²⁺-dependent repair of micro-lesions that occur in the muscle sarcolemma. Of the seven C2 domains in dysferlin, only C2A is reported to bind both Ca²⁺ and phospholipid thus, acting as a key sensor in membrane repair. Dysferlin C2A exists as two isoforms, the "canonical" C2A, and C2A variant 1 (C2Av1). Interestingly, these isoforms have markedly different responses to Ca²⁺ and phospholipid. Structural and thermodynamic analyses are consistent with the canonical C2A domain as a Ca²⁺-dependent, phospholipid-binding domain, whereas C2Av1 functions as a Ca²⁺-independent, membrane-sensing domain. Additionally, both isoforms display remarkably low free energies of stability, indicative of a highly flexible structure. The inverted ligand preference and flexibility for both C2A isoform suggest a complexity in effector interactions ranging from constitutive to Ca²⁺-regulated interaction, likely relevant to its role as mediator of membrane repair.

Work supported by the Jain Foundation

Notes:

Lined area for notes

Jorge A Bevilacqua, MD, PhD

University of Chile, Santiago, Chile
jbevilac@med.uchile.cl



Clinical and Genetic Characterization of Dysferlinopathy in the Chilean Population: Preliminary Results

Jorge A Bevilacqua^{1,2}, Gabriella A Di Capua³, Lisanne Woudt¹, Claudia Castiglioni⁴, Jorge Díaz⁵, Beatriz Belásquez⁶, Mario Campero¹, Ricardo Hughes¹, Cristián Garrido⁵, Patricio González-Hormazábal³, Raúl Godoy-Herrera³, Nicolas Levy⁷, Martin Krahn⁷, Lilian Jara³

¹Dpto. Neurología y Neurocirugía, Hospital Clínico Universidad de Chile, Santiago, Chile; ²Programa Anatomía y Biología del Desarrollo, ICBM, Facultad de Medicina, Universidad de Chile, Santiago, Chile; ³Programa de Genética Humana, ICBM, Facultad de Medicina, Universidad de Chile, Santiago, Chile; ⁴Unidad de Neurología, Dpto. de Pediatría Clínica Las Condes, Santiago, Chile; ⁵Departamento de Imagenología, Hospital Clínico Universidad de Chile, Santiago, Chile; ⁶Departamento de Medicina Física y Rehabilitación, Hospital Clínico

Universidad de Chile, Santiago, Chile; ⁷Aix-Marseille Université, INSERM UMR_S 910, Equipe Myologie Translationnelle, Faculté de Médecine de Marseille, and AP-HM, Département de Génétique Médicale, Hôpital d'enfants de la Timone, Marseille, France.

Mutations in the dysferlin gene lead to limb girdle muscular dystrophy 2B, Miyoshi myopathy and several other clinical myopathic phenotypes. A cohort of Chilean patients affected by dysferlinopathy is described. Based on clinical findings or absence of dysferlin in muscle biopsy, 39 patients suspected to have dysferlinopathy were selected. Assessment workup consisted of clinical evaluation, Motor Function Measure (MFM) scale, CPK levels, electrodiagnostic testing, whole body MRI, echocardiogram, basal spirometry and direct sequencing of the DYSF gene. We identified 29 patients from 22 non-related Chilean families harboring point mutations in DYSF. Eight mutations were consistently found in the cohort, four of which (c.5979dupA; c.2858dupT; c.2779delG and c.4390G>T) accounted for 78% of the total, these are considered recurrent mutations. In three patients only one mutation was found after complete DYSF gene sequencing. Symptoms at onset ranged from 10 to 33 years, invariably as weakness in lower legs, either distally (21/29) or in the pelvic girdle (8/29), progressing later to upper limbs. Electrodiagnostic assessment showed consistently normal NCV and repetitive stimulation testing, with distinct degrees and distribution of myopathic changes on needle EMG. Single fiber EMG was normal in four confirmed dysferlinopathy patients. Muscle impairment observed through MRI in 27/29 was proportional to disease duration, but distribution of affected muscles was similar, despite of clinical phenotype. MFM scale score in 26/29 patients at different disease's stages showed major impairment for standing and transfers and axial and proximal motor function, with relative sparing of distal motor function. Cardiac and respiratory evaluation was normal in all patients assessed (50%). The clinical spectrum of dysferlinopathy in the series is in agreement with similar cohorts reported. The relative high frequency of some mutations suggests a founder effect for such mutations in the Chilean population. Funding: FONDECYT grant #1110159 (Conicyt, Chile).

Notes:
