QIBA Proton Density Fat Fraction Biomarker Committee (PDFF BC) Call
Thursday, February 4, 2021 at 3 p.m. (CT)
Call Summary

Participants

RSNA

Takeshi Yokoo, MD, PhD (Co-chair)   Dariya Malyarenko, PhD   J.M. (Hans) Peeters, PhD   Joe Koudelik

Jean Brittain, PhD   Michael Middleton, MD, PhD   Jonathan Riek, PhD   Susan Stanfa

Gavin Hamilton, PhD   Nancy Obuchowski, PhD   Suraj Serai, PhD

Discussion on In-House Solutions (non-product), e.g., LipoQuant (LQ)

- It was noted that though it is used by a variety of entities, LQ is not a commercially available software
- If LQ were to be included in the Profile, users developing new PDFF quantification techniques would be able to rely on a phantom to improve the accuracy of their method vs. being required to conduct a major validation study
- Discussion re: whether to provide Profile users a choice, e.g., complex sequences and magnitude, vs. magnitude only
  - While complex is better, there are obstacles to using it such as availability, cost, and/or incompatibility with scanners containing old magnets
  - If complex sequences become more accessible over time, the Profile can be updated to make it a requirement
  - Consensus was to allow drug studies to use the sequences of their choice
  - There are plenty of other reliable, FDA-accepted techniques that have been used for decades and they will be included in the Profile

- It was noted that temperature correction is needed for phantom studies (not needed for human studies)
- The value in the longitudinal Profile claim: +5% change = true change, however, this may not be true for LQ; Dr. Obuchowski to be consulted on how to address this issue
- A reference standard for bias is needed for the cross-sectional claim; phantom data are used for bias and reproducibility; clinical data are used for repeatability
- Dr. Obuchowski recommended that the wSD and Bias assumptions underlying the Claims be documented
- Suggestion to include MR Spectroscopy as an adjunct to verify the phantom's PDFF values for a cross-sectional Claim
- Consensus was reached re: the inclusion of magnitude data to the greatest feasible extent
- Due to limited data for complex sequences, PDFF BC support for a magnitude Claim was greater than the support for complex
- Dr. Yokoo to follow up with Drs. Reeder and Hernando with an update on this discussion and revised cross-sectional and longitudinal claim values

Next QIBA PDFF BC call: Thursday, March 4, 2021 at 3 p.m. (CT)