QIBA PET Myocardial Blood Flow (MBF) Biomarker Committee (BC)

Monday, April 12, 2021 at 9 am CT

Call Summary

In attendance		**RSNA Staff**
Robert deKemp, PhD (Co-Chair)	Nancy Obuchowski, PhD	Joe Koudelik
Jonathan B. Moody, PhD (Co-Chair)	Richard Wahl, MD, FACR	Julie Lisiecki
P. David Mozley, MD	Gudrun Zahlmann, PhD	

***Moderator**: Dr. deKemp*

Discussion

- Dr. deKemp agreed to create a sample size spreadsheet for Dr. Obuchowski to review and run a metanalysis to determine the coefficient of variation
- From previous conversations, it was agreed that it was incorrect to simply divide by the average blood flow value
    - Need to consider each individual patient's mean, not just the grand mean
- Dr. Moody is working on extracting and summarizing data from the graphs for same-day datasets and noted that the method of stress is an important variable to identify
- Dr. deKemp requested that Dr. Obuchowski determine whether there are any systematic differences between the tracers
- Dr. Moody noted that there is variability among the tracers and stress response is one of the big variables
- Dr. Wahl said that using the same scanner and software is the basis of the Profile and should be required for baseline and follow up
    - Length of time for the effects of the stress test may be the biggest source of variability as this varies from patient to patient
- Dr. Mozley noted that, in general, the focus of QIBA is on "total systems variance": the assumption is the biology has not changed if you are studying a subject on the same day.
- Drs. Obuchowski and Wahl agreed that estimating "minimum change" needs to include biological variability to better understand "real change"
    - Patients may relax on the second scan, may be affected by lunch or a snack, and may also be affected by any news they receive in between scans
    - Isolating any systems variance is helpful if possible, as it is not possible to eliminate biological variability
- Testing preparations include every effort to standardize the software and machine to isolate variance; standardizing patient prep as much as possible is critical

Action items:

- Dr. Moody to begin work on drafting the longitudinal claim for discussion on the next call
- Dr. deKemp to follow up with Dr. Obuchowski re: sample size to determine coefficient of variation

Next Call: April 26, 2021 at 9 am CT (2nd and 4th Mondays) at 9 am CT

Parties interested in joining the QIBA LinkedIn page for QIBA updates should visit: https://www.linkedin.com/company/rsna-qiba

Process Committee

- All Profile Editors are encouraged to join the QIBA Process Committee to learn about QIBA writing tips and processes and network with other Profile Editors to exchange best practices

Contact information for QIBA Process Committee Leaders:

- Kevin O'Donnell, MASc (Chair) | Michael Boss, PhD (Co-Chair)

QIBA Wiki Resources:

- Dashboard updates | Profiles | QIBA Profile template | How to Write a QIBA Profile | Claim Guidance

Inventory of QIBA tools:

- QIBA LinkedIn page (please join / follow) | QIBA News | QIBA Community (discussion board)

Other: QIBA Webpage | QIBA Wiki | QIBA Biomarker Committees | QIBA Organization Chart | Dropbox

EndNote: To obtain access to the RSNA EndNote citations, please send an email request to: sstanfa@rsna.org.