|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| MAC lung disease | | M. abscessus lung disease | | Both MAC-LD & M. abscessus-LD | | Other NTM-LD | |
| N=??? | | N=??? | | N=??? | | N=??? | |
| MAC alone | MAC + non-NTM | M. abscessus alone | M. abscessus + non-NTM | MAC + M. abscessus alone | MAC + M. abscessus + non-NTM | Other NTM alone | Other NTM + non-NTM |
| n=??? | n=??? | n=??? | n=??? | n=??? | n=??? | n=??? | n=??? |

Notes:

* MAC includes M. avium, M. intracellulare, and M. chimaera (technically a subspecies of M. intracellulare) and maybe some others (ask me)
* M. abscessus (group) includes M. abscessus, M. bolletti, and M. massiliense
* “Other NTM” would be NTM other than MAC or M. abscessus group
* non-NTM includes bacteria other than NTM (mycobacteria) or fungi

**Edward**: for our subsequent CT analyses based on microbial culture results, we should analyze CT findings based on the rows 1 and 2 and possibly based on rows 3 and 4 too. The issue with analyzing CT findings based on rows 3 and 4 is the numbers could be relatively small (as there are 8 subgroups). Also, the “non-NTM” data may not be completely reliable as we (NJH) may have only a “snapshot” of their total number of culture results as most patients are from out-of-state.