**Table S2** Distribution of NTM Species causing NTM infection stratified by site of infections (335 isolates from 150 cases).

|  |  |  |  |
| --- | --- | --- | --- |
| **Organisms** | **Number of isolates (335 isolates):****n (%)** |  | **Number of cases (150 cases):****n (%)** |
| **Pulmonary**  | **Extra pulmonary**  | **Total** |  | **Pulmonary**  | **Extra pulmonary**  | **Total** |
| *M. abscessus* | 34 (35.05) | 88 (36.97) | 122 (36.42) |  | 10 (27.78) | 29 (25.44) | 39 (26) |
| *M. arupense* | 0 (0) | 0 (0) | 0 (0) |  | 0 | 0 | 0 (0) |
| *M. asiaticum* | 0 (0) | 2 (0.84) | 2 (0.6) |  | 0 | 1 (0.88) | 1 (0.67) |
| MAC (all species) | *30 (30.93)* | *69 (28.99)* | *99 (29.56)* |  | *5 (13.89)* | *17 (14.91)* | *22 (14.67)* |
|  *M. avium*  | 0 (0) | 3 (1.26) | 3 (0.9) |  | 0 | 3 (2.63) | 3 (2) |
|  *M. intracellulare* | 22 (22.68) | 38 (15.97) | 60 (17.91) |  | 3 (8.33) | 7 (6.14) | 10 (6.67) |
| Unidentified MAC | 8 (8.25) | 28 (11.76) | 36 (10.75) |  | 2 (5.56) | 7 (6.14) | 9 (6) |
| *M. chelonae* | 3 (3.09) | 7 (2.94) | 10 (2.99) |  | 1 (2.78) | 3 (2.63) | 4 (2.67) |
| *M. florentinum* | 0 (0) | 0 (0) | 0 (0) |  | 0 | 0 | 0 (0) |
| *M. fortuitum* | 6 (6.19) | 5 (2.1) | 11 (3.28) |  | 3 (8.33) | 2 (1.75) | 5 (3.33) |
| *M. genavense* | 0 (0) | 1 (0.42) | 1 (0.3) |  | 0 | 1 (0.88) | 1 (0.67) |
| *M. gordonae* | 4 (4.12) | 0 (0) | 4 (1.19) |  | 1 (2.78) | 0 | 1 (0.67) |
| *M. interjectum* | 0 (0) | 0 (0) | 0 (0) |  | 0 | 0 | 0 (0) |
| *M. kansasii* | 1 (1.03) | 6 (2.52) | 7 (2.09) |  | 0 | 0 | 0 (0) |
| *M. lentiflavum* | 0 (0) | 0 (0) | 0 (0) |  | 0 | 0 | 0 (0) |
| *M. malmoense* | 1 (1.03) | 0 (0) | 1 (0.3) |  | 0 | 0 | 0 (0) |
| *M. marinum* | 0 (0) | 1 (0.42) | 1 (0.3) |  | 0 | 1 (0.88) | 1 (0.67) |
| *M. monacense* | 0 (0) | 0 (0) | 0 (0) |  | 0 | 0 | 0 (0) |
| *M. mucogenicum* | 0 (0) | 0 (0) | 0 (0) |  | 0 | 0 | 0 (0) |
| *M. palustre* | 0 (0) | 0 (0) | 0 (0) |  | 0 | 0 | 0 (0) |
| *M. saskatchewanense* | 0 (0) | 0 (0) | 0 (0) |  | 0 | 0 | 0 (0) |
| *M. scrofulaceum* | 3 (3.09) | 8 (3.36) | 11 (3.28) |  | 0 | 3 (2.63) | 3 (2) |
| *M. simiae* | 1 (1.03) | 0 (0) | 1 (0.3) |  | 1 (2.78) | 0 | 1 (0.67) |
| *M. szulgai* | 0 (0) | 1 (0.42) | 1 (0.3) |  | 0 | 0 | 0 (0) |
| *Mycobacterium* spp. | 11 (11.34) | 17 (7.14) | 28 (8.36) |  | 1 (2.78) | 8 (7.02) | 9 (6) |
| Rapidly grower | 1 (1.03) | 25 (10.5) | 26 (7.76) |  | 0 | 6 (5.26) | 6 (4) |
| Mixed NTM isolation | 2 (2.06) | 8 (3.36) | 10 (2.99) |  | 14 (38.89) | 32 (28.07) | 46 (30.67) |
| Multiple site infection | - | - | - |  | 0 (0) | 11 (9.65) | 11 (7.33) |
| **Total** | **97 (100)** | **238 (100)** | **335 (100)** |  | **36 (100)** | **114 (100)** | **150 (100)** |

**Note:** NTMs were isolated from 97 pulmonary samples (36 cases) and 238 extra-pulmonary samples (114 cases). Mixed NTM refers to isolation of >1 species of NTM from the specimens, i.e. from pulmonary samples includes *M. intracellulare* and *M. avium* (1 case) and *M. massiliense* and *M. abscessus* (1 case), and from extra-pulmonary samples includes MAC and *M. intracellulare* (1 case), *M. gordonae* and *M. simiae* (2 cases), *M. fortuitum* and *M. abscessus* (1 case), *M. fortuitum* and *M. peregrinum* (3 cases) and *M. intracellulare* and *M. scrofulaceum* (1 case). MAC=*Mycobacterium avium* complex.