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Magnetic resonance imaging techniques for the quantitative analysis of skeletal muscle: State of the art



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Keywords:

Dixon

Clinical trials

Muscle MRI

T2 mapping

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ARTICLE INFO

Diffusion tensor imaging

Quantitative analysis

ABSTRACT

Background: Magnetic resonance imaging (MRI) is the dominant 3D imaging modality to quantify muscle properties in skeletal muscle disorders, in inherited and acquired muscle diseases, and in sarcopenia, in cachexia and frailty.

Methods: This review covers T1 weighted and Dixon sequences, introduces T2 mapping, diffusion tensor imaging (DTI) and non-proton MRI. Technical concepts, strengths, limitations and translational aspects of these techniques are discussed in detail. Examples of clinical applications are outlined. For comparison ³¹P-and ¹³C-MR Spectroscopy are also addressed.

Results: MRI technology provides a rich toolset to assess muscle deterioration. In addition to classical measures such as muscle atrophy using T1 weighted imaging and fat infiltration using Dixon sequences, parameters characterizing inflammation from T2 maps, tissue sodium using non-proton MRI techniques or concentration or fiber architecture using diffusion tensor imaging may be useful for an even earlier diagnosis of the impairment of muscle quality.

Conclusion: Quantitative MRI provides new options for muscle research and clinical applications. Current limitations that also impair its more widespread use in clinical trials are lack of standardization, ambiguity of image segmentation and analysis approaches, a multitude of outcome parameters without a clear strategy which ones to use and the lack of normal data.

1. Introduction

Magnetic resonance (MR) is an established technique for imaging skeletal muscle disorders. Traditionally, MR sequences sensitive to water such as T1-weighted images (T1w), short-tau inversion recovery (STIR) or T2-weighted images (T2w) with or without fat suppression have been used to determine progression and treatment effects in inherited and acquired muscle diseases [1–5]. Typically, semi quantitative scores such as Mercury [6,7], Jungbluth [8], Lamminen [9] Goutallier [10,11] or Poliachik [12], were used to grade structural integrity, fatty muscle

infiltration, muscle edema and MR signal intensity.

Predominant locations were muscles of the lower extremities, which are large and relatively easy to assess. Chemical shift imaging sequences [13] to quantify fat infiltration and T1w imaging [14] have been explored in the last century to allow earlier detection of muscle diseases compared to the use of semi quantitative scores. In 2009 and 2010 two TREAT-NMD (https://treat-nmd.org/) workshops on skeletal muscle MRI recommended the use of "whole body T1w imaging, for the screening of disease extension, Dixon imaging with water–fat separation, for the quantitation of fatty infiltration and parametric T2 imaging, for the quantitation of inflammation" as outcome measures for

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https://doi.org/10.1016/j.jot.2023.07.005

Received 17 February 2023; Received in revised form 4 July 2023; Accepted 19 July 2023

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Abbreviations		MR	magnetic resonance
		MRE	MR elastography
ADC	apparent diffusion coefficient	MRI	magnetic resonance imaging
AT	adipose tissue	MRS	magnetic resonance spectroscopy
BMI	body mass index	MT	muscle tissue
CT	computed tomography	NMD	neuromuscular disease
DMD	Duchenne muscular dystrophy	PDFF	proton density fat fraction
DWI	diffusion weighted imaging	PDWF	proton density water fraction
DTI	diffusion tensor imaging	SAT	subcutaneous adipose tissue
DXA	dual X-ray absorptiometry	SE	spine echo
EMCL	extra myocellular lipids	STIR	short-tau inversion recovery MRI sequence
FA	fractional anisotropy	T1w	a specific so called T-weighted MRI sequence
FF	fat fraction	T2w	a specific so called T2-weighted MRI sequence
IMAT	intermuscular adipose tissue	TMS	tetramethylsilane
IMCL	intra myocellular lipids	wb-MRI	whole body MRI
MD	mean diffusivity		

neuromuscular diseases (NMD) [15]. New MR imaging and spectroscopy techniques for NMD were also summarized in a workshop report of a funded COST action project (co-operation in science and technology) of the European Union "BM1304 MYO-MRI" [16].

In the last two decades interest in muscle imaging has been extended to muscle atrophy or muscle wasting caused by or associated with inactivity, denervation, fasting, malnutrition, chronic obstructive pulmonary disorder, cancer-associated cachexia, diabetes, renal failure, cardiac failure, Cushing syndrome, sepsis, burns and trauma [17]. Further areas of interest are the association of quantitative muscle parameters with back pain [18–21], myosteatosis [22] and sarcopenia [23,24]. The interdependence of myosteatosis and inflammation that propagates tissue degeneration is increasingly been recognized as an important component of aging and frailty [25,26].

The focus of this contribution is on technical aspects of quantitative MR techniques currently used to image skeletal muscle. Imaging of muscle perfusion and imaging of smooth and cardiac muscle is not considered. For comparison, a section on MR spectroscopy (MRS) is included. A comprehensive review of medical applications is beyond the scope of this article, only selected examples can be illustrated. Muscle size/volume and fat infiltration can also be measured with computed tomography (CT). One recent focus of muscle CT was on the prediction of osteoporotic fractures [27–32]. Techniques of quantitative muscle CT were covered by an earlier review [33].

2. Muscle fat infiltration

In muscle, lipids are either stored as adipocytes, with fat imaging characteristics, or as intramyocellular lipid droplets (IMCL: intramyocellular lipids). Adipocytes can be located sub fascial between muscle groups (perimuscular adipose tissue), or as interstitial (intramuscular) adipose tissue within an individual muscle as extramyocellular lipids (EMCL) (Fig. 1). T1w images provide good contrast between muscle and adipose tissue but IMCL and smaller EMCL aggregations are not visible in the T1w images.

Historically, in the thigh the combination of all visible adipose tissue (AT) below the deep fascia, be it perimuscular AT or larger EMCL aggregations has been denoted as intermuscular adipose tissue (IMAT) [25, 34]. Unfortunately, the term IMAT is used inconsistently throughout the literature. A different definition of IMAT was given in a recent Interdisciplinary Workshop at the National Institute on Aging, which stated that myosteatosis included three components "(a) intermuscular adipose tissue (IMAT), the extra-myocellular adipose tissue found beneath the fascia and in-between muscle groups; (b) intramuscular adipose tissue, the extramyocellular adipose tissue found within an individual muscle; and (c) intramyocellular lipids (IMCL)" [35]. According to this definition,

IMAT is equivalent to perimuscular AT as shown in Fig. 1 but does not include any intramuscular adipose tissue. Standardization of terminology is needed. In this contribution we will use IMAT in the traditional way and will divide the tissue beneath the fascia into IMAT, which in T1w images appears bright and muscle tissue (MT), which appears dark.

From an anatomical and physiological perspective muscle tissue is the contractile tissue, composed of cells, which can shorten or contract. This definition excludes all EMCLs. However, due to limited spatial resolution of in vivo imaging small EMCL aggregations cannot be visualized and cannot be separated from the contractile tissue. Thus, the term MT used in imaging is usually less strict as MT will contain smaller aggregations of non-contractile EMCL.

Skeletal muscle fat infiltration which is also known as myosteatosis [35] differs from sarcopenia, which according to the more recent definitions focusses on external muscle function, whereas myosteatosis focusses on the internal muscle property of fat infiltration [22].

3. MR spectroscopy

MRS of skeletal muscle is primarily used to assess the muscle metabolism using ³¹P-MRS or ¹³C-MRS to measure concentrations of high energy phosphates or muscular glycogen, respectively, or using ¹H-MRS to assess the muscle lipid composition [36–38]. An excellent summary of ³¹P- and ¹³C-MRS [16] and consensus recommendations for ³¹P-MRS of skeletal muscle [39] have recently been published. ¹H-MRS generates an intensity spectrum as a function of relative chemical shifts of lipid metabolites measured in ppm versus the universal reference, the methyl ¹H signal of tetramethylsilane (TMS), which is assigned a value of 0 ppm [40]. In this reference system water protons in living tissues resonate at ~4.7 ppm, EMCL at ~1.5 ppm and IMCL at ~1.28 ppm.

In MR imaging the chemical shift between water and fat is either used to suppress the fat signal and to selectively excite the water signal or for example in Dixon imaging (see section 6.2) to separate fat and water signals. However, very small chemical shift difference of ~0.2 ppm between EMCL and IMCL as well as between other liquid metabolites cannot be detected by Dixon imaging [36,41]. In contrast, MRS allows for a differentiation of IMCL and EMCL despite their similar chemical composition, due to small susceptibility effects of structural differences between the more spherical lipid droplets (IMCL) and the plate- or tube-like structures of EMCL [42]. The detection of these differences requires long acquisition times, thus the MRS signal is typically obtained from a small (≈ 1 cm³) volume of interest, the so-called spectroscopy voxel. Consensus recommendations on how to perform ¹H-MRS in skeletal muscle have been published recently [43].

One main difficulty of MRS is the repositioning of the spectroscopic voxel in the same anatomical location. Muscle is an elastic tissue and the



Fig. 1. Muscle fat infiltration shown schematically in the semimembranosus of the mid-thigh. The T1w image provides good contrast and shows the individual muscles separated by perimuscular adipose tissue (orange) and intramuscular adipose tissue (red). However, the amount of visible intramuscular adipose tissue depends on the spatial resolution and smaller aggregations of intramuscular adipose tissue either cause partial volume artifacts or cannot be detected in T1w images at all. The muscle tissue (dark) contains contractile tissue, and lipids, either as EMCLs and IMCLs that contribute to the fat faction signal in Dixon images. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

high and inhomogeneous muscle fat infiltration present in elderly and diseased subjects further complicates the reproducible positioning. This results in poorer precision compared to Dixon imaging (see section 6.2).). For comparison, precision is much less problematic in the liver, another organ for which Dixon imaging is frequently used, because liver is a more homogeneous tissue than skeletal muscle. A solution could be MRS imaging but applications in muscle are still rare [44–46].

¹H-MRS has been used in muscular dystrophies but is increasingly been replaced by Dixon imaging and T2 mapping [47–50]. Quantification of IMCLs is a powerful tool in exercise and nutrition research, for bioenergetics studies and for studies of insulin resistance [36,51].

4. MR imaging

4.1. T1 weighted sequences

T1w fast spin echo (SE) sequences have long been the dominant sequence in muscle imaging as they provide excellent contrast between muscle and adipose tissue (Fig. 2a), which is the basis for qualitative or semi quantitative radiological assessments. In combination with appropriate segmentation, T1w images are also used for the quantitative measurement of area or volume of tissue compartments such as subcutaneous adipose tissue (SAT), IMAT or MT. Compared to gradient echo sequences, SE sequences are less sensitive to susceptibility artifacts that can arise from fatty inflation. SE T1w sequences can be obtained with good spatial resolution ($0.5 \times 0.5 \times 3 \text{ mm}^3$) and in extremities a stack of 30 images can be obtained in less than 5 min (Table 1). The intensity values of T1w images vary among sequences and manufacturers. They can be used to guide the segmentation but they are of limited value with regard to other quantitative measurements.

T1w sequences are standard sequences, available on all MR scanners and easy to use. They are still a good choice for measurement of muscle volume and semiquantitative assessment of muscle fat infiltration, although this is also the realm of computed tomography, which due to faster scan times is less sensitive to motion artifacts. Whole body MRI (wb-MRI) sequences originally developed for oncologic screening are of interest for myopathies affecting a large variety of muscles throughout the body [52-54]. For such a scan, typically multiple coils are used to cover the whole body. As an alternative, separate scans along the body are stitched together.

4.2. Dixon imaging

T1w cannot be used to quantify muscle fat infiltration. This is the realm of Dixon techniques. If the advanced imaging and signal processing techniques described in the Technical Appendix are used to correct for confounding factors, Dixon techniques deliver parametric water and fat maps denoted as 'proton density fat fraction' (PDFF) and 'proton density water fraction' (PDWF) maps. 'PDFF is defined as the ratio of density of mobile protons from fat (triglycerides) and the total density of protons from mobile triglycerides and mobile water'. PDFF reflects tissue fat concentration and correlates with tissue triglyceride concentration but is not equivalent to mass fat fraction. PDFF has been suggested to be used as standardized MRI and MRS parameter to measure the tissue fat concentration [55]. Conversion of PDFF to absolute fat mass in grams has been reported [56]. For a given voxel, PDFF + PDWF = 1, as only water and fat protons contribute to the measured MR signal. In the presence of edema or fibrosis, PDWF differs from the absolute water content.

Depending on scanner model, intensity values of the PDFF map scale from 1 to 100 or from 1 to 1000 and linearly code the fat fraction from 1% to 100% or from 0.1 to 100%, respectively. An intensity range from 1 to 1000 provides higher sensitivity as PDFF differences of 0.1% can be resolved. In principle, tissue specific differences of the triglyceride spectrum have to be considered in the signal models of the advanced Dixon techniques but spectral differences observed in nonalcoholic steatohepatitis for example, had little impact on PDFF outcome [57]. In humans the triglyceride composition of subcutaneous adipose tissue and bone marrow did not differ for a given subject [58]. Nevertheless, the impact of differences in the triglyceride spectra of muscle and liver should be further investigated as most manufacturer implemented Dixon sequences used for muscle assessments are optimized for the liver.

In the liver multiple studies have reported PDFF accuracy [59] but



Fig. 2. T1w images of elderly subject with sarcopenia (top) and of young healthy subject (bottom). A: T1 weighted sequence, B: Dixon fat fraction sequence and C: Dixon water fraction sequence. The T1w image in A is affected by bias (upper left corner of the image in the upper row), Dixon fat and water images are also affected but this effect cancels out the PDFF and PDFW images (upper row B and C).

Table 1

Representative values of spatial resolution and acquisition time for MRI sequences for a 10 cm long scan of the mid thigh. Values apply to 1.5 and 3 T MRI scanners; for 1.5 T scanners similar values apply. Please note: covering 10 cm with T2 mapping and DTI using 5 slices with a thickness of 10 mm implies a gap of 10 mm between slices*values for 7 T scan of the calf.

Sequence	Resolution [mm ³]	No of slices	Acquisition time [min]	Typical applications
T1w	$0.5\times0.5\ x\ 3.0$	36	3–5	quantification of muscle volume and atrophy in sarcopenia and cachexia, semiquantitative assessment of fat infiltration in muscle myopathies
Dixon	$1.6 \times 1.6 \ x \ 3.0$	36	0.5–1	quantification of muscle fat infiltration in muscle myopathies and for body composition
Dixon high res.	$0.8\times0.8~x~3.0$	36	1-2	
T2 map (10 echos)	$1.3\times1.3x10.0$	5	2–4	quantification of muscle edema in muscle myopathies, muscle injury and exercise
T2 map (32 echos)	$1.3\times1.3x10.0$	5	3–6	
DTI	$1.3\times1.3x10.0$	5	4–6	quantification of muscle fiber architecture in exercise and muscle myopathies
39 K (AW-SOSt)*	$7.5 \times 7.5 \ge 30$	8	8-10	experimental
23Na (AW-SOSt)*	$2.5\times2.5 \ x \ 15$	16	8-10	experimental

studies in skeletal muscle are rare. PDFF accuracy is typically reported as correlation and bias between Dixon and MRS measurements where MRS serves as gold standard. Correlations between 6 pt Dixon and MRS of $r \ge 0.95$ and absolute differences in FF of $\le 5\%$ have been reported in vivo [60,61]. Absolute differences in FF among a variety of 2 pt, 3 pt, and 6 pt Dixon sequences implemented on a Siemens 3 T MAGNETOM Skyrafit were $\le 4.5\%$ with the exception of much higher inaccuracies of a 2 pt Dixon sequence that did not use exact in (2.4 ms) and out of phase (1.2 ms) echo times [62].

Dixon sequences have become the method of choice to quantify muscle fat infiltration. However, it is a limitation that IMCL and EMCL cannot be separated thus PDFF results contain contributions form IMCL that are vital for the energy metabolism of the cell, whereas fatty muscle infiltration attributable to EMCL has a negative impact on muscle function. Acquisition of Dixon images is faster than of T1w images (Table 1) but typically spatial resolution is inferior. Thus T1w images are often preferred over Dixon images for assessment of muscle volume and for muscle segmentation, although Dixon images can also be used for these tasks. As a disadvantage to Dixon, T1w images may be affected by bias (Fig. 2a) causing an inhomogeneous contrast across the images, which cancels out in the Dixon images.

Recently, whole body Dixon MRI has been developed for body

composition studies [63–66] as an alternative to whole body dual X-ray absorptiometry (DXA). In contrast to DXA, with a 3D imaging technique such as Dixon MRI, fat and water fractions of individual organs and muscles can be quantified separately. However, it should be considered whether separate MR acquisitions that can be optimally adapted to a given anatomical region are advantageous to a whole body MRI scan [67].

4.3. T2 maps

In addition to PDFF, T2 relaxation times are increasingly used as a quantitative MR marker for disease activity in skeletal muscle tissue in part replacing STIR sequences that have been used for semiquantitative assessment of edema [68,69]. Skeletal muscle edema can be caused by trauma and is also observed in early myositis ossificans and inflammatory myopathies. Edema results in increased muscular T2 relaxation times and is an indicator for inflammatory processes, which often precede the replacement of muscle tissue by adipose tissue [70]. Alterations in T2 are generally non-specific, however, they can represent the intensity of underlying pathological changes [71]. To assess T2 in skeletal muscles, multi-spin-echo (MSE) sequences are commonly used. Different fitting approaches have been proposed to evaluate the resulting signal evolution

and determine the T2 relaxation times.

The simplest approach is to fit a mono-exponential signal decay (Figure-A 1), which results in an overall, so-called "global T2 relaxation time" [71]. This global T2 represents an average of all compartments within the muscle, containing both muscle and adipose tissue. It highly depends on the amount of fat infiltration, as lipids possess significantly longer T2 times than (muscle) water. For example, at 3 T, T2 of muscle water (T2_{water}) in the range of 25–30 ms and T2 of fat (T2_{fat}) of approx. 150 ms have been reported [72]. Thus, an enhanced intramuscular FF results in an increased global T2 [73]. This effect is particularly prominent in subjects with a high amount of intramuscular fat such as patients with neuromuscular disorders [73,74]. Increases in global T2 due to fat infiltration may even mask actual pathological changes in T2_{water}, which are usually relatively small (approx. 10 ms) [71].

Different approaches have been proposed to selectively determine the T2 of muscle water in the presence of fat infiltration. For example, the water signal can be selectively excited or the signal of fat can be suppressed using conventional fat suppression techniques [70,75]. However, the quality of fat suppression usually relies on correct flip angles and therefore fails in regions of an inhomogeneous transmit (B1+) field. Another approach is multi-exponential T2 fitting [73] described in detail in the Technical Appendix.

4.4. Diffusion weighted imaging

Diffusion-weighted imaging (DWI) maps the thermal energy related random motion of water molecules. Outcome is the water diffusion rate [76]. However, in a tissue like muscle impermeable or semi permeable walls around the muscle fibers and other structures restrict the diffusion of molecules. This restriction is anisotropic. In mathematical terms it is described by a 3 \times 3 matrix called the diffusion tensor D as described in detail in the Technical Appendix. Diffusion tensor imaging (DTI) [77] is an extension of DWI to determine the degree of anisotropy of the diffusion. Further outcomes of DTI are the mean diffusivity (MD) also termed apparent diffusion coefficient (ADC) and the fractional anisotropy FA as described in more detail in the Technical Appendix. DTI is an important technique for quantification of muscle fiber architecture because water diffusivity in the axial muscle fiber directions higher than in the radial fiber direction [78,79]. ADC and FA values for various muscles have been published [80-83]. In edematous muscle diffusivity in both, axial and radial directions, and FA are increased compared to healthy muscle [82-84] indicating the relevance of DTI in inflammatory myopathies [83, 85], although no effect of myositis on ADC or FA has been observed in a recent study [86]. Discrepancies have also been reported in patients with Duchenne Muscular Dystrophy (DMD): higher ADC and lower FA values compared to healthy subjects in one [87] and opposite effects in other studies [81,88]. Reasons are lower ADC in adipose tissue compared to skeletal muscle [79,85] and impact of noise on FA values [78,89]. Consequently, it has been suggested to combine assessments of water T2, PDFF and signal to noise ratio for a correct interpretation of DTI measures [90].

For DTI image acquisition typically a single-shot diffusion weighted SE echo planar imaging (EPI) pulse sequence is used. As described above, DTI assessments are affected by the amount of adipose tissue, thus fat suppression is required in DTI. Accuracy further depends on acquisition parameters such as TE, TR or voxel size and age, sex or BMI. Further details have been addressed in recent reviews [91–93].

DTI is still not widely used for or muscle imaging. Examples in addition to myopathies discussed above are changes in muscle diffusivity associated with denervation [94], metabolic disease [95,96] muscle fiber tears [97,98], and differences in muscle diffusivity between osteoporotic and osteoarthritic subjects [99]. Another interesting field is the relation between muscle properties and external muscle strength that has important implications for optimizing training effects in athletes and for exercise or pharmaceutical interventions in sarcopenia and frailty [100–106].

Given adequate image quality of the DTI dataset [92,107] special algorithms can be applied to visualize the 3D muscle fiber architecture (Figure-A 2) or to be more accurate, to visualize the diffusivity in the axial muscle fiber direction. With this method termed tractography also parameters such as pennation angle, fiber length and curvature, and physiological cross-sectional area, which is the muscle area perpendicular to its fibers, can be quantified. Obviously, interpretation of results must consider that fiber tractography is not a real representation of muscle structure but a computational estimation. Applications of tractography used in trunk or leg muscles may have great potential in assessing the risk of falls and related fractures.

4.5. Non-proton MRI methods

Non-proton MRI techniques can provide valuable insights into the composition of muscle tissue [113]. For example, ²³Na MRI enables the quantitative measurement of the tissue sodium concentration (TSC), and, thus can provide important information about the tissue ion homeostasis. One of the main regulators of the tissue ion homeostasis is the Na⁺/K⁺-ATPase (or Na⁺/K⁺-pump). In healthy tissue, the Na⁺/K⁺-ATPase helps to maintain a concentration gradient between intra- ([Na⁺]_{in} = 10–15 mmol/L) and extracellular sodium ([Na⁺]_{ex} = 145 mmol/L), which is of utmost importance for the excitation and inhibition of muscle cells.

The TSC is a volume-weighted average of intra- and extracellular sodium concentrations. For healthy muscle tissue, a mean intracellular volume fraction of approximately 0.92 can be assumed [114]. This results in a TSC of 21–25 mmol/L. Changes of the intracellular sodium concentration, or slight changes of the intracellular volume-fraction can result in large TSC changes, which can be assessed by ²³Na MRI. In addition to TSC measurements, relaxation-weighted ²³Na MRI techniques such as ²³Na inversion recovery MRI can be applied to achieve a weighting of the contrast towards the intracellular sodium [115]. ²³Na MRI of skeletal muscle tissue has been applied in several clinical research studies [115–117]. For instance, sodium anomalies were observed in patients with DMD, and were present even in absence of fatty degenerative changes and water T2 increases [118].

Using dedicated ultra-high field MRI systems ($B_0 \ge 7$ T), also other ions such as potassium or chloride can be investigated using ³⁹K or ³⁵Cl MRI to provide a more comprehensive analysis of the tissue ion homeostasis [119,120]. However, so far, ³⁵Cl and ³⁹K MRI of skeletal muscle tissue have only been performed in small feasibility studies [121–123].

4.6. MR elastography

In clinical practice, the manual examination of palpation is frequently used for the qualitative assessment of biomechanical tissue properties. MR elastography (MRE) enables quantitative evaluation of these biomechanical tissue properties. In MRE, shear waves that are typically introduced by a vibrating actuator, are imaged with a motion-sensitive MRI sequence [124]. A detailed description of principles and guidelines for MR elastography can be found in Ref. [125]. Applications of MRE to skeletal muscle research has recently been summarized [16]. For example, it has been shown that altered elastic properties of dystrophic muscle of patients with DMD can be detected by MRE [126,127].

5. Muscle analysis and quantitative parameters

5.1. Muscle segmentation

Quantitative muscle measurements such as fat fraction, or T2 water require a prior segmentation. The general trend from analysis of single towards analysis of multiple slices, for example covering the whole thigh, requires a higher degree of automation to limit overall operator efforts. A number of muscle segmentation algorithms have been developed in particular for NMD [128,129] but comparison of performance is difficult because of differences in acquisition parameters, sequences and assessments. One strategy used in subjects with sarcopenia, is to segment the *fascia lata* (of the thigh) or *fascia cruris* (of the calf) and then separate IMAT and muscle tissue within the fascia. In this case segmentation of individual muscles is not performed. Segmentation of individual muscles is usually required for NMD as muscles are affected differently by the disease [4,130,131].

One example workflow is outlined in Fig. 3. The T1w dataset is used for an automatic segmentation of the fascia lata. The segmentation map is then transferred by 3D co-registration to a Dixon fat fraction map where segmentation of IMAT and muscle tissue is performed (Fig. 4). Finally, T2 water results are obtained in muscle tissue using a T2 map (Fig. 3 right) 3D registered to the Dixon fat fraction map. This workflow demonstrates a number of important requirements of advanced MR muscle analysis. First, the combination of multiple MR sequences, which typically have different spatial resolutions and which may also be affected by subject motion between acquisitions requires sophisticated 3D registration algorithms. Second, a differentiation of SAT and IMAT, which was not performed in earlier studies of the thigh [132] requires a segmentation of the fascia lata, which is hardly visible in Dixon images. Thus T1w may be preferable for the segmentation of the fascia lata although it is still difficult to track in T1w images. In younger subjects (Fig. 2a) a tight muscle envelope, which is relatively easy to segment [133-136], can be used as substitute of the fascia lata. However, in elderly subjects the fascia lata is no longer in overall contact with muscle but locally separated by layers of adipose tissue (Fig. 5). Recently advanced semi-automatic [137,138] as well as deep learning based [139,140] fascia segmentation procedures with good accuracy and precision have been developed but current deep learning models are based on rather small amounts of training and validation data. Thus they are still very specialized and further validation of more general models is needed.

In a second workflow shown in Fig. 6 individual muscles are manually segmented in the T1w images and segmentation masks are 3D registered to Dixon maps. In the Dixon image a PDFF threshold is applied to differentiate muscle and adipose tissue of each segmented muscle. Obviously the manual segmentation of multiple slices is challenging but high agreement among experts with ICC values of >0.94 in the thigh [141–143] and of >0.98 in the spine [144] have been reported. An excellent review of segmentation of individual muscle has recently been published [128]. So far in NMD, the performance of automated segmentation techniques was poor because of varying degrees of replacement of muscle by adipose tissue. However, recently accurate results with Dice ratios of around 0.9 when comparing of automated and manual segmentation results have been reported [138,139,145,146].

A third workflow (Fig. 7) shows the segmentation of paraspinal muscles, left and right psoas and erector spinae muscles of the lumbar spine. In some publications multifidus, longissimus and ilocostalis lumborum of the erector spinae are further differentiated [147–149] and the quadratus lumborum has also been analyzed [150,151]. Depending on available data and parameters to be quantified other workflows may be preferable to the ones discussed above.

5.2. Quantitative measurements

Table 2 lists common parameters to quantify muscle properties with MRI or MRS. Muscle area/volume can be obtained directly from T1 weighted images, which provide good spatial resolution but are often affected by inhomogeneity artifacts, which as shown in Fig. 3 may still persist after bias correction using N3 or N4 algorithms [152]. Also T1w grey values are not standardized or normalized, which complicates any threshold based segmentation. A large variety of methods to determine muscle area/volume have been published [153]. For comparability absolute measurements such as volume or area should be normalized, for example to body height or in the thigh to the leg volume/diameter. IMAT and muscle tissue volume could also be normalized to the fascia volume [154]. PDFF, T2_w, T2_f, and TSC values are measured directly in the corresponding images as mean intensity values, however, as outlined in the preceding sections, these sequences require dedicated signal reconstruction or post processing to generate the specific parameter maps.

For the differentiation between adipose and muscle components a threshold applied to a Dixon PDFF map and sometimes even to T1w images has been used. For example, a 50% PDFF threshold [155,156] has been suggested but in healthy and even sarcopenic subjects this seems high as muscle tissue PDFF is below 20%. One level of sophistication is the use of subject adaptive thresholds obtained from a histogram analysis [137,157,158] but different threshold techniques may result in large differences in IMAT volume [159]. Other authors have developed k-means clustering [160] or fuzzy c-means algorithms [161] to differentiate IMAT and muscle tissue. A comparison of more advanced methods such as level sets, Gaussian mixture models, graph cuts and shape prior level sets showed that the choice of the best method depended on the severity of fat infiltration [162].

It is important to note that analysis results depend on spatial resolution as shown for IMAT and muscle tissue in Fig. 4. In vivo imaging is always affected by partial volume artefacts caused by small agglomerations of adipocytes. Thus PDFF of those muscle tissue voxel located at the border with IMAT will be too high and a peeling operation of the muscle tissue VOI before calculation of PDFF may be indicated but here further research and standardization is required.



Fig. 3. Left: T1 weighted sequence after bias correction, with segmented fascia lata (pink); center Dixon fat fraction map after 3D registration to T1w sequence and registration of fascia lata. Right: T2 map after registration to Dixon sequence. One axial slice of 3D dataset shown each. Bias correction did not remove all artifacts in the T1w image.



Fig. 4. Dixon fat fraction map without (top) and with (bottom) segmentation of IMAT and muscle tissue. Left: high resolution (in plane pixel size x slice thickness - $0.98 \times 0.98 \times 3.0 \text{ mm}^3$); center: standard resolution ($1.56 \times 1.56 \times 3.0 \text{ mm}^3$); right: same resolution as center but muscle tissue peeled by one voxel. The figure shows one slice out of 29 of the acquired 3D dataset. Results of the complete dataset for muscle tissue (MT) volume and proton density fat fraction (PDFF) depend on spatial resolution and on segmentation technique. Left: MT vol = 985 cm³, PDFF = 8.7%; center: MT vol = 923 cm^3 , PDFF = 13.2%; right: MT vol = 500 cm^3 , PDFF = 10.2%.



Fig. 5. In elderly subjects the fascia lata is not always in direct contact with muscle but partly separated by layers of adipose tissue (pink), which are part of intermuscular adipose tissue (IMAT). A tight muscle envelope excluding most or all of the pink ROI would significantly decrease the volume of IMAT (yellow). In younger subjects Fig. 2a there is no or very little adipose tissue located between muscle and fascia. (For interpretation of the references to color in this figure legend, the reader is referred to the Web version of this article.)

6. Muscle imaging in clinical trials

Muscle MRI has been increasingly used for quantification of muscle

properties in longitudinal studies to evaluate efficacy of therapeutic interventions or to document disease effects over time [163–170] Only a few multicenter trials have been published [171–176]. Outcome of clinical trials is typically the comparison of percentage change over time between a treated and a control group for a given quantitative parameter such as PDFF. Minimization of longitudinal precision errors is of high importance. Low accuracy errors are important to compare assessments across scanners but as long as accuracy errors do not change longitudinally their impact on a clinical trial endpoint is less relevant. Precision errors for parameters listed in Table 2 are summarized in Table 3.

In designing multicenter trials special challenges must be considered so that imaging is performed in a consistent manner when utilizing scanners from different manufacturers with different field strength. The design of MRI subject positioning procedures, sequence parameters, and data analyses must be standardized to ensure that imprecision does not mask the expected physiological change.

Change in muscle tissue volume over time specifically in the thigh has been the main MRI based biomarker used in single- and multicenter trials. MRI data acquisition for this task can be easily standardized across multiple sites as it does not require advanced sequences or modern hardware. Spin echo-based sequences should be used either for a set number of slices acquired at the center of the muscle or for the entire length of the muscle bundle. Spin echo sequences are superior to Gradient recalled echo sequences in producing sharper images, because they are less sensitive to susceptibility artifacts that can arise from fatty inflation [185]. Axial images with an in-plane resolution close to 1 mm and 5–8 mm slice thickness in the thighs have been used [186], as compared to approximately 0.5–0.75 mm and 2–4 mm slices in the arms and calves [187].

Fat fraction is another biomarker that has been implemented in multicenter trials. 2 pt Dixon based approaches are widely available but not all sites participating in a multi center trial may have used them in clinical routine. Sometimes the Dixon sequence still must be set up on a scanner, which typically requires tuning and optimization. Dedicated training of the technicians performing the muscle scans may also be required Three or more echoes have been used [60] but these sequences



Fig. 6. Left: Manual contouring of individual muscles (here: vastus medialis, rectus femoris and biceps femoris) in T1 weighted sequence; center Dixon FF map after 3D registration to T1w sequence and registration of muscle contours. Right: Threshold based separation of muscle tissue and adipose tissue compartments of each segmented muscle.



Fig. 7. Segmentation and analysis of paraspinal muscles of the lumbar spine. Left. T1w images with segmented psoas, erector spinae and quadratus lumborum muscles; right: Dixon FF map 3D registered to T1w sequence and registered segmentation maps.

Table 2

Determination of common quantitative muscle parameters by technique. ADC: apparent diffusion coefficient; DTI: diffusion tensor imaging; EMCL: extramyocellular lipids; FA: fractional anisotropy; IMAT: intermuscular adipose tissue; IMCL intramyocellular lipids; MRS: magnetic resonance spectroscopy; PDFF: proton density fat fraction; T2_w: T2 water [ms]; T2_w: T2 fat [ms]; *DTI based tractography.

Parameter	T1w	Dixon FF	T2 map	DTI	MRS
SAT area/volume (cm ² /cm ³)	++	+	+/-	_	
muscle area/volume (cm ² /cm ³)	++	+	+/-	_	
IMAT area/volume (cm ² /cm ³)	+	++	+/-	_	
muscle tissue area/volume (cm ² /cm ³)	+	++	+/-	_	
intra fascia PDFF (%)	_	++	_	_	
muscle tissue PDFF (%)	_	++	_	_	+
T2 _w (ms)	_	_	++	_	
T2 _f (ms)	_	_	++	_	
EMCL (mmol/kg)	_	_	_	_	++
IMCT (mmol/kg)	_	_	_	_	$^{++}$
ADC, FA				$^{++}$	
pennation angle, curvature, fiber length, and physiological cross- sectional area				++*	

are not as widely available as 2 pt Dixon sequences. For a multi-center trial the scan of a phantoms to evaluate the accuracy of the fat fraction maps and to determine if water/fat swap artifacts occur is recommended [178]. A simple fat and water phantom suffices to configure the sequence but phantoms with a larger range of fat fractions such as the PDFF phantom from Calimetrix (Calimetrix, Inc, Madison, WI, USA) could be useful (Fig. 8). In a recent multicenter study with different scanner types initiated by the PDFF Biomarker Committee within the Quantitative Imaging Biomarkers Alliance (QIBA) of the Radiological Society of North America, PDFF accuracy errors were below 5% [188].

T2 mapping is even more challenging to implement in multicenter trials due to the variability in the implementation of the MSE sequences

among different manufactures. On many scanners the number of echos is limited preventing the fit of multi exponential fits (see section on T2 maps). Thus $T2_w$ and $T2_f$ cannot be differentiated. As a consequence, fat suppressed T2 sequences must be used. However, fat suppression is usually not perfect and accuracy of $T2_w$ is lower than with non-fat suppressed T2 sequences. For these around 20 echos are required, which is only feasible with modern scanners.

7. Future directions

Quantitative MR imaging techniques have significantly matured during the last decade, however, assessments must be better standardized. Even the terminology with respect to IMAT is not unequivocal. The clinical interpretation of outcome parameters is not always obvious and small differences in segmentation algorithms may have a significant impact on numerical results. There is a lack of data on accuracy and precision. Given the large variety of MR sequences and implementation differences between manufacturers, standardization of accuracy measurements is of high importance. One potential avenue is the use of phantoms, as demonstrated in a recent PDFF study [188] but these efforts must be extended to all the techniques described above. Also, mid- and long-term stability of phantoms, which often contain fluids, is still questionable.

Further, gender and ethic specific normal data such age-related changes of quantitative outcome parameters are required for putting intervention effects into perspective. Very little data have been published [189–194] so far. Published data on precision, which are summarized in Table 3 are encouraging but it remains to be shown whether these data typically obtained in very experienced research centers can be achieved in clinical routine or in multicenter trials. Currently, multicenter trials with quantitative endpoints are rather difficult to conduct in particular if scanners from different manufactures or even of different makes from a given manufacturer are used. Missing standardization of installed MR sequences and available coils further complicates and increases cost of such trials.

K. Engelke et al.

Table 3

Precision errors of quantitative parameters shown in Table 2. The time period between repeated measurements is indicated in column 'Period'. ST: short term (same day); the digit after ST denotes the number of total acquisitions;/repos: subjects were repositioned between acquisitions. Depending on publication, precision errors are either reported as root mean square coefficient of variation (CV_{RMS}) in % [177] or as intraclass correlation coefficients (ICC). IF: intra fascia; PDFF: proton density fat fraction; wb: whole body.

ref	parameter	Anatomy	technique	population	Period	Statistics	Value
[178]	SAT volume	abdomen	2 pt wb Dixon	18 subjects ♂ & ♀	ST 2	%CV	4.4
				age range 24–51	5 different scanners		
[179]	IF muscle area	thigh	T1w	14 subjects ♂ & ♀	ST 3	%CV _{RMS}	1.3
	muscle area	hip adductor		age range 21–68			1.6
		hip flexor					1.8
[178]	muscle volume	total thigh	2 pt wb Dixon	18 subjects ♂ & ♀	ST 2	%CV	0.87
				age range 24–51	5 different scanners		
[180]	muscle tissue volume	thigh adductors	2 pt wb Dixon	16 subjects ♂ & ♀	4–12 weeks	%CV	3.4
		quadriceps		age range 23–65			3.5
		spinus erectae					7.0
[181]	muscle tissue volume	thigh	T1w	20 subjects ♂ & ♀	ST 2/repos	ICC	0.996
				age range 25–76			
[182]	muscle tissue volume	thigh	6 pt Dixon	23 young healthy ♂	ST 2/repos	%CV _{RMS}	1.2
				24 elderly sarcopenic ♂			1.5
[178]	muscle fat infiltration	anterior/posterior lef/right thigh	2 pt wb Dixon	18 subjects ♂ & ♀	ST 2	%CV	10.8-14.4%
				age range 24–51	5 different scanners		
[182]	IF PDFF	thigh	6 pt Dixon	23 young healthy ♂	ST 2/repos	%CV _{RMS}	2.1
				24 elderly sarcopenic ♂			1.6
[183]	IF PDFF	thigh	4 pt Dixon	65 young healthy ♂ & ♀	ST 3	ICC	0.999
[184]	IF PDFF	thigh	3 pt Dixon	14 young healthy ♂ & ♀	2 weeks	ICC	0.91
		calf					0.89
[182]	muscle tissue PDFF	thigh	MRS	23 young healthy ♂	ST/repos	%CV _{RMS}	15.3
				24 elderly sarcopenic ♂			9.0
[183]	T2 _w	thigh	T2/17 echos	65 young healthy ♂ & ♀	ST	ICC	0.986
[183]	ADC	thigh	DTI	65 young healthy ♂ & ♀	ST	ICC	0.963



Fig. 8. Phantoms for calibration of Dixon sequences. Top: Clario FF phantom with pure water and fat inserts; bottom: Calimetrix PDFF phantom with 5 inserts containing 0, 10, 20, 30, and 40% fat fraction.

It is a promise to clinicians that via the use of quantitative MRI using PDFF and T2_w maps muscle disease can be diagnosed earlier than with standard techniques. PDFF and T2_w are related to inflammatory processes preceding muscle fat infiltration and destruction. DTI and perhaps ²³Na MRI, which probe pathophysiological changes at the cellular or

fascicular level, hold some promise to allow for diagnosis at even earlier stages of the disease and eventually may allow for design of personalized interventions. The use of multiple MRI scans such as T1w, Dixon and T2 maps has been reported in many studies but overall scan time should be shortened, sequences should have similar spatial resolution and a common reference system so that they can easily be registered together.

The association of quantitative MRI parameters with muscle function warrants further investigations. In NMD, for example many cross-sectional studies have demonstrated clinically relevant correlations between MRI and muscle function but only a few studies have presented longitudinal results [130]. Even less is known on how age or for example exercise related changes of MRI parameters can predict direct changes in muscle strength. In normal or sarcopenic subjects muscle strength can be rapidly increased by about 30% through exercise. Thus exercise is an important intervention for sarcopenia but its pathophysiological effect on muscle is still difficult to evaluate. First studies have shown the potential of DTI based fiber tractography.

In summary, quantitative MRI provides new avenues for significant advances in muscle research using in vivo imaging but standardization of almost all of its procedures combined with a tighter integration of the analysis into the workflow will be key to its more widespread clinical use.

15 Technical Appendix

15.1 Dixon Imaging

Author contributions

Each author contributed manuscript text according to his or her specific expertise. KE assembled all text blocks into the final manuscript, which was reviewed, edited and approved by all coauthors.

Funding

There was no specific funding available for this study.

Declaration of competing interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest. KE is a part time and MABE a full time employee of Clario, Inc.

In 1984, Dixon introduced a 'simple proton spectroscopic imaging' technique [195], which decomposes fat and water components of the proton signal into two separate image maps by exploiting the difference in resonance frequencies between fat and water protons (chemical shift). Dixon showed that there is an oscillation of the free induction decay (FID) of the magnetization of a voxel containing fat and water after a 90° pulse. At the start (t = 0) of the free induction decay the magnetization vectors of water and fat point in the same direction (IP: in phase. The first minimum of the FID occurs at t_{min1}

$$t_{\min 1} = \frac{1}{2(\nu_w - \nu_f)}$$

at t_{min1} magnetization vectors of water and fat point in opposite direction (OP: opposed phase). ν_w and ν_f are the Lamor frequencies of water and fat, respectively. The chemical shift between water and fat is ≈ 3.4 ppm which translates into $\Delta \nu = \nu_w - \nu_f \approx 220$ Hz at 1.5 T and $\Delta \nu \approx 440$ Hz at 3 T.

In theory the sum of IP and OP images divided by 2 results in a so-called water image and the difference divided by 2 in a so-called fat image. Fat fraction (FF) and water fraction (WF) images can then be calculated as:

FF = fat image/(fat image + water image)

WF = water image / (fat image + water image)

In reality, fat quantification accuracy of the simple IP-OP approach is impaired by magnetic field inhomogeneities, $T2^*$ -decay, T_1 -bias, spectral complexity of fat, noise bias and eddy currents [164,196–200]. Magnetic field inhomogeneities for example increase the probability of wrong phase assignments which cause local fat-water swaps [201–203]. These limitations have triggered significant improvements of the original 2 pt Dixon technique incorporating more sophisticated signal models such as the use of flexible echo times [61,197,204,205] and the introduction of 3 pt or 6 pt echo techniques [206–210]. With these advanced Dixon techniques exact IP and OP imaging is no longer required [211–213]. Another area of improvement is signal processing. For example, the T2* decay caused by increasing echo times after RF excitation can be corrected by incorporation of T2* into the signal model used to calculate the fat fraction [214–218].

15.2 T2 maps

Multi-exponential T2 fitting [73] exploits the strong differences in relaxation times between water and fat. The total signal decay is modeled as a combination of the individual water and fat signals, weighted by the respective volume fractions. The fat signal is further assumed to consist of multiple components possessing different relaxation properties. For example, a tri-exponential T2 model (Figure-A 1) assumes two dominant fat components, one possessing a shorter relaxation time (T2_{s,fat}) and a signal fraction of $f_{s,fat}$ possessing a longer relaxation time (T2_{l,fat}) and a contribution of (1- $f_{s,fat}$). The total resulting signal is therefore [73]:

$$S = S_f \left(f_{s,fat} \exp\left(-\frac{TE}{T2_{s,fat}} \right) + \left(1 - f_{s,fat} \right) \exp\left(-\frac{TE}{T2_{l,fat}} \right) \right) + S_w \exp\left(-\frac{TE}{T2_{water}} \right).$$

here, S_f and S_w describe the overall signal intensities of fat and water, respectively. As this model requires the determination of several fit parameters, it is unstable if only a limited number of echoes are acquired. Therefore, relaxation parameters of adipose tissue are usually determined first, e.g. within subcutaneous fat or bone marrow, and then fixed in the tri-exponential model to enhance fit stability [73]. However, multi-exponential fitting models generally do not consider inhomogeneities in the B1 field as well as stimulated echoes [219], which can influence the resulting T2 values.

To overcome these limitations, T2 fitting exploiting extended phase graphs (EPG) has been proposed [220]. Using the EPG approach, the signal evolution is simulated for various combinations of T2 as well as relative B1 and FF values. Then, a mapping of the measured signal decay to the

simulated curves is performed to find the corresponding parameters for each voxel [220,221]. By including B1 in the simulation, EPG approaches offer higher stability with respect to an inhomogeneous transmit field, and correct for stimulated echoes. Recent implementations of EPG T2 fitting also consider the slice flip angle profiles and chemical shift displacement in slice direction, enabling a reliable T2 determination even in case of large FF > 50% [222].

15.3 Diffusion tensor imaging

Diffusion tensor imaging (DTI) [77] is a technique to determine a map of the six components of the diffusion tensor D with its eigenvalues λ_1 , λ_2 and λ_3 [223]. The magnitude of the eigenvectors characterizes the degree of anisotropy of the diffusion, which in the axial muscle fiber direction (λ_1) is higher than in the radial fiber direction (λ_2 and λ_3). Further outcomes of DTI are MD also termed apparent diffusion coefficient (ADC) and the fractional anisotropy FA as given by the formulas below

$$D = \begin{cases} D_{xx} & D_{xy} & D_{xz} \\ D_{yx} & D_{yy} & D_{yz} \\ D_{zx} & D_{zy} & D_{zz} \end{cases} \quad \text{with } D_{xy} = D_{yx}; \ D_{xz} = D_{zx}; \ D_{yz} = D_{zy} \end{cases}$$

$$MD = ADC = \frac{\lambda_1 + \lambda_2 + \lambda_3}{3} = \overline{\lambda}$$
$$FA = \sqrt{\frac{2}{3}} \cdot \sqrt{\left[\left(\frac{(\lambda_1 - \overline{\lambda})^2 + (\lambda_2 - \overline{\lambda})^2 + (\lambda_3 - \overline{\lambda})^2}{\lambda_1^2 + \lambda_2^2 + \lambda_2^2} \right) \right]}$$



15.4 Appendix - Figures

Fig. A1. T2 maps and corresponding Dixon FF maps of a subject with lower and a subject with higher muscle tissue FF (patient 1, mean FF = 4.9%; patient 2, mean FF = 13.1%). In subject 2 with higher FF, T2 values are elevated, particularly in the vendor-provided T2 map, but also in the mono-exponentially fitted T2 map. In contrast, T2 values were similar for both patients in the tri-exponential T2 map. Moreover, within the thigh muscle of subject 1, a variation could be observed between individual muscles in the product T2 map, which was not present in the custom-fit T2 maps.



Fig. A2. Illustration of paraspinal muscle fibers of a rat using tractography.

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K. Engelke et al.

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K. Engelke et al.

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