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COMPARISON OF 3D T2-WEIGHTED SEQUENCE WITH CONVENTIONAL 2D MRI SEQUENCES IN THE ASSESSMENT OF SHOULDER JOINT PATHOLOGIES

Radio-Diagnosis

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ABSTRACT

Background: Conventional 2D MR protocol routinely used in the institutions for assessment of shoulder joint pathologies have good tissue contrast and in-plane spatial resolution, but they must be repeated in several planes which takes more examination time, and the thicker slices can miss some pathologies due to partial volume averaging. Instead, procuring thin slices is possible with 3D acquisition and can be post-processed into other planes using multiplanar reformation techniques, thereby reducing overall examination time and provides good patient compliance, fewer motion artefacts. This study's goal is to determine the agreement between conventional 2D sequences and 3D T2 weighted sequence in the assessment of rotator cuff and other shoulder joint pathologies. **Methods:** 50 patients with suspected shoulder joint pathologies were examined with 2D and 3D protocol in the same session. In the assessment of shoulder joint pathologies, agreement between T2-weighted 3D sequence and conventional 2D sequences is evaluated with kappa statistics. Diagnostic accuracy of T2-weighted 3D sequence with conventional 2D sequences as standard of reference is evaluated using McNemar and Chi square test. **Results:** Perfect agreement (k=1.00) between 2D and 3D sequences seen in the assessment of full thickness tears of supraspinatus and infraspinatus, partial thickness tears of subscapularis, tendinitis of rotator cuff muscles, biceps tendon, AC joint, bursitis and joint effusion. Strong agreement is seen with assessment of partial thickness tears of supraspinatus (k=0.811), moderate agreement with articular cartilage lesions (k=0.79) and bone marrow edema (k=0.779). **Conclusion:** Perfect agreement is seen between 2D and 3D sequences in the assessment of most of the rotator cuff and other shoulder pathologies in our series. With 3D sequence being capable of reducing overall examination time, it provides more patient compliance and reduced motion artefacts. We recommend further studies with arthroscopy as gold standard before relying purely on 3D sequence for shoulder evaluation.

KEYWORDS

shoulder, rotator cuff, 2D, 3D

INTRODUCTION

The shoulder joint is one of the most frequent sites of musculoskeletal pain of which rotator cuff disease accounts for approximately half to two-thirds of these shoulder discomfort patients (1). Rotator cuff diseases include impingement, tendinopathy and tear. According to the extrinsic theory, acromioclavicular joint hypertrophy causes impingement on the rotator cuff tendons and eventually leads to tendon tears, whereas the intrinsic theory quotes tendon degeneration as the cause.

In MR imaging, many institutions use 2D sequences for the assessment of shoulder joint pathologies. Although the 2D sequences give good tissue contrast and in-plane spatial resolution, they must be repeated in several planes in order to visualize the joint, which takes more examination time, and the thicker slices can miss some pathologies due to partial volume averaging. On the other hand, procuring thin slices is possible with 3D acquisition and also reduces the total examination time as the single 3D sequence can be post-processed into other planes using multiplanar reformation techniques. Due to reduced examination time with 3D protocol, there are more chances of good patient compliance and fewer motion artefacts (2) (3).

Current literature showing 3D sequence to have substantial concordance with conventional 2D sequences for most shoulder joint pathologies needs more studies so as to determine the clinical reliability and feasibility to implement the usage of 3D protocol alone in our daily clinical practice in our hospital settings. Hence, this study's goal is to determine the agreement between conventional 2D sequences and 3D T2 weighted sequence in the assessment of rotator cuff and other shoulder joint pathologies.

AIM & OBJECTIVE

To determine the agreement between 3D T2-weighted sequence and conventional 2D sequences in the assessment of rotator cuff tears and other shoulder joint pathologies.

MATERIALS & METHODS

50 patients with suspected shoulder joint pathologies were examined with a 2D and 3D protocol on the same side and during the same session on a 1.5 T machine. The diagnostic study is conducted over a period of 2 years (2020 to 2022) in the Department of Radiology, AIMS, Kochi.

Table 1 1.5T 2D MR Imaging Protocol

1.5T 2D MRI Parameters	Coronal PD FS	Axial PD FS	Sagittal PD FS	Coronal T1
TR (msec)	2550	2583	2600	620
TE (msec)	42	42	42	Minimum
FOV (cm)	14x16	14x16	14x16	14 x 16
Slice thickness (mm)	4	4	4	4
Spacing (mm)	0.5	0.5	0.5	0.5

Table 2 1.5T 3D MR Imaging Protocol

1.5T 3D MRI Parameters	Coronal CUBE T2
TR (msec)	2500
TE (msec)	143
FOV (cm)	28
Slice thickness (mm)	1.4
Spacing (mm)	0
Echo train length	100 echoes
Slab	1

In the assessment of shoulder joint pathologies, the agreement between T2-weighted 3D sequence and conventional 2D sequences was evaluated with kappa statistics. Diagnostic accuracy of T2-weighted 3D sequence with conventional 2D sequences as the standard of reference is evaluated using McNemar and Chi square test with the help of validity parameters such as sensitivity(Sn), specificity(Sp), accuracy, negative predictive value (NPV) and positive predictive value (PPV). A p-value of <0.05 was considered statistically significant.

RESULTS

I. Agreement Between 2D And 3D Sequences In The Assessment Of:

1) Full Thickness Tears: All the full thickness tears of supraspinatus (27 out of 50) and infraspinatus (10 out of 50) are evident both on 2D and 3D sequences showing perfect agreement (k=1.00) between 2D and 3D sequences which is statistically significant (p value <0.001).

2) Partial Thickness Tears: 7 out of 50 patients are shown to have partial thickness tears of supraspinatus on 2D sequences where the 3D

sequence missed 2 out of these 7 patients. In this context, 3D sequence showed strong agreement (k=0.811) between 2D and 3D sequences which is statistically significant (p value <0.001). On the other hand, perfect agreement (k=1.00) is seen in the assessment of partial thickness tears of subscapularis where it is seen evident in all the 6 patients in both 2D and 3D sequences.

3) Tendinitis Of Rotator Cuff Tendons: All the tendinitis of supraspinatus, infraspinatus, subscapularis show perfect agreement (k=1.00) between 2D and 3D sequences which is statistically significant (p value <0.001).

4) Long Head Of Biceps Tendon Pathologies: Long head of biceps tendon pathologies – tendinopathy (6 out of 50 patients), rupture (2 out of 50 patients), subluxation (2 out of 50 patients) are evident on both 2D and 3D sequences showing perfect agreement (k=1.00) between 2D and 3D sequences which is statistically significant (p value <0.001).

5) Articular Cartilage Lesions: Moderate agreement (k=0.790) is seen between 2D and 3D sequences in the assessment of articular cartilage lesions where the 3D sequence missed 1 out of 3 patients. This is statistically significant with p value of <0.001.

6) AC Joint Degenerative Changes: 35 out of 50 patients showed AC joint degenerative changes in both 2D and 3D sequences. This showed perfect agreement (k=1.00) between 2D and 3D sequences which is statistically significant (p value <0.001).

7) Bone Marrow Edema: Moderate agreement (k=0.779) is seen between 2D and 3D sequences in the assessment of bone marrow edema where the 3D sequence missed 2 out of 6 patients. This showed perfect agreement (k=1.00) between 2D and 3D sequences which is statistically significant (p value <0.001).

Table 3: Agreement Between 2D And 3D Sequences In The Assessment Of Shoulder Joint Pathologies (K – Coefficients).

	2D vs 3D		
	k value		p value
SSP FTT	1.000	Perfect	< 0.001
ISP FTT	1.000	Perfect	< 0.001
SSP PTT	0.811	Strong	< 0.001
SSC PTT	1.000	Perfect	< 0.001
SSP Tendinitis	1.000	Perfect	< 0.001
ISP Tendinitis	1.000	Perfect	< 0.001
SSC Tendinitis	1.000	Perfect	< 0.001
LHBT Tendinopathy	1.000	Perfect	< 0.001
LHBT Rupture	1.000	Perfect	< 0.001
LHBT Subluxation	1.000	Perfect	< 0.001
Cartilage	0.790	Moderate	< 0.001
AC Joint	1.000	Perfect	< 0.001
Marrow edema	0.779	Moderate	< 0.001
Bursitis	1.000	Perfect	< 0.001
Joint Effusion	1.000	Perfect	< 0.001

SSP – Supraspinatus, ISP – Infraspinatus, SSC – Subscapularis, LHBT – Long head of biceps tendon, AC Joint – Acromio-clavicular joint, FTT – Full thickness tear, PTT – Partial thickness tear

Table 4: Sensitivity, Specificity, PPV, NPV, Accuracy Of 3D Sequence In The Assessment Of Shoulder Joint Pathologies With 2D As Standard Of Reference.

	3D CUBE T2 sequence			
	Sn	Sp	Accuracy	p value
SSP FTT	100%	100%	100%	1.000
ISP FTT	100%	100%	100%	1.000
SSP PTT	100%	95.56%	96%	0.500
SSC PTT	100%	100%	100%	1.000
SSP Tendinitis	100%	100%	100%	1.000
ISP Tendinitis	100%	100%	100%	1.000
SSC Tendinitis	100%	100%	100%	1.000
LHBT Tendinopathy	100%	100%	100%	1.000
LHBT Rupture	100%	100%	100%	1.000
LHBT Subluxation	100%	100%	100%	1.000
Cartilage	100%	97.92%	98%	1.000
AC Joint	100%	100%	100%	1.000
Marrow edema	100%	95.65%	96%	0.500
Bursitis	100%	100%	100%	1.000
Joint Effusion	100%	100%	100%	1.000

SSP – Supraspinatus, ISP – Infraspinatus, SSC – Subscapularis, LHBT – Long head of biceps tendon, AC Joint – Acromio-clavicular joint, FTT – Full thickness tear, PTT – Partial thickness tea, Sn – Sensitivity, Sp- Specificity

8) Bursitis: 46 out of 50 patients showed bursitis in both 2D and 3D sequences with perfect agreement (k=1.00) between 2D and 3D sequences which is statistically significant (p value <0.001).

9) Joint Effusion: 34 out of 50 patients showed joint effusion in both 2D and 3D sequences with perfect agreement (k=1.00) between 2D and 3D sequences which is statistically significant (p value <0.001).

II. Diagnostic Accuracy Of 3D Sequence With 2D Sequences As The Standard Of Reference:

With 2D sequences as gold standard, 100% diagnostic accuracy of 3D sequence seen in the assessment of most of the shoulder joint pathologies except for partial thickness tears of supraspinatus (96%), articular cartilage lesions (98%), bone marrow edema (96%). Statistically, no significant difference seen between 2D and 3D sequences in the assessment of shoulder joint pathologies.

DISCUSSION

With the introduction of 3D sequences along with the available advanced workstations and PACS capabilities, a single 3D acquisition can be reformatted into other planes without significant loss of quality using multiplanar reconstruction techniques. The possibility of procuring thin continuous slices reduces the partial volume averaging artefacts. As it does not require repeat imaging in other planes, the total examination time will be reduced and improves patient compliance (2).

There was perfect agreement (Kappa value of 1.00) between 2D & 3D sequences in the assessment of full thickness tears of supraspinatus and infraspinatus. Similar observations were seen in a study done by Kloth et al in 2014 (3) where substantial agreement was seen in the assessment of full thickness tears involving rotator cuff muscles. Higher sensitivity of 3D sequence in the assessment of rotator cuff tears was also observed in the studies by Lee et al (4) and Park et al in 2014 (5).

Out of 7 patients that showed partial thickness tears of supraspinatus in 2D sequences, the 3D acquisition could not reveal in 2 patients; however strong agreement with kappa value of 0.811 seen in this context. This was also noted by Jung, Joon-Yong, et al (6) where they stated that they felt difficulty in the detection of small partial thickness tears and in differentiating between full thickness tears and partial thickness tears. In the course of our study, we observed that pain was a major limiting factor in imaging patients with shoulder pathologies. In these patients with poor compliance, the movement artefacts might not affect the 2D acquisition in all three orthogonal planes, but that is not the case with 3D where the resulting artefacts affect the entire data set and thereby affects the reconstructed images in all three orthogonal planes. In a small subset of patients, manipulation of the scan parameters by our technologists to reduce scan time resulted in anisotropic resolution of the 3D sequence. In these patients, the reconstructions in the orthogonal planes resulted in sub-optimal image quality due to poor spatial resolution. We believe that the above two reasons could be attributed to the lack of perfect agreement between 2D & 3D in the assessment of partial thickness tears of supraspinatus in our series. Similar observations were also made by Lee et al in 2014 (4) where they observed high diagnostic accuracy for full thickness tears but varied diagnostic accuracy for partial thickness tears. They noticed that 3D sequence was susceptible to more motion artefacts due its longer acquisition time than 2D sequence. The long echo train length of the 3D sequence results in minimal blurring that can give way to false interpretations. On the other hand, perfect agreement was seen in the assessment of partial thickness tears of subscapularis where all the 6 patients were found to have partial thickness tears on both 2D as well as 3D sequences. In the study done by Choo et al in 2012 (7), they observed more false positives with both 2D & 3D sequences in the assessment of partial thickness tears of subscapularis.

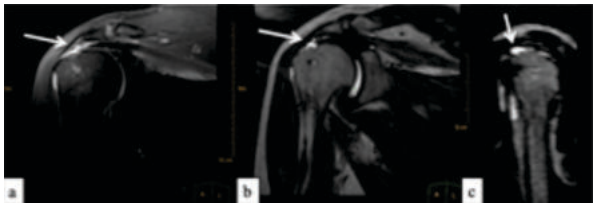

Figure 1 Full-thickness Tear Of The Supraspinatus Tendon (arrow) From Its Attachment With Tendon Retraction Visible In The 2D Coronal PDFS Sequence (a) As Well As In The Coronal T2 CUBE Sequence (b) And In Its Sagittal Multiplanar Reformation Image (c).

Perfect agreement between 2D & 3D sequences seen in the assessment of tendinitis of supraspinatus, infraspinatus and subscapularis. We also had a perfect agreement in the assessment of the tendinopathy, rupture and subluxation of the long head of biceps tendon (LHBT). Kloth et al (3) observed a perfect agreement in subluxation of LHBT but only moderate agreement in the assessment of tendinopathy of LHBT. Rybak et al (8) observed that they were more confident to assess small and obliquely positioned structures, such as curved sections of glenoid labrum and intraarticular portion of LHBT with 3D sequence as it provides more anatomical detail due to its thin slice acquisition and reduced partial volume averaging.

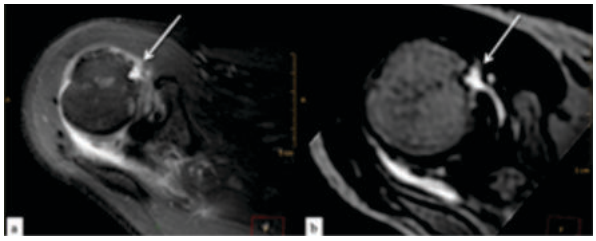

Figure 2 Empty Bicipital Groove (arrow) Seen In Both 2D Axial PDFS Sequence (a) As Well As In The Reformatted Axial T2 CUBE Sequence (b) Suggesting LHBT Subluxation With Suspicion Of Rupture Of THL.

There was no perfect agreement in the assessment of articular cartilage lesions (kappa value of 0.79). Moderate agreement was observed by Kloth et al (3) in the assessment of articular cartilage lesions.

Moderate agreement (kappa value of 0.779) was seen in the assessment of bone marrow edema and this could be due to the lack of fat suppression in the 3D sequence resulting in poor visualization of mild marrow oedema. Our observation is in discordance with Kloth et al (3) where they observed almost perfect agreement in the assessment of marrow edema. Perfect agreement is seen in the assessment of AC joint degenerative changes, bursitis and joint effusion which is similarly observed by Kloth et al in 2014 (3). With 2D sequences as standard, 3D sequence showed > 90% diagnostic accuracy in the assessment of rotator cuff and other shoulder joint pathologies included in our study with no significant statistical difference. This is also observed by Lee et al (4), Park et al (5), Oh et al (9). Foti et al (10) also showed a comparable diagnostic accuracy of 3D sequence with the 2D sequences in the assessment of rotator cuff pathologies.

Limitations

In our series, we studied the agreement between 2D & 3D sequences in MR evaluation of shoulder pathologies and the diagnostic accuracy of 3D sequence using 2D sequences as the standard of reference. Arthroscopy as the standard of reference would have been ideal. We have not studied the agreement between 2D & 3D sequences in the evaluation of labral tears. Manipulation of the scan parameters by our technologists to reduce scan time resulted in anisotropic resolution of the 3D data in a small subset of patients.

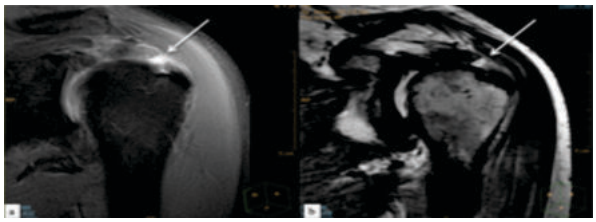

Figure 3 Full Thickness Tear Of SSP Involving The Anterior Fibres Just Proximal To Its Insertion (arrow) Seen In 2D Coronal (a), 2D Sagittal (c) PDFS Sequences As Well As In The Coronal T2 Cube (b), Reformatted Sagittal T2 CUBE (d) Sequences.

CONCLUSION

Perfect agreement is seen between 2D & 3D sequences in the assessment of most of the rotator cuff and other shoulder joint pathologies in our series. Statistically, there is no significant difference between 2D & 3D sequences in their diagnostic accuracy with the 2D sequence taken as the standard of reference.

3D sequence has the potential to reduce the overall examination time and thus may ensure more patient compliance. However, in patients with severe shoulder pain and poor cooperation, the entire data set of 3D sequence can get compromised by movement artefacts and this can result in the suboptimal characterization of some shoulder pathologies like partial thickness tears.

We recommend further studies with arthroscopy as the gold standard before relying purely on 3D sequence for shoulder evaluation.

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