Review

Exploration of New Contrasts, Targets, and MR Imaging and Spectroscopy
Techniques for Neuromuscular Disease –
A Workshop Report of Working
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ADDDEVIATIONS

Abstract. Neuromuscular diseases are characterized by progressive muscle degeneration and muscle weakness resulting in functional disabilities. While each of these diseases is individually rare, they are common as a group, and a large majority lacks effective treatment with fully market approved drugs. Magnetic resonance imaging and spectroscopy techniques (MRI and MRS) are showing increasing promise as an outcome measure in clinical trials for these diseases. In 2013, the European Union funded the COST (co-operation in science and technology) action BM1304 called MYO-MRI (www.myo-mri.eu), with the overall aim to advance novel MRI and MRS techniques for both diagnosis and quantitative monitoring of neuromuscular diseases through sharing of expertise and data, joint development of protocols, opportunities for young researchers and creation of an online atlas of muscle MRI and MRS. In this report, the topics that were discussed in the framework of working group 3, which had the objective to: Explore new contrasts, new targets and new imaging techniques for NMD are described. The report is written by the scientists who attended the meetings and presented their data. An overview is given on the different contrasts that MRI can generate and their application, clinical needs and desired readouts, and emerging methods.

Keywords: Neuromuscular disease, muscle, MRI, MRS, biomarker, outcome measure, myo-mri

ABBREVIATIONS		Gr	gracilis
		GRAPPA	generalized autocalibrating partial
ADC	apparent diffusion coefficient		parallel acquisition
ADP	adenosine diphosphate	GRMD	golden retriever muscular dystrophy
ATP	adenosine triphosphate	IDEAL	iterative decomposition of water and
bSSFP	balanced steady state free precession		fat with echo asymmetry and
cCSA	contractile cross sectional area		least-squares estimation
CK	creatine kinase	IR	inversion recovery
COST	cooperation in science and technology	ISIS	image-selected in vivo spectroscopy
CS	corticosteroid/compressed sensing	NMD	neuromuscular diseases
	(in the context of MR image	MIRACLE	motion-insensitive rapid configuration
	reconstruction methods)		relaxometry
CSA	cross sectional area	MOLLI	modified look-locker inversion
CT	computed tomography		recovery
CV	coefficient of variation	MR	magnetic resonance
DENSE	displacement encoding with	MRE	magnetic resonance elastography
	stimulated echoes	MRI	magnetic resonance imaging
DESS	double echo steady state	MRS	magnetic resonance spectroscopy
DMD	Duchenne muscular dystrophy	MSE	multi-spin-echo
DWI	diffusion weighted imaging	MT	magnetization transfer
DTI	diffusion tensor imaging	MTR	magnetization transfer ratio
EPG	extended phase graph	NBD	nemo-binding-domain
¹⁸ F-FDG	¹⁸ F-fluorodeoxyglucose	PC	phase contrast
FH	foot-head	PCr	phosphocreatine
FSHD	facioscapulohumeral dystrophy	PDE	phosphodiesters
GCL	gastrocnemius lateral head	PDFF	proton density fat fraction
GCM	gastrocnemius medial head	PER	peroneus

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PET positron emission tomography

Pi inorganic phosphate
PME phosphomonoesters
PS pulsed saturation
PSR pool size ratio

pSSFP partially spoiled steady state free

precession

qMT quantitative magnetization transfer RF rectus femoris/radio frequency (in the

context of MRI excitation pulses and

signal acquisition)

SIR selective inversion recovery

sLASER semi-localized by adiabatic selective

refocusing

SMA spinal muscular atrophy SNR signal-to-noise ratio

SOL soleus Sr Sartorius

SSFP steady state free precession STEAM stimulated echo acquisition mode STIR short-TI inversion recovery

TA tibialis anterior

TESS triple echo steady state

TIRM turbo inversion recovery magnitude

TP tibialis posterior
TSE turbo spin echo
UTE ultra-short echo time
VI vastus intermedius
VL vastus lateralis
VM vastus medialis.

INTRODUCTION

Neuromuscular diseases (NMD) form a large group of individually rare diseases that are present in all populations and affect people of all ages. They are often, particularly at chronic stages, characterized by progressive muscle degeneration and muscle weakness resulting in functional disabilities. Many of them result in chronic disability, which poses a significant healthcare burden for society, and most of them lack an effective therapy. Even though NMDs have very different causes and pathogenic mechanisms, fibrosis, edema, and fat replacement are frequently observed histological features. Diagnosis and therapy development for NMD has rapidly expanded in recent years [1-3] and there is an urgent need to develop objective, non-invasive outcome measures to monitor disease progression and treatment effect [4, 5]. Muscle biopsies have been used extensively

to classify NMD and to gain a better understanding of their underlying pathomechanisms. However, because they are invasive, it is undesirable to repeat them often. Also, they only assess a small sample in a single muscle, leading to non-representative results and making them less suitable as outcome measures for clinical trials. Functional measures are often used in clinical trials as the primary outcome, but most of them heavily rely on patient cooperation and motivation, and are therefore inherently variable and subjective.

The use of magnetic resonance imaging and spectroscopy techniques (MRI and MRS) applied to NMD is showing increasing promise as an outcome measure in clinical trials [6, 7]. Unfortunately, progress has been hindered by the rarity of individual NMDs and lack of options for pooling data from different groups. Therefore, in 2013, the European Union funded the cooperation in science and technology (COST) action BM1304 called MYO-MRI (www.myo-mri.eu). The overall aim of MYO-MRI was to advance novel MRI and MRS techniques for both diagnosis and quantitative monitoring of neuromuscular diseases through sharing of expertise and data, joint development of protocols, opportunities for young researchers and creation of an online atlas of muscle MRI and MRS. There were four working groups in the action, which all held two working group meetings a year, where data were shared and discussed in an open and informal atmosphere. In this report, the topics that were discussed in the framework of working group 3, which had the objective to explore new contrasts, new targets and new imaging techniques for NMD are described.

This report is written by scientists who attended the meetings and presented their data. The report starts with the different contrasts that MRI can generate, and describes their recent developments as applied to skeletal muscle. Clinically, the two most used contrast mechanisms are those that determine fat infiltration and from that muscular fraction (area), in the form of T₁-weighted imaging, and those that use T₂ relaxation to characterize a combination of various states of water in muscles (T2-weighted imaging with fat suppression, or inversion-recovery based short-tau inversion recovery (STIR) or turbo inversion recovery magnitude (TIRM) sequences). As the focus of the working group 3 meetings was on new contrasts, T₁and T₂-weighted imaging will not be discussed, and the report will focus on the more experimental imaging sequences that can generate quantitative image contrasts. This report will describe the different

contrasts and their applications, followed by a section on the most pressing clinical needs, with an overview of applied and desired readouts for NMD, as well as combinations of MR techniques. In addition, an overview is given of emerging methods, including new developments in post-processing technology and acceleration techniques. The report ends with summarizing perspectives.

CONTRASTS

Dixon imaging

The increased number of potential treatments for NMDs results in a higher need for a reliable and sensitive biomarkers which would allow objective quantification of disease progression [8-13]. Since one of the main characteristics of chronic NMDs is fatty infiltration of muscle tissue, a method quantifying fat content would be a natural choice for such a biomarker. A technique commonly employed in MRI to measure fat content is the Dixon method [14–16]. It utilizes the difference in resonance frequencies of water and fat to produce separate maps of water and fat distribution. While solely water or fat images remain qualitative, the combination of the two becomes quantitative by giving the relative content of the two species, generally defined through a fat fraction FF = f/(w + f), where w and f are water and fat signals, respectively.

The Dixon technique is well-established, but many variants exist, and one of the objectives of working group 3 was to reach a consensus on the optimal approach to apply it in the muscles. In particular a number of confounding factors needs to be addressed to make the method independent of the protocol and system where the data is acquired, and some trade-offs need to be addressed. First, to properly compensate for main field inhomogeneities, it is recommended that at least 3 echoes (Dixon points) are acquired [15, 16]. The sequence parameters need to be chosen so that the sequence is minimally T₁-weighted, since water and fat tissue have very different T₁ values. This can be avoided by using long repetition times and low flip angles [17, 18]. Also, the complexity of the fat spectrum needs attention - basic implementation of Dixon reconstruction assumes a single spectral peak, however around 30% of the fat protons resonate at frequencies different from that of the main peak [19-21]. T₂* relaxation effects need to be accounted for. This can be included in

the reconstruction model, but often requires acquisition of additional echoes to be stable [22]. Moreover, noise bias from magnitude correction can influence the measurements, so a post-processing correction method is advised, particularly if the signal-to-ratio (SNR) of the images is low [17]. Finally, phase data from the scanner needs to be reliable – this can be confounded by bipolar readouts, eddy currents, and gradient delays. Using monopolar readout sequences helps to mitigate some of these, otherwise modeling is needed [23–25].

If these confounders are accounted for, the Dixon technique is considered to produce a setup-independent measurement of fat fraction, generally referred to as proton density fat fraction (PDFF), and working group 3 published a consensus paper detailing what is necessary to achieve this goal, as well as listing important NMD studies to date utilizing the Dixon technique [26].

T₂ Relaxation time mapping

The transverse relaxation time (T_2) is one of the main variables that determine the MR signal intensity. It describes the nuclear spin-spin interactions and its value highly depends on the molecular tumbling rate. T₂ relaxation time mapping can be performed for the T₂ of the water signal (commonly referred to as water- T_2 or MRS- T_2), the fat signals or of all signals combined (commonly referred to global-T₂ or $MRI-T_2$). Muscle water T_2 variations provide relevant information about disease activity and muscle physiological status but are highly nonspecific. They may indeed reflect inflammatory processes, myocyte swelling, sarcoplasmic leakiness, cell necrosis, denervation, or simply hydrostatic edema. More about T₂ as a biomarker for inflammation in NMD can be found in section 3.1.

The standard way to measure T₂ consists of adjusting an exponential model to the signal decay measured with a multi-spin-echo (MSE) sequence. Quantitative relaxometry in fat infiltrated muscles should be interpreted with care though since water and fat protons T₂ largely differ. Because of the long T₂ of fat compared to the T₂ of normal muscle tissue, a single-component analysis of non-fat-suppressed signal results in a global T₂ that primarily reflects the fat content in tissues and may hide underlying alterations of the muscle tissue itself [27]. Different approaches were proposed to decompose the global signal decay into a sum of fat and water contributions. A bi-exponential fit was introduced by Yao

et al. and combined with a Dixon acquisition to determine water T_2 [28]. More recently, a tri-exponential model was introduced, where the fat signal decay was approximated by a bi-exponential (based on the analysis of subcutaneous fat) and the muscle tissue decay by a single exponential and resulted in the simultaneous estimation of water T_2 and the fat fraction [29]. However, in practice, the signal resulting from an MSE sequence rarely displays a pure T_2 decay. It is sensitive to instrumental imperfections like non-ideal slice pulse profiles, B_1^+ inhomogeneities, and insufficient crushing schemes. This leads to the generation

of T_1 -weighted stimulated echoes that contaminate the signal decay curves [30]. This can be resolved applying more complex models based either on Bloch equations [31] or extended phase graph (EPG) analysis [30]. Recently, a bi-component EPG approach was proposed to simultaneously quantify the muscle water T_2 and fat fraction from a standard MSE acquisition (Fig. 1) [32].

Alternatively, a method that exploits the chemical shift between fat and water [33, 34] has been proposed, combining an IDEAL (iterative decomposition of water and fat with echo asymmetry and

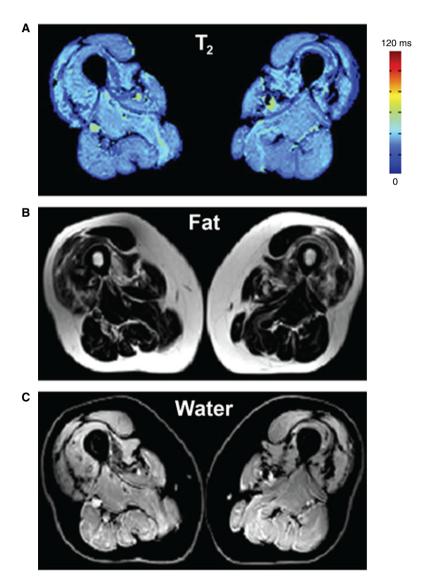


Fig. 1. Bi-component extended phase graph (EPG) approach to simultaneously quantify the muscle water T_2 and fat fraction. (A) Water T_2 map. (B) Fat image. (C) Water image. Figure adapted from Marty et al. with permission [32].

least-squares estimation) decomposition of water and fat signals with an MSE sequence was also specifically designed for simultaneous estimation of water T_2 and fat fraction.

Several rapid T_2 -mapping sequences based on 2D- or 3D-SSFP sequences have been developed for musculoskeletal imaging, including bSSFP [35, 36], pSSFP [37, 38], DESS [39], TESS [40]. These methods are generally sensitive to B_1^+ inhomogeneities and flip angle profiles, and some of them show, in addition, some sensitivity to motion. Recently a rapid B_1^+ , B_0 , and motion-insensitive 3D-SSFP relaxometry approach, MIRACLE [41], was presented. It allows accurate T_1 and T_2 mapping within one single scan, but was to date only applied in the brain. To mitigate the effects of B_1^+ inhomogeneities on muscle water T_2 quantification T_2 -prepared 3D-TSE sequences employing an adiabatic T_2 preparation have been also proposed [42, 43].

Although rarely mentioned, the T_2 -relaxation of muscle water is multi-exponential [44], as revealed by spectroscopic studies. At least three T_2 components can be observed: a short one ($T_2 < 5 \, \mathrm{ms}$) attributed to hydration water, and two others around 30 and 150 ms, with respective relative fractions of about 90% and 5%, reflecting the water compartmentation into intracellular, interstitial, and vascular spaces [45]. On standard single-exponent T_2 -mapping methods the signal is dominated by the longer T_2 components. Multicomponent T_2 decay analysis has the potential of determining compartment-specific T_2 values, relative volumes, and compartmental exchange rates.

Diffusion-weighted imaging

Diffusion-weighted imaging (DWI) has been widely applied in various medical and non-medical fields, ranging from solid material, phantom and animal experiments to human tissue studies. DWI uses diffusion-sensitizing pulsed-field gradients to assess displacement of water protons in vitro and in vivo [46]. This has motivated its use to probe microstructural information beyond the resolution of conventional MR imaging, i.e. in the range of several 10's of micrometers. Depending on the pulsed-field diffusion gradient scheme and strategy of analysis of the acquired DWI data, different parameters can be estimated from the investigated object: the apparent diffusion coefficient (ADC) and the directional diffusivity [47], the displacement probability [48], the sizes of the diffusion-restricting boundaries, e.g. pore

or cell diameter [49], and the transition probability between compartments delimited by semi-permeable boundaries [50–52].

When applying DWI in a clinical setting, especially the analysis of the directional diffusivity and the time-dependent analysis of DWI parameters have shown to be a promising tool for the non-invasive investigation of human skeletal muscle architecture [53, 54]. However, its use can be hampered by the time-consuming acquisitions, as measurement time is directly proportional to the number of diffusion-sensitizing gradient directions, the steps of diffusion weighting (the number of b-values), and for specific sequences also the diffusion time (time between diffusion gradients). The ADC can be estimated easily and fast using one image without diffusion weighting and three images with orthogonal gradient directions in order to get the trace image. Prior studies in pathological human skeletal muscle have demonstrated a change in ADC due to muscle denervation (24% increase) [55], in inflammatory myopathies (17% increase) [56], and deformation-induced injury (between 16% increase and 10% decrease, depending on time after injury) [57] - hence the ADC could serve as a biomarker in muscular disorders. However, analysis of ADC in resting healthy human muscles has yielded a broad range of normal values between 1.26×10^{-3} and 1.99×10^{-3} mm²/s [54–56, 58–61], *i.e.* a 58% difference between the lowest and the highest values. Additionally, changes in muscle ADC are rather unspecific. Changes in ADC and directional diffusivity in healthy human muscles have previously been reported to be dependent on exercise [62, 63], training condition [64], active muscle contraction [65], and passive joint position [66, 67]. Recent systematic evaluations of DWI in healthy human skeletal muscle have furthermore described the DWI parameters to be dependent on different technical issues during acquisition and post-processing, such as spatial resolution, diffusion-encoding parameters, signal-tonoise ratio, and phase-sensitive variations due to microcirculation [68-71]. Fatty infiltration of muscle tissue is a hallmark of NMD and confounds DWI measurements [72, 73]. Hence new acquisition methods for robust fat suppression need to be used in such cases [74, 75]. Careful planning of MR examinations can take the DWI parameter dependences mentioned above into account, but the variability of values in resting healthy human muscle means that interpreting DWI changes in pathological conditions remains challenging.

Magnetization transfer

Magnetization transfer (MT) MRI is sensitive to the relative sizes of, and exchange between, the free water and solid-like macromolecular proton pools in tissues. One mechanism for this exchange is a through-space interaction between magnetic dipoles, commonly termed cross-relaxation. Another mechanism is the chemical exchange of protons in free water protons and certain functional groups on macromolecules, thought to occur by way of the intermediate pool of the macromolecule's interfacial water. The MT's sensitivity to the relative proportions of free water and macromolecules may make this technique sensitive to common aspects of muscle pathology such as inflammation and fibrosis. Because the rate of chemical exchange between water and functional groups such as amides is sensitive to pH [76], MT methods may potentially afford insight into a tissue's metabolic status as well.

Two common MT methods are the pulsed saturation (PS-MT [77]) and selective inversion recovery (SIR-MT [78, 79]) approaches. Both approaches take advantage of the broad linewidth of the macromolecular proton signal, relative to the narrow linewidth of the water proton signal. In PS-MT, the macromolecular signal is saturated with an RF pulse centered on a resonance frequency sufficiently different from the water signal. Typically, the saturation pulse is applied several kHz off-resonance to water. MT takes place between the solid and free water proton pools, and as the saturated magnetization enters the free water pool, the water signal is reduced in amplitude. In SIR-MT, a narrow-bandwidth RF pulse is used to invert the water signal selectively. MT between the solid and free water proton pools causes the water signal to recover as a bi-exponential function.

Semi-quantitative methods based on PS-MT methods express the reduction in water signal amplitude following off-resonance saturation relative to the signal observed in a control condition (typically achieved by centering the saturation pulse $\sim\!50\,\mathrm{kHz}$ off-resonance to water, beyond the reasonable limits of the macromolecular peak). This quotient is called the MT-ratio (MTR). A disadvantage of this approach is that the MTR is sensitive to the saturation pulse power and offset frequency. Consequently, if studies have employed different RF saturation pulse parameters, then strict quantitative comparisons of the results are not possible. In truly quantitative MT (qMT) methods, data are collected at a variety of saturation offsets (for the PS-MT method) or inversion

times (for SIR-MT). These data are then fitted to a biophysical model, allowing estimation of the ratio of macromolecular to free water protons (the pool size ratio, PSR), the relaxation rates of these pools, and the rates of exchange between them.

MT has been developed and applied in healthy muscles [80-90]. Some of these works have provided fundamental quantitative or semi-quantitative descriptions of the MT process in healthy muscle tissue. For example, Harrison et al. observed that the amount of signal loss due to off-resonance MT saturation pulses is greater in the T₂ signal component associated with the intracellular space than in the T₂ component associated with the extracellular space [82]. Normative values for exchange rate, PSR, and other important parameters have been reported [83, 85, 86, 88, 89], as a function of variables such as age [85, 88] and sex [88]. Other studies have advanced the understanding of the MT process in muscle or implemented technical advances. For example, Louie et al. studied the effect of intracellular pH on the MT rate and observed a direct, linear dependence of the MT rate on pH [84], which they postulated may reflect base-catalyzed amide-water proton exchange [76]. Other advances have included the correction of MT parametric maps for RF inhomogeneity [91, 92], the effects of fat signal contamination [90], the reduction of data acquisition time by adopting reduced parameter models [90], and establishment of the reproducibility of the technique [88, 89].

MT has also been used to characterize human NMD and animal models of human disease. Quantitative MT has been used to study small animal models of muscle inflammation, wherein it has been shown that inflammation decreases the PSR [93]. Inasmuch as MT reflects both the macromolecular and free water proton pools, the PSR may also be influenced by fibrosis [94, 95]. Also consistent with inflammation, Sinclair et al. have observed a reduced MTR in patients with peripheral neuropathies [87]. They further observed that the MTR was correlated with clinical severity and was even reduced in otherwise normally appearing images. In a study of patients with Charcot-Marie-Tooth disease and inclusion body myositis, Sinclair et al. likewise observed reductions in MTR [91].

MR Elastography

Palpation is frequently used in the physical examination of patients with NMD. Pathological features related to NMD such as fat infiltration, fibrosis, and

edema affect the muscle biomechanical properties and can be detected using palpation by the sense of touch. Although very practical in the clinical setting, assessment of skeletal muscle biomechanical properties using manual palpation is of a qualitative nature and therefore less useful to objectively assess disease progression and for treatment evaluation. A quantification of the biomechanical properties of tissue can be done with a specialized MRI technique called MR Elastography (MRE). Since the invention of this *palpation by imaging* technique, it is increasingly used to quantify the biomechanical properties of skeletal muscle [96, 97].

MRE is based on the imaging of shear waves, most often introduced in the tissue by an external vibrating actuator mechanically coupled to the tissue, usually the skin. During vibration, the tissue displacements, *i.e.* the shear waves, are imaged with a motion-encoded MRI sequence synchronized to the motion [98]. By inversion of these shear wave images, viscoelastic biomechanical properties, such as the complex shear modulus G* can be subsequently estimated [99].

Current applications of skeletal muscle MRE can be roughly divided in four categories. A first application involves skeletal muscle rheology. Skeletal muscle exhibits nonlinear viscoelastic anisotropic material behavior, which makes accurate determination of the biomechanical properties challenging. Several research groups focused on sophisticated experimental and analysis techniques to approximate the true mechanical properties. Most effort was put into including the anisotropic behavior of skeletal muscle. Some proposed a linear (visco-) elastic transverse isotropic material approach as intermediate solution [101–106]. Other relevant rheological features for skeletal muscle, including nonlinear viscoelasticity, frequency dependence (power-law) behavior, incompressibility, tissue fluid content, tension-compression nonlinearity, and inhomogeneity are currently often neglected, however, could be worthwhile to investigate further [107]. Secondly, the study of the biomechanical properties of healthy skeletal muscle is an active field of research, since it is believed that there are relevant differences in stiffness between muscles and because thorough understanding of muscle's baseline biomechanical properties is considered essential to study muscle injury or disease. Most studied are the individual skeletal muscles in the lower extremities, upper extremities, and shoulder [108-117]. Furthermore, MRE-derived biomechanical properties during skeletal muscle contraction and relaxation can be used as readout for skeletal muscle function. Several groups have studied the relationship between muscle biomechanical properties and load [115, 116], as well as the effects of skeletal muscle exercise on muscle biomechanical properties, and the difference in relaxed versus contracted skeletal muscle [100, 105, 109, 113, 118–120]. The fourth application is MRE applied for studying skeletal muscle pathology. MRE has been applied to study mechanical changes due to neuromuscular dysfunction, myositis, deformation-induced damage, testosterone treatment, aging, disuse, hyperthyroidism, myofascial pain, and Duchenne muscular dystrophy (DMD) [100, 110, 120-127]. For example, in boys with DMD. Bensamoun et al. have observed elevated vastus medialis muscle stiffness at rest and decreased muscle stiffness in contracted state compared to healthy controls (Fig. 2) [100].

³¹P and ¹³C MR Spectroscopy

Following initial animal experiments, MR spectroscopy (MRS) was first applied to human subjects in the 1980s, using the ³¹P nucleus to monitor the levels and fate of high-energy phosphates in skeletal muscle [128]. The technique was initially applied in healthy individuals at rest and during exercise, and rapidly also in NMD patients [129, 130]. ³¹P MRS offers a unique non-invasive window on some key high-energy phosphate metabolites such as ATP, phosphocreatine (PCr) and inorganic phosphate (Pi), which are present at sufficient tissue levels to generate resonances with good SNR. Other compounds that may be estimated from usually less intense signals in ³¹P MR spectra of muscles are total NAD(H), phosphomonoesters (PME) and phosphodiesters (PDE) [131]. In addition, intracellular pH can be derived from the chemical shift of the Pi resonance [132], free Mg⁺⁺ from shifts of the α -ATP and γ -ATP peaks and a measure of free cytosolic ADP may be derived from the creatine kinase (CK) equilibrium assuming its substrates to be free in solution [133]. The enzyme kinetics of the CK reaction and of ATPases may be estimated from saturation transfer experiments [134, 135]. During in-magnet exercise bioenergetics data involving PCr, ATP, Pi, and tissue pH can also be acquired [136], Recent studies have identified socalled ³¹P-³¹P nuclear Overhauser effects for ATP due to its transient binding to large molecular structures like mitochondria [137].

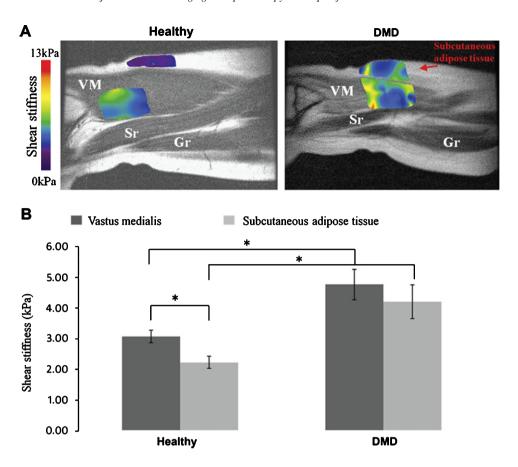


Fig. 2. Biomechanical characterization of skeletal muscle in DMD children. (A) MR Elastography derived sheer stiffness color maps projected on parts of the legs of a healthy subject and a child with DMD. VM = vastus medialis, Sr = sartorius, Gr = gracilis. (B) Quantification of the shear stiffness in the vastus medialis and the subcutaneous adipose tissue (*=P < 0.1). Figure reproduced with permission from Ref. [100].

To be able to excite and acquire 31P spectra, or any other nucleus apart from ¹H, a dedicated coil is needed. ³¹P MR spectroscopy of skeletal muscle is traditionally done by only using a ³¹P surface coil (for transmit and receive) close to the muscles of interest, sampling mostly signal from tissue adjacent to the coil. However, spectra acquired in this way are not very well localized and do not arise purely from one muscle which can complicate interpretations, especially in NMDs where muscles of clinically asymptomatic patients can already show fatty infiltration in some muscles, while others still appear to be normal [138]. This has been addressed in several ways, including localization methods like ISIS or sLASER to select single voxels within a muscle [139, 140] or spectroscopic imaging [141–143]. As these methods usually sacrifice some of the total information present in ³¹P MR spectra of muscles an educated selection of a method for a specific purpose is required. It was recently discovered that

high-energy phosphate metabolism and fatty infiltration may be very different within a muscle and therefore localization is also required to capture this heterogeneity [144–147].

A major advantage of using ³¹P MRS in NMD is that the metabolites sampled are hardly present in fat and are therefore representative of muscle and to a lesser extent interstitial tissue rather than the fat. This is potentially very useful in therapy development, as drugs are commonly designed to preserve or improve muscle tissue. It is generally thought that fat replacement of muscle tissue is irreversible, while other processes may be at least partially reversible. Typical findings in resting ³¹P spectra of skeletal muscle affected by NMD are a low total P-compound level due to atrophy and fatty infiltration, a low PCr/ATP ratio indicating a loss in contractile elements or unbalanced energy metabolism, high Pi/PCr ratio which may indicate increased ADP and thus unbalanced ATP production versus consumption, changes in PDE

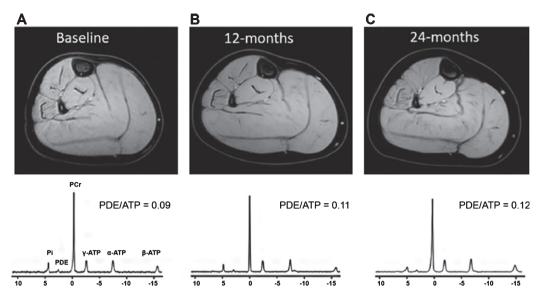


Fig. 3. (top row) Representative reconstructed water images of the right lower leg and (bottom row) 31 P spectra of the TP muscle of a DMD patient at (A) baseline, (B) 12-months and (C) 24-months. PDE/ATP ratios in TP muscles are shown in the graph and %fat for the all analyzed muscle for all three time points are as follows. Baseline: GCL = 5.6%; GCM = 7.3%; SOL = 7.1%; PER = 14.4%; TA = 6.24%; TP = 4.2%; 12-months: GCL = 6.6%; GCM = 8.8%; SOL = 5.2%; PER = 20.6%; TA = 5.71%; TP = 4.3%; TP = 4.3%;

levels and an increased tissue pH [148–150]. However, not all NMDs show the same changes, and even if the metabolic alterations are similar, they likely arise from different mechanisms for each pathology [150, 151]. As a result, it is unlikely that metabolic alterations as shown by ³¹P MRS are specific markers for disease in NMD.

The technique has also been used to study pathophysiology and timing of events in the disease cascade. Recently, it was postulated that the increased tissue pH in patients with DMD is due to a splitting of the Pi peak, with an interstitial Pi associated with damaged dystrophic myocytes and/or expanded interstitial space related to fibrosis [152]. An additional Pi peak has also been assigned to a mitochondrial compartment in healthy muscles [153]. Using chemical shift imaging, it was shown that in patients with facioscapulohumeral dystrophy (FSHD), metabolic changes were only present in fat infiltrated muscles [154], while in both Becker and Duchenne muscular dystrophy, the PDE peak was increased already in muscles without fat infiltration [155, 156]. PDE is often assigned to membrane breakdown products and its signal may be used as a biomarker for treatments [6]. Longitudinal studies which followed ³¹P MRS changes over time in NMD patients are scarce [9, 152, 157]. In the

forearms of patients with DMD, it was shown that the ratio of the alkaline Pi signal over Pi and Pi/PCr were increased over one year in non-ambulant patients only [9, 152]. In the legs of patients with DMD (an example is demonstrated in Fig. 3), no changes in ³¹P MR indices were observed in a 2-year follow up, but in this study no distinction was made between ambulant and non-ambulant patients [157].

Studies with ³¹P MRS during and after exercise to assess the dynamics of high-energy phosphate metabolism have only rarely been performed in patients with muscular dystrophies, but have been done in metabolic and inflammatory myopathies. In general, changes in tissue pH and PCr depletion during exercise and differences in metabolite and tissue pH recovery after exercise were noted in a number of diseases [149, 158–160]. More recent studies on this topic are scarce [161–163], and maybe more practical to assess the kinetics of CK and ATPase is the application of saturation transfer experiments at rest. It has been performed in muscles of patients such as diabetics type II, but not yet in NMD [164].

As ¹³C MRS is a relatively insensitive method and ¹³C nuclei only occur at 1% natural abundance it is only feasible to detect highly concentrated compounds at natural abundance such as lipids and glycogen [165]. As a result, application of this

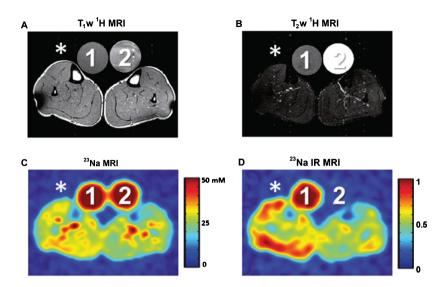


Fig. 4. ¹H and ²³Na MR images of a patient with a muscular channelopathy (paramyotonia congenita). The right lower leg (*) was cooled with an ice bag, which results in an increase of the intracellular Na⁺ concentration and in severe muscle weakness. Two reference tubes were used for signal normalization (1:51.3 mmol/L NaCl and 5% agarose gel, 2:51.3 mmol/L NaCl solution). (A) T₁-weighted and (B) T₂-weighted ¹H MRI revealed no pathological signal differences between the cooled (*) and the non-cooled muscle. (C) The cooled leg shows a slightly increased total Na⁺ concentration. (D) ²³Na inversion recovery (IR) MRI revealed a distinct increase of the signal in the cooled leg and, thus, visualizes the increase of the intracellular Na⁺ content. Note, reference tube 2 (pure saline solution) shows no signal intensity in ²³Na IR MRI. Images adapted from Ref. [172] with permission.

method in NMD is limited to a study in adult onset acid maltase deficiency [166]. As an alternative, ¹³C labeled compounds can be used, such as ¹³C1-glucose, as this allows following metabolic conversions. As ¹³C labeled material is costly and the method requires special hardware it is not much applied and only in a rare case to a neuromuscular disease [167]. A much higher sensitivity can be achieved with so-called hyperpolarized ¹³C, but this new approach is still in development and has not been applied yet to neuromuscular diseases [168].

Sodium imaging

Sodium ions (Na^+) play an important role in the ion homeostasis of skeletal muscle tissue. In healthy tissue, the intracellular concentration ($[Na^+]_{in} = 10-15 \text{ mmol/L}$) is about 10-fold lower than the extracellular concentration ($[Na^+]_{ex} = 145 \text{ mmol/L}$). This concentration gradient across the cell membrane is maintained by the Na^+/K^+ -ATPase pump and is of utmost importance for the excitation and inhibition of muscle cells. Sodium MRI enables non-invasive imaging of the stable and naturally occurring (100% natural abundance) isotope (^{23}Na). However, its quadrupolar nature leads to a fast transverse relaxation and, thus,

requires acquisition techniques that enable ultra-short echo times [169]. In addition, dedicated hardware such as transmit/receive coils that are tuned to the Larmor frequency of ²³Na are required [170].

During the last decades, ²³Na MRI has evolved into a versatile tool in biomedical research [171]. It enables non-invasive determination of the total tissue Na⁺ concentration (Fig. 4C) and relaxation-weighted measurements (Fig. 4D). The latter allows at least a partial separation between different Na⁺ compartments. For example, it was shown that ²³Na inversion recovery MRI can visualize changes of the intracellular Na⁺ content in muscular channelopathies [172] that are not visible in conventional ¹H MRI (Fig. 4). ²³Na inversion recovery MRI and conventional ²³Na MRI in combination with sophisticated modelling have also been applied to provide a quantitative estimation of the intracellular Na⁺ concentration in brain tissue [173].

Although ²³Na MRI largely benefits from the increased signal-to-noise ratio at ultra-high magnetic field strength (*e.g.* 7 T), ²³Na MRI of skeletal muscle can also reliably be performed at clinical field strengths (3 T).

In NMD, it has been shown that muscle tissue of patients with myotonic dystrophy [174] and DMD [175] have increased sodium concentrations. Also in

the muscles of mdx-mice (a model for DMD), abnormally high intracellular concentrations have been reported [176]. In DMD, the absence of dystrophin modifies the gating properties and expression level of the voltage-gated Na⁺ channel (Nav1.4). This results in an increased Na⁺ concentration under the sarcolemma [177]. It was hypothesized that the elevation of the intracellular Na+ concentration contributes to an elevated rate of cell death in dystrophic muscle. In vitro studies demonstrated that both effects can be reversed by a specific Nav1.4 channel blocker (tetrodotoxin) [177]. In DMD patients, it has been shown, that the K+-sparing diuretic agent eplerenone reduces muscular Na⁺ overload and edema [178]. However, long-term studies with larger patient numbers are required to investigate treatment effects of eplerenone in more detail. In future, ²³Na MRI might be used in clinical studies that investigate disease progression or therapy effects in neuromuscular diseases.

CLINICAL NEEDS

Inflammation & disease activity

Multiple MR imaging strategies have been shown to be sensitive to muscle inflammation and muscle damage in the NMDs. For instance, STIR sequences are commonly used to enhance the contrast generated by in areas of muscle inflammation and edema. In many NMDs it is believed that areas that are hyperintense on STIR images precede the eventual deposition by fibrofatty tissues. For instance, Marden et al. [179] observed regions of increased signal intensity on STIR images in the muscles of young DMD boys in the absence of fatty infiltration. This finding is consistent with the conjecture that inflammation, as well as necrosis and edema, occurs early in DMD, prior to the loss in contractile tissue and accumulation of fatty infiltration. The importance of inflammation in DMD is supported by the 100-fold higher serum levels of TNF- α in boys with DMD compared to controls (27.8 vs. 0.27 ng/L) [180]. Changes in the serum levels of TNF- α with age are also consistent with the observations that muscle expression of TNF- α and IL-6 decreases with age [181]. In another type of muscular dystrophy, FSHD, a direct relationship between inflammatory markers (serum and tissue) and hyperintensity observed on STIR images has also been documented [182]. Due to these early inflammatory changes a wide range of therapeutics are in clinical trials for NMD targeting specific inflammatory pathways [183].

Changes in muscle T2, MT, and diffusion have all been commonly used to look at acute muscle damage and inflammation. Damage and inflammation has been induced in animal models using myotoxins [184, 185], a local inflammatory agent [93, 186–188], and in humans [189-191] and preclinical models [192–195] following eccentric muscle contractions. Due to the close association between muscle damage (loss of sarcoplasm integrity), inflammation, and edema, it is often difficult to separate these individual components from net changes in MRI signal. Despite this, careful animal studies along with detailed histological analysis at specific time points [93, 186] and multimodal MR acquisitions are providing insight into sources of the different contrast mechanisms [57, 93, 184, 186]. Often in these analyses it is necessary to take into account the multicomponent nature of relaxation or diffusion that are occurring on the subpixel scale [186]. Due to the fact that the primary problem in many of the muscular dystrophies is related to a mutation or absence of a structural protein, many modern therapeutics aim at replacing or mitigating these defective or missing proteins which leads to bouts of muscle damage and inflammation [183].

Agents that are known to decrease inflammation have also been shown to lower muscle T2. Currently the only intervention that has been shown to be successful in mitigating some of the effects of dystrophy are glucocorticosteroids. Studies have shown that corticosteroid treatment can significantly improve muscle strength and function, reduce the incidence of scoliosis, maintain the respiratory and cardiac function, as well as prolong ambulation and survival in boys with DMD [196-198]. Although there is increasing evidence of long-term benefits of corticosteroids in DMD, the exact mechanism of action of these drugs in dystrophic muscle is unclear but a primary mechanism is believed to reduce muscle inflammation possibly by modulating NF-κβ activation. Arpan et al. measured the muscle water T₂ in 5 to 7 year-old DMD boys whom were using corticosteroids and age matched corticosteroid naïve subjects and found that muscle water T₂ measured by ¹H-MRS was significantly reduced in both the vastus lateralis and soleus muscles of the boys on corticosteroids [199], consistent with the anti-inflammatory effect of corticosteroids (Fig. 5). At the low levels of fatty tissue deposition in these young DMD patients, they also found lower T2 values in both thigh and lower leg muscles of boys on corticosteroid treatment. Of the muscle groups studied, the gracilis muscle was the only exception. Where, the gracilis is known to

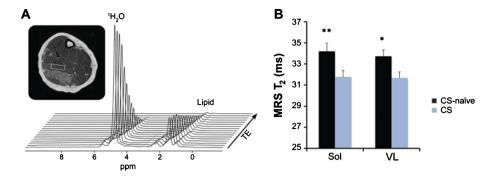


Fig. 5. Cross-sectional comparisons of water T₂ measured by MRS between corticosteroid- treated (CS) and corticosteroid-naïve (CS-naïve) boys with Duchenne muscular dystrophy. (A) Spectroscopic relaxometry measurement using ¹H-MRS STEAM to quantify water T₂ in individual muscles. (B) T₂ values for both the soleus (Sol) and vastus lateralis (VL) muscles were lower in CS boys compared to the CS-naïve boys, indicating less damage in the muscles of boys on corticosteroid treatment. Figure reproduced with permission from [199].

be one of the most preserved muscles in DMD and hence might not reveal treatment response at such a young age. Both MRI and MRS measures detected the beneficial effects of corticosteroids on the skeletal muscles as early as 3 months after drug initiation. Additional evidence of ability of water T₂ to be a readout for inflammation was shown by Marty et al. [32] in which they found an almost complete recovery to normal water T₂ values after 3 months of steroid treatment in patients with juvenile dermatomyositis.

Whereas the clinical benefits of steroids in DMD are clear, their use also comes with significant side effects and great effort has been spent to identify new anti-inflammatory agents for the NMDs [183]. Preclinical studies in the golden retriever muscular dystrophy (GRMD) model revealed that MRI water T₂ changes following the treatment with a nemo-binding-domain (NBD) peptide, which is a specific inhibitor of NF-κβ [200]. Post NBD treatment, GRMD dogs had normalized postural changes and a trend towards lower tissue injury on T2 images. Unfortunately, despite phenotypic improvement in the dystrophic dogs, NBD administration over time led to infusion reactions and an immune response in both treated GRMD and wild type dogs. Other drugs that target inflammation that have shown great success in preclinical models such as Vamorolone (VBP-15; NCT03439670), Edasalonexent (CAT-1004; NCT02439216), Histone deacetylase 2 inhibitor (Givinostat; NCT02851797) are now in clinical trials [183] and either plan to or include MRI and MRS measures as secondary outcome measures.

²³Na imaging – see also section 2.7 – showed that areas of hyperintensity on STIR images from skeletal muscle in DMD subjects are directly related to muscle edema [201]. In a pilot study, Glemser et al. per-

formed a longitudinal assessment of edema in 2 DMD patients treated with eplerenone or steroid using a combination of ²³Na, Dixon, and STIR imaging [178]. This study demonstrated that longitudinal changes in sodium content, and presumably tissue edema, can be noninvasively monitored throughout therapeutic intervention.

Taken together, these findings indicate that multiple MR sequences may be sensitive to early inflammation in the NMDs and emphasize the potential of MRI and MRS as biomarkers for the quantification of early and subtle muscle changes caused by the disease process and evaluation of therapeutic interventions in NMD.

Fat infiltration

Muscle fat infiltration has been extensively investigated in NMDs with single-voxel ¹H MRS and 2D and 3D imaging. Over the past decade, fat infiltration has been evaluated with respect to functional measures, the rate of disease progression, in clinical trials, and to assess differences between and within individual muscles. A listing of important NMD studies to date assessing muscle fat fraction can be found in the recently published article from our COST action [26]. All these findings together showed that muscle fat infiltration differs between muscles and diseases, is highly associated with disease progression and that functional and strength measures are correlated to the fat fraction in NMD. A recent large longitudinal study in DMD reinforced this finding, with correlations to functional endpoints and sentinel events ranging from 0.59 to 0.78 depending on the muscle studied [202]. Besides all the possible readouts used for fat fraction itself — i.e. whole

muscle fat fraction, specific volume fat fraction for an individual muscle or muscle groups, delta %fat etc. - other closely related measures, such as contractile cross-sectional-area (cCSA = %fat \times total CSA) or muscle volume have also been widely investigated and it was shown that specific strength is reduced in a number of NMD [10, 203-205]. Recently, this analysis was extended by obtaining physiological cross-sectional areas in patients with FSHD, showing that specific strength is also reduced in these patients [206]. Besides the relation with function, some recent studies also focused on the methodological aspects of fat infiltration as outcome measure. Different MR fat quantification methods have been assessed and benchmarked against each other and other methods for fat quantification [13, 26, 207-210]. Muscle fat fraction measurements showed to be highly reproducible from day-to-day and across centers, with CV values ranging between 1.8–7.3% [10, 88, 211]. However, in situations where muscles inevitably change in between measurements, for instance in a maturing study population (for instance in patients with DMD and patients with spinal muscular atrophy, SMA), repositioning according to internal muscle references and bony landmarks becomes more challenging and could affect the reproducibility.

It is important to consider the non-uniform fat distribution patterns along the proximodistal muscle axis in various NMDs [145-147, 212, 213]. This non-uniform shape emphasizes the need for accurate spatial localization between measurements, as a slight shift of the imaging stack or volume can result in over- or underestimation of fat fraction between measurement points. Subsequently, the choice of intrinsic parameters of most imaging and spectroscopy approaches, i.e. slice gaps, slice thickness, restricted voxel size, results in limited and location specific information, which could amplify the effect of inaccurate spatial localization. 3D acquisitions with full limb coverage would allow accurate offline matching of datasets in a standardized way as well as the possibility to retrospectively decide which readout is most suitable for the study set-up.

Fibrosis

Besides fatty infiltration of skeletal musculature, patients with NMD often show excessive accumulation of extracellular matrix proteins as collagen (fibrosis) in their skeletal muscles. The process

of formation of proteins in the extracellular space between remaining myocytes and resulting scars is physiologically active during repair of damaged musculature (e.g. after injuries). This repair involves several cell types acting in response to various local and systemic signals, but those activities are not persisting in healthy subjects. In contrast, during chronic tissue damage in muscular dystrophies, an inflammatory cell infiltration persists, leading to activation of fibroblasts and their transformation to myofibroblasts, which are continuously building up excess amounts of connective tissue, while the reparative capacity of muscle stem cells is more and more attenuated.

Volume share and composition of the extracellular space in musculature involved in NMD strongly depends on the intensity and duration of inflammatory activity (Fig. 6). Their non-invasive detection is of high clinical interest in order to better stage the disease and monitor therapeutic interventions. In early involvement of musculature, inflammatory activity leads to increasing amounts of interstitial fluid without fibers. Thus, an increased amount of free water is detectable by prolonged T2 values in MRI, and also other MR detectable features of musculature (e.g. proton density, diffusion, magnetization transfer, ²³Na content) undergo changes due to inflammation. Persistent inflammatory activity often leads to an irreversible and increasing accumulation of protein fibers in the extracellular space (fibrosis). It is evident that mechanical properties (stiffness) and signal characteristics of musculature in MRI depend on the composition of the extracellular compartment containing variable amounts of fluid and increasing volume share of protein fibers.

However, since fibrotic areas and remaining muscular elements are distributed microscopically, it is impossible to selectively record MR signals from the interstitial compartment only. We have to deal with a superposition of signal contributions from remaining functional musculature, from the components of the interstitial space (mainly water and protein fibers, but also cellular elements), and in some cases from fat in cases with fatty degeneration. So, valid and unambiguous interpretation of results from MR imaging with respect to fibrosis of musculature is very challenging. The gold standard for assessment of fibrosis (in any type of tissue) is biopsy. Unfortunately, this procedure is invasive, and results are often not representative for extended tissue areas, since fibrosis is often not disseminated homogenously, neither microscopically nor macroscopically.

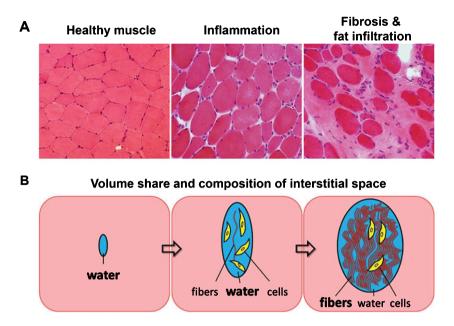


Fig. 6. (A) Histological sections of healthy muscle, inflamed muscle, and heavily fat infiltrated and fibrotic muscle tissue. (B) Schematic of changes in volume share and composition of the interstitial space due to inflammation and as a consequence of fibrosis and fat infiltration.

Therefore, non-invasive imaging techniques for reliable assessment of the degree of fibrosis are highly desired.

The most common MR approach for examination of muscle stiffness is MR elastography [101, 123]. This technique works with mechanical stimulation and assessment of mechanical wave propagation inside musculature and is established for assessment of fibrosis in other organs like liver and breast. Applications in musculature are more difficult because of the variable muscle tone and geometric anisotropy of muscle tissue (see section 2.5).

Other approaches to non-invasively measure fibrosis by MRI are currently investigated. Changes in water diffusion, magnetization transfer, prolonged T_1 , prolonged T_1 -rho, short T_2 components, and late enhancement after administration of a contrast agent were correlated to fibrosis in myocardium, liver, and bone marrow [94, 214-217]. However, only a few approaches have been discussed regarding applications in NMD [6, 93]. Pathological events concurrent to fibrosis in muscular dystrophy, such as inflammation and muscle damage, may affect the contrast in the same direction or in opposite direction than fibrosis, which poses a challenge to disentangle the contribution of fibrosis. Nevertheless, a promising technique that deserves further attention in the context of NMD is ultra-short echo time (UTE) imaging, which was

already applied to characterize age-related difference in collagenous tissue in muscle [218].

Muscle cell morphology/architecture

Routine clinical MRI investigation in patients with NMD continues to rely largely on T₁-weighted, T₂-weighted and STIR methods to obtain high definition anatomical information. These methods primarily distinguish between apparently normal appearing muscle fibers and muscle tissue with strong fatty infiltration, which represents the end stage of the disease process. In the context of clinical patient management and treatment there is an important need to visualize the early and ongoing pathological changes, which are occurring in the remaining muscle fibers. For clinical trials, such information is vital to understand drug-target interaction and to identify early treatment response. In the muscular dystrophies, disease progression is characterized at the cellular level by cycles of degeneration and regeneration of muscle fibers. Over time, the ability to regenerate fibers is lost and fibers are eventually replaced by fibrotic tissue and fat. Histological measurement of muscle in animal models shows that the distribution of muscle fiber sizes changes in dystrophic muscle over and above differences driven by maturation or healthy ageing [219]. Specifically, an increase in the proportion of fibers with much larger or smaller diameter than normal muscle is observed, represented by a shift and broadening of the muscle fiber size histogram [220]. In addition, muscle sarcolemma permeability to large tracer molecules is increased in dystrophic muscle, driven by damage to the membrane [221, 222].

These two basic morphological properties (fiber size and permeability) are fundamental determinants of the effective (apparent) diffusivity of water within the tissue microstructure. Indeed, the earliest in vivo studies of self-diffusion characteristics of water in tissue by magnetic resonance methods were made in excised muscle specimens [223]. In that early work Tanner demonstrated that measurement of water diffusivity at extremely long diffusion time (hundreds of milliseconds to seconds, achieved through the use of stimulated echoes) showed evidence of restricted behavior. The magnitude of the effect increased with diffusion time as each water molecule has an increased probability of interacting with major barriers in the tissue such as the sarcolemma itself. More recently such measurements have been revisited as imaging experiments in living tissue, both in animal models and in human subjects [50, 220, 224-226]. In the context of NMD, studies in wild type mice have shown that clear maturation related changes can be seen in diffusion restriction [220], while in the mdx-mouse model significant differences are reported, particularly at long diffusion times with reduced restriction compared to wild type animals [227]. Applications of the DWI technique in humans are also described in section 2.3.

To quantify the changes seen using diffusion methods, Tanner et al. applied a simple biophysical model of regularly spaced semi-permeable membranes to estimate muscle fiber size and permeability [223]. It is however clear from the progressively complex models which have subsequently been proposed to quantify muscle water diffusion behavior [224, 226, 228], that sarcolemmal permeability and muscle fiber scale are inherently opposing factors - increasing permeability reduces restriction whatever the change in muscle fiber size. In diseased muscle, such as in the muscular dystrophies where significant changes are expected in muscle fiber permeability, it seems unlikely that a unique solution is possible and that the effects of altered permeability will dominate the ability to assess muscle fiber sizes [229]. Nevertheless, the potential to differentiate normal from diseased muscle using long diffusion times and to detect changes with time [227], as suggested by recent

animal data suggest that further development is warranted.

EMERGING IMAGING TECHNOLOGY

Muscle segmentation

Segmentation of individual muscles is of high interest in NMD, as fat infiltration can differ greatly even between adjacent muscles. This issue is also of interest if one aims at monitoring changes resulting from training and/or pharmaceutical interventions.

The task of segmenting MR images into meaningful compartments has been recognized as challenging for a variety of reasons. In addition to the high muscle shape variability among subjects, fatty infiltration and muscle atrophy can change the visibility and location of borders between muscles and therefore greatly complicate the segmentation task. So far, manual segmentation of anatomical structures is the gold standard and has been used in multiple studies. However, this approach is widely acknowledged as very time-consuming and can be operator-dependent [230]. For example, accurate segmentation of the quadriceps femoris compartment in controls may take a few hours.

More recently, several semi-automated and automated methods have been tested on MR images of healthy subjects. An example by Ogier et al. is shown in (Fig. 7) [231]. They implemented an algorithm allowing a semi-automatic transverse propagation of a number of manually drawn masks, resulting in an 85% reduction in segmentation time. A random walk algorithm based on graphs has been reported by Baudin et al. [232, 233], while Gilles et al. [234] proposed a method based on mesh deformable registration models. In order to take into account the large inter-individual variability, Prescott et al. [235] used a semi-automatic segmentation method based on the pre-selection of appropriate templates selected from a database. Using atlas-based registration, Ahmad et al. proposed a semi-automatic segmentation tool for quadriceps muscles [236]. At the whole body-level and using a multi-atlas based method, Karlsson et al. reported a 3% volume error for the quadriceps femoris compartment [237]. Using a similar approach, Le Troter et al. further confirmed a 3% volume error for the quadriceps femoris compartment but reported much larger errors when considering individual muscles [238]. The corresponding muscle volume

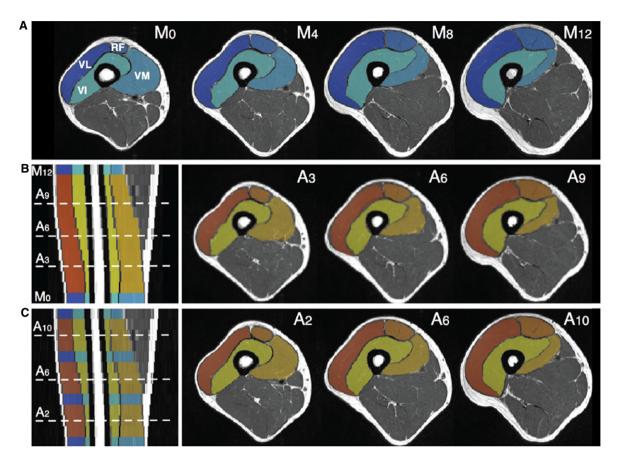


Fig. 7. Semi-automatic segmentation of the upper leg muscles on axial slices. (A) Manual segmentations (blue colored ROIs) of vastus lateralis (VL), rectus femoris (RF), vastus medialis (VM) and vastus intermedius (VI). Sagittal and axials views of the automatic segmentations of intermediate slices (yellow-orange colored ROIs) based on (B) 2 and (C) 4 initial manual segmentations. Figure reproduced from Ref. [231] with permission.

errors measurements ranged from 4 (vastus medialis muscle) to 17% (rectus femoris and vastus lateralis muscles).

Overall, segmentation methods have been developed and tested so far mostly in healthy subjects so that the issues of fat infiltration and muscle atrophy as confounding factors still need to be systematically addressed.

Accelerated imaging

The acquisition time of quantitative MRI is a barrier to the expanded use of these methods in NMD, particularly for DMD and SMA, where restricting the duration of the protocol is critical to ensuring child compliance and avoiding motion artifacts.

The acquisition time of an MRI acquisition is conventionally limited by the need to acquire a matrix of raw data (k-space) of an equivalent size to the even-

tual desired imaging matrix (the Shannon-Nyquist criterion). Whereas the read dimension is acquired rapidly, the other dimensions using phase encoding require multiple repetition times. If the amount of k-space data points to be acquired can be reduced by the use of additional information, then the number of repetition time delays and hence the acquisition time can be reduced.

Parallel imaging, now available on all modern scanners, achieves this by exploiting the spatial sensitivity of multi-channel array coils. More recently, research effort has exploited a different source of additional information, the sparsity of the image under a mathematical transform, such as discrete wavelets or the calculation of total variation. If the k-space is undersampled quasi-randomly, such that no coherent aliasing is produced under inverse Fourier transformation, then the sparsity in spatial and/or temporal domains can be exploited to permit a high

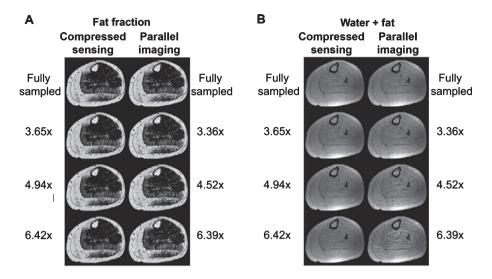


Fig. 8. Reconstructions of the left lower leg of a subject showing (A) the calculated fat fraction maps and (B) the total water and fat signal map for a fully sampled acquisition (top row) using CS and traditional parallel imaging (GRAPPA) with different undersampling ratios (subsequent rows). Figure reproduced with permission from Hollingsworth et al. [239].

quality iterative reconstruction. This method has been coined compressed sensing.

Research into the use of compressed sensing in MRI has proliferated [240], with applications in skeletal and cardiac muscle relevant to NMD. It has been demonstrated that combined compressed sensing and parallel imaging could be applied to a 3D IDEAL-type fat fraction measurement in skeletal muscle at acceleration factors of up to $5\times$ without significant loss of image quality or impairment of fat fraction fidelity (Fig. 8) [22, 239, 240].

The measurement of cardiac function is of increasing interest in NMD. In preclinical cardiac imaging, a Cartesian spatiotemporal undersampling scheme has been used to allow an acceleration of up to $3\times$ [241] while producing comparable results for end systolic and end diastolic volumes and the early to late filling ratio in diastole. Subsequently, a 2D multislice golden-angle radial acquisition was applied to a sequence with ultra-short echo time, which reduces artifacts due to flow and susceptibility [242]. Goldenangle radial schemes permit post-hoc decisions to be made about the number of spokes to be reconstructed per cardiac phase and the number of cardiac phases resolved in the spatiotemporal scheme. This permitted accelerations of 2, 4 and $5 \times$ to be assessed for end-systolic-volume, end-diastolic-volume, ejection fraction and cardiac output, using Bland-Altman analysis.

The assessment of myocardial extra-cellular volume by pre- and post- contrast gadolinium T_1

measurement has found an increasing role in cardiac studies, with potential applications to monitoring the neuromuscular disease process [243]. Marty et al. have demonstrated T_1 measurement using compressed sensing reconstruction with a 2D multi-slice radial MOLLI sequence which permits accurate reconstruction of T_1 maps in a breath hold of 5 heart beats, a substantial time saving over the 12–17 heart-beats conventionally required [244]. This has recently been extended to rapid T_1 -mapping of skeletal muscle in Becker muscular dystrophy [245].

Measuring muscle contraction & strain

The MRI techniques used for dynamic muscle contraction and strain imaging can be categorized in three main groups: MR tagging, phase contrast (PC), and displacement encoding with stimulated echoes (DENSE). Tagging has been used to monitor tissue displacement and deformation during active isometric contraction in humans [246, 247] as well as for muscle indentation in rats [248] and in humans [249, 250]. The PC method, which enables tissue velocity measurements in three directions, has been applied to quantify muscle inertial forces [251], as well as changes in fascicle length [252] and strain rate [253, 254]. DENSE is conceptually similar to PC, as it encodes displacement on the phase of the signal, but it is based on the acquisition of stimulated echoes. One of the advantages of DENSE over PC is that it allows to encode motion over longer time

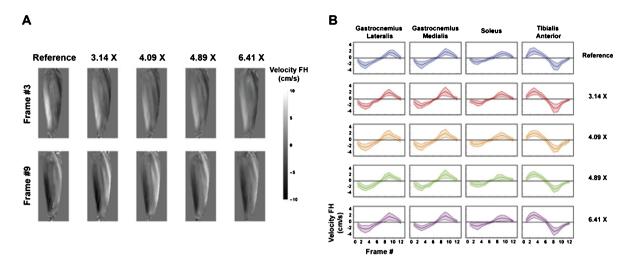


Fig. 9. Accelerated 3D dynamic muscle contraction imaging of the lower leg during active plantarflexion and dorsiflexion. (A) Two velocity-imaging frames from a 12-frame movie with varying degree of image acceleration. The reference image required 10:52 min of scan time and 326 repetitions of the motion task, whereas the 6.41 times accelerated scan was only 2:46 min and 83 repetitions. (B) Velocities in foot-head (FH) direction for 4 muscles of the lower leg during the motion cycle for various degree of image acceleration. Figure was reproduced with permission from Mazzoli et al. [259].

intervals, which is especially beneficial for skeletal muscles, that are characterized by low velocities [255].

Dedicated MRI technology has been developed to visualize and quantify muscle deformation during active and passive contraction [256]. Dynamic muscle imaging can be performed in real time [257] or in a triggered fashion by mechanically restricting muscle motion to repeatable patterns, or by using electrical muscle stimulation [254, 258]. Because of imaging speed restrictions, real-time imaging is commonly limited to a 2D single slice approach, or 3D with coarse spatiotemporal resolution [250, 257]. When the motion task can be consistently repeated, displacements or velocities can be acquired in a segmented way, allowing for volumetric acquisition and 3D strain measurements. Mazzoli et al. [259] have recently introduced a 4D PC method for quantification of velocities and strain rate of the muscles in the lower leg during active plantarflexion and dorsiflexion, using the latest compressed sensing acceleration technology requiring only 2:46 min of scan time (Fig. 9).

Dynamic imaging offers great opportunities to study musculoskeletal healthy function and dysfunction from (neuromuscular) disease, particularly when combined with structural information and modeling of muscle function. PC MRI in skeletal muscles showed non-uniform strain values in the biceps brachii during elbow flexion, as well as in the

soleus aponeurosis-tendon complex [260, 261]. A later study combined such information with finite element modeling and confirmed that a different fascicle length and curvature within the muscle are the main cause for non-uniform strains [262]. Non-uniform strain values were also reported in the tibialis anterior [263], as well as changed strain rate values in the gastrocnemius muscle [264].

Sinha et al. observed significant differences in strain rates between young and elderly subjects in the medial gastrocnemius, as well as smaller angles between the principal strain rate and the fiber direction in the older cohort [253]. Since acquisition was limited to a single slice, the out-of-plane component of the strain rate could not be measured, and was estimated under the assumption of volume incompressibility [265, 266]. Non-collinearity of the strain directions and fiber directions and non-uniform strains observed are believed to be caused by architectural heterogeneity in terms of fiber lengths and pennation angles [263]. Diffusion tensor imaging (DTI) combined with appropriate postprocessing, allows for determination of fiber lengths [267, 268], fiber curvatures [68, 269, 270], and pennation angles [268]. We foresee that combining these architectural parameters with local 3D strain measurement will assist in a better understanding of mechanisms of altered muscle force production and lateral force transmission as a consequence of healthy aging and NMD.

MRI/PET

MRI/PET is a relatively new multimodal imaging technique, which combines superior anatomical, structural, and functional information provided by MRI, with the greater sensitivity of PET for providing molecular information via the detection of radiolabeled molecular tracers. The evolution of MRI/PET has been rapid over the past decade and has successfully addressed the technical challenges, which are related to the design of PET detectors that operate in the presence of the strong magnetic field in the MR scanner. Initially this resulted in high-performance preclinical prototype and research systems, but by now both preclinical and clinical PET/MRI systems are available from several vendors [271].

There may be added value to PET/MRI in the field of NMD, considering that MRI/PET is practically the combination of a standard MRI, which means that all the MRI techniques described in this paper may be enriched with molecular information from PET. Currently, because of its young age, there are only few examples of application of MRI/PET in the neuromuscular field. Behera et al. [272] observed increased ¹⁸F-FDG uptake in the affected nerve of animals with neuropathic pain. Based on these findings Lee et al. showed increased ¹⁸F-FDG uptake in the ipsilateral trapezius muscle in a limited number of patients with varying degree of severity of spinal accessory neuropathy [273]. Priola et al. showed that the combination of PET and MRI can provide additional information to the standard computed tomography (CT) for the identification of myasthenia gravis, the detection and type of the thymic abnormality, and preoperative planning [274]. Haddock et al. employed hybrid MRI/PET to determine the relationship between relative ¹⁸F-FDG uptake and MRI T2 changes in skeletal muscles following resistance exercise. They found a high correlation between ¹⁸F-FDG uptake and changes in muscle T₂ with physical exercise, leading to an improved insight into the metabolic changes that occur with muscle activation [275]. Since the family of neuromuscular disorders is associated with a large number of muscle pathologies the role of this technology is expected to increase as new protocols and PET tracers become available.

SUMMARIZING PERSPECTIVES

For the seven working group three meetings of COST action BM1304, research teams from a large number of universities have contributed unpublished

preclinical and clinical data with the intention to discuss the potential and pitfalls of a large range of advanced imaging techniques. The workshops were attended by a core group of attendees and a selected group of invited experts per topic. In this workshop report, an overview of the topics that were discussed was presented.

Of the techniques that were discussed, fat fraction by MRS or Dixon imaging as well as T2 relaxation time mapping are already used as an outcome measure in a number of clinical trials as a primary or secondary endpoint (e.g. NCT02851797, NCT02439216) [276]. In the research realm, a significant number of publications have appeared on DTI and ³¹P; for DTI several groups have been working together on consensus protocols for application in skeletal muscle, whereas the commercial availability of higher field human MR systems has resulted in renewed interest in phosphorous MRS and MRI by several groups. In terms of practical implementation, both (semi-) automatic segmentation and scan acceleration are areas of great interest, and a number of groups are actively pursuing these goals. Imaging of fibrosis and/or other aspects of muscle tissue apart from fatty infiltration is being regarded as a great clinical need, but the optimal technique to assess this remains a topic for further study.

The atmosphere during the workshops was open and informal, and the frequency of the meetings created common ground for new collaborations and strengthening of existing ones. The action brought the community together and had several tangible outputs in the form of shared publications. The final activity of MYO-MRI consisted of the first International Conference on Imaging in Neuromuscular Disease [277]. The conference was very successful, with 200 participants and almost equal contribution from clinical and academic partners, with more than 10% industry participation. This illustrates the large interest in imaging in NMD and shows that collaboration between disciplines in this field is very active.

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