T1-mapping in the liver: The need for standardization

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Background

Quantitative MRI is used to assess liver disease burden, fibrosis, and inflammation. The standardized, MRI T1 mapping metric, corrected T1 (cT1), is recommended in guidelines to stratify metabolic dysfunction-associated steatotic liver disease (MASLD) and it predicts cardiovascular and liver outcomes. cT1 correlates well with histologic features of the NAFLD activity score (NAS) and fibrosis grading. cT1 is measured using the MRI Modified Look-Locker inversion recovery (MOLLI) method and is adjusted with an algorithm which aligns T1 across scanner manufacturers and magnetic field strengths, while correcting for elevated iron levels which reduces T1 values and masks disease. Here we assess the impact of the standardization to MOLLI T1 provided by cT1.

Methods

Participants with MASLD who underwent biopsies and MRI scans were grouped into 1 of 5 groups by MRI scanner and field strength. To ensure comparable disease states, we excluded patients with purely steatotic livers (both inflammation and ballooning of 0) and included those with fibrosis scores between 1–3. Liver iron concentration (from MRI T2*) and cT1 were calculated using LiverMultiScan. Median and interquartile range (IQR) of T1 and cT1 scores across all scanners were compared. The previously defined threshold of 875ms for cT1 has been suggested as the optimal cut-off for identifying at-risk MASH patients (NAS ≥4 and fibrosis ≥2 on biopsy). We compared the accuracy of this threshold applied to cT1 and T1 for identifying at-risk MASH patients.

Results

373 individuals scanned on 5 MRI scanners (GE 1.5T [n=70], GE 3T [n=79], Philips 3T [n=9], Siemens 1.5T [n=134], and Siemens 3T [n=81) were included. 33% of patients had elevated iron levels indicating the need for correction. The median and IQR of T1 across the scanners was 774ms (716–842, GE 1.5T), 882ms (802–932, GE 3T), 974ms (884–1011, Phillips 3T), 645ms (606–696, Siemens 1.5T) and 931ms (882–994, Siemens 3T). The spread of cT1 was significantly smaller across the respective scanners with median and IQR of 960ms (891–1045), 888ms (830–941), 955ms (905–990), 829ms (780–892), and 919ms (852–984), allowing for comparison of values across scanners. 65% had biopsy confirmed at-risk MASH. cT1 ≥ 875ms identified 60% of patients with at-risk MASH, versus 35% for T1 ≥ 875ms.

Conclusion

Standardizing the MOLLI T1 signal with cT1 provides a reference that is independent of MRI hardware resulting in better classification of disease and a more versatile biomarker to assess MASH.

Figure

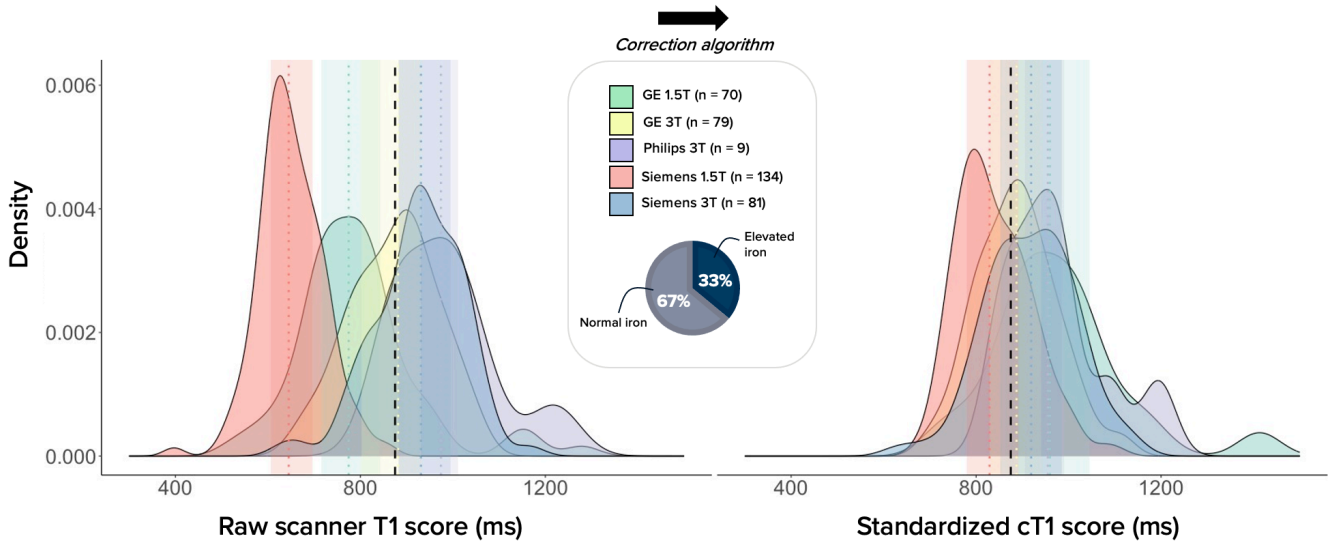

Figure 1. Standardized cT1 provides a signal reference that is applicable across scanners while correcting for increased levels of iron. The colored dotted lines represent the medians, and the shaded regions represent the interquartile range of T1 and cT1 across each scanner. The black dotted line represents the optimal threshold (875ms) at identifying patients with at-risk MASH.