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VALIDATION OF STRAIN ASSESSMENT IN THE ACHILLES TENDON USING ULTRASOUND SPECKLE TRACKING IN AN IN VITRO EXPERIMENTAL SETUP

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INTRODUCTION

In order to design and compare rehabilitation protocols or orthotic devices for treatment of injuries to the Achilles tendon their biomechanical effects on the tendon need to be studied. Speckle tracking algorithms applied to ultrasound images offer a noninvasive means of measuring tissue displacement or strain in the distal free portion of the Achilles tendon. Ultrasound speckle tracking is based on tracking of unique patterns created by interference of reflected ultrasound between a series of frames in an ultrasound sequence. A block-matching speckle tracking algorithm adapted for tendon tissue has previously been validated on human flexor digitorum superficialis tendons and a relative error in displacement of 1.6 % was found when it was compared to displacement estimated from tracking of the musculotendinous junctions [1]. Others have found high correlation (r=0.997) between gastrocnemius tendon displacement assessed by speckle tracking and tracking of the musculotendinous junctions during isometric contractions [2]. The aim of this study was to validate strain assessment in the Achilles tendon by applying a commercially available and an in-house developed speckle tracking algorithm on ultrasound acquisitions of motion in a tendon phantom, a porcine tendon and a human Achilles tendon allograft in an in vitro experimental setup.

METHODS

A custom-made polyvinyl alcohol tendon phantom, a porcine flexor digitorum profunda tendon and a human Achilles tendon allograft were successively mounted in a materials testing machine (ElectroPuls E3000, Instron, MA, USA) and loaded to mimic strain in the Achilles tendon during the stance phase of walking as seen in pilot data. Motion was monitored by a sensor on the motor shaft and the observed displacement was divided by the initial length of the tendon phantom or tendon to find the true value of strain. An ultrasound transducer (Vivid*i*, linear array transducer 8L GE, Horten, Norway) was fixed in a holder and placed on the tendon phantom or tendon and acquisitions with 13 MHz and 39.4 frames per second were made during ten strain cycles for each condition. The gray scale ultrasound recordings were analysed for strain using EchoPAC 2D Strain (General Electrics, Horten Norway) and an in-house algorithm developed in Matlab (normalized cross-correlation, kernel size 52λ×25λ) Four strain peaks were identified (Figure 1) and compared to true strain. Mean strain curves were calculated for true strain and each condition and algorithm respectively. Time between peak one and two was calculated and compared to that of the true strain curve.

RESULTS AND DISCUSSION

Mean absolute errors for each peak, condition and speckle tracking algorithm are shown in Table 1. Mean strain curves with standard deviations are shown in Figure 1. Mean absolute errors for time between peak one and two were small, not exceeding -0.09±0.03 s for any tendon type or algorithm. Both algorithms performed well in estimating magnitude and timing of strain peaks on the tendon phantom. On the porcine tendon both algorithms tended to overestimate both positive and negative peaks. On the human tendon, peaks were underestimated and both algorithms failed to identify the negative peak 3. However, it is worth noting that the algorithms were accurate in detecting when a change in direction of strain occurred even though they were poor at determining the magnitude thereof.

Some limitations in the experimental testing setup may have affected the results. It was difficult to centre the tendon ends in the materials testing machine accurately and any failure to do so would lead to an oblique pull on the tendon. This in turn may have contributed to out of plane motion of speckles which is a known source of error in speckle tracking [3].

After peak 2, there was a rapid decrease in strain. The tendon phantom was more elastic than the tendons and it is possible that the tendons did not follow the motion of the

materials testing machine during this negative strain as well as the phantom did. This may have resulted in coiling rather than retraction of the tendons and is a possible source of error in peak 3.

It is desirable to measure tendon strain rather than displacement as it is more likely to be the cause of injury. However, assessing strain instead of displacement is more challenging as it requires tracking of differences in displacements within a region [4]. It seems that further development is needed before speckle tracking assessment of the comparably small strains common in tendons can be performed with high reliability and validity.

CONCLUSIONS

The results indicated that ultrasound speckle tracking may have potential in non-invasive assessment of tendon mechanics and deformation. However, further advances in ultrasound speckle tracking methodology are required before it can be routinely used to estimate magnitude of strain in the human Achilles tendon.

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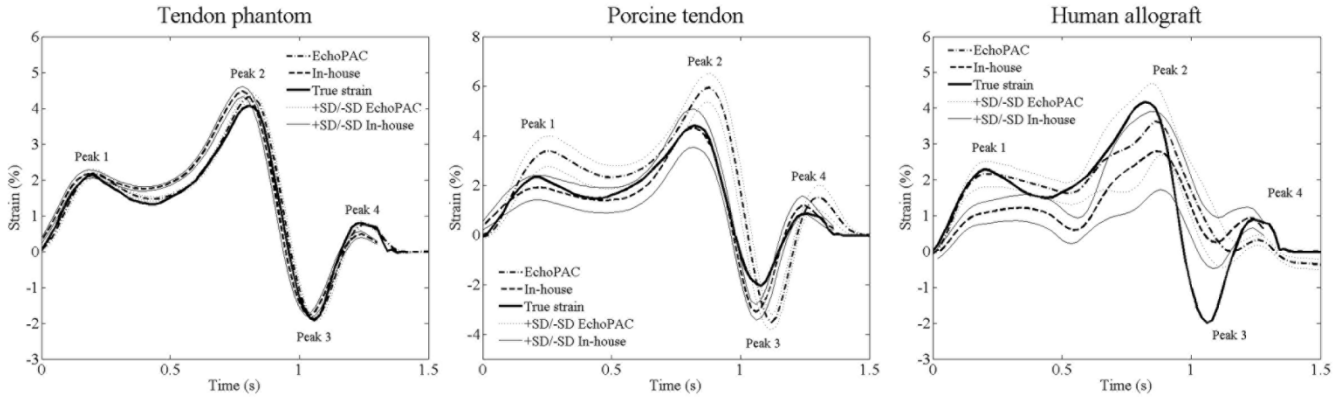

Figure 1: True strain and mean strain curves with standard deviations for the two algorithms for a) the tendon phantom, b) the porcine tendon and c) the human Achilles tendon allograft.

Table 1: Mean absolute errors for strain with standard deviations at peak 1-4 for the tendon phantom and tendons and the two algorithms respectively. The "true strain" column shows the true values for strain separated by commas for the four peaks respectively.

	Absolute error peak 1 mean ± SD (%)	**Absolute error peak 2** mean ± SD (%)	**Absolute error peak 3** mean ± SD (%)	**Absolute error peak 4** mean ± SD (%)	**True strain (%)** mean (%)
EchoPAC					
tendon phantom	0.06 ± 0.11	0.29 ± 0.12	0.00 ± 0.05	0.03 ± 0.03	2.13, 4.07, -1.92, 0.82
porcine tendon	1.07 ± 0.62	1.6 ± 0.59	-1.58 ± 0.31	0.66 ± 0.49	2.34, 4.41, -2.06, 0,88
human allograft	-0.12 ± 0.34	-0.42 ± 0.89	1.9 ± 0.56	-0.57 ± 0.14	2.29, 4.19, -2.01, 0.91
In-house algortihm					
tendon phantom	0.03 ± 0.11	0.42 ± 0.14	0.13 ± 0.06	-0.32 ± 0.08	2.13, 4.07, -1.92, 0.82
porcine tendon	-0.43 ± 0.49	-0.07 ± 0.78	-1.11 ± 0.33	0.37 ± 0.36	2.34, 4.41, -2.06, 0,88
human allograft	-1.06 ± 0.37	-1.26 ± 1.02	2.22 ± 0.71	0.09 ± 0.26	2.29, 4.19, -2.01, 0.91