Table 1. Patient epidemiological and demographic data of the present study

|  |  |  |
| --- | --- | --- |
| Variants | Number | Ratio |
| Sex | Male | 169 | 73 |
|  | Female | 45 | 20 |
|  | No data | 16 | 7 |
| Governorates | Cairo | 112 | 49 |
| (patients origin) | Alexandria | 44 | 19 |
|  | Others | 60 | 26 |
|  | No data | 14 | 6 |
| Treatment history | Treated cases | 190 | 83 |
|  | New cases | 24 | 10 |
|  | No data | 16 | 7 |

Table 2. Frequency distribution of major lineages/subclades of *M. tuberculosis* in Egyptian isolates.

|  |  |  |
| --- | --- | --- |
| Global lineage/Subclades\* | No. of isolates | % of isolates |
| Lineage 1 | - | 0 | 0 |
| Lineage 2 | - | 0 | 0 |
| Lineage 3 | CAS |  | 14 | 6.1 |
|  | Orphan strains |  | 2 | 0.87 |
| Lineage 4 | T superfamily | T1 | 89 | 38.7 |
|  |  | T2 | 2 | 0.87 |
|  |  | T3 | 6 | 2.6 |
|  |  | T4 | 5 | 2.2 |
|  | Haarlem |  | 1 | 0.43 |
|  |  | H1 | 5 | 2.2 |
|  |  | H3 | 19 | 8.3 |
|  | LAM | LAM | 7 | 3 |
|  |  | LAM1 | 1 | 0.43 |
|  |  | LAM3 | 2 | 0.87 |
|  |  | LAM5 | 1 | 0.43 |
|  |  | LAM6 | 1 | 0.43 |
|  |  | LAM7\_TUR | 8 | 3.5 |
|  |  | LAM9 | 9 | 3.9 |
|  |  | LAM10\_CAM | 2 | 0.87 |
|  | S |  | 17 | 7.4 |
|  | Orphan strains |  | 25 | 10.87 |
|  | Unknown |  | 14 | 6.1 |
| Lineage 5 | - | 0 | 0 |
| Lineage 6 | - | 0 | 0 |
| Lineage 7 | - | 0 | 0 |
| Total |  | 230 | 100 |

**Table 3** Individual and cumulative HGDI of MIRU-VNTR loci in [SIT53T1 + SIT34/S + SIT4/Unknown] versus independent SIT53/T1.

|  |  |
| --- | --- |
| SIT53T1 + SIT34/S + SIT4/unknown clade a |  |
|  |  | No. of | No. of | No. of clustered | Size of | Unique | Clustering | Individual | Cumulative |
| locus | Alias | patterns | clusters | isolates | clusters | patterns | rate (%) | HGDI c | HGDI c |
| 4052 | QUB-26 |  |  |  |  |  |  |  |  |
| 2165 | ETR-A | 16 | 13 | 74 | 2 to 16 | 3 | 96.1 | 0.6992 | 0.9056 |
| 3690 | Mtub39 | 30 | 19 | 66 | 2 to 9 | 11 | 85.7 | 0.6651 | 0.9586 |
| 2163b | QUB-11b | 43 | 16 | 50 | 2 to 7 | 27 | 64.9 | 0.5971 | 0.9761 |
| 1644 | MIRU16 | 45 | 16 | 48 | 2 to 6 | 29 | 62.3 | 0.5386 | 0.9798 |
| 960 | MIRU10 | 49 | 14 | 42 | 2 to 6 | 35 | 54.5 | 0.5311 | 0.9829 |
| 424 | Mtub04 | 54 | 14 | 37 | 2 to 6 | 40 | 48.1 | 0.4788 | 0.9870 |
| 1955 | Mtub21 | 54 | 14 | 37 | 2 to 6 | 40 | 48.1 | 0.4617 | 0.9870 |
| 802 | MIRU40 | 55 | 13 | 35 | 2 to 6 | 42 | 45.5 | 0.4392 | 0.9874 |
| 2996 | MIRU26 | 56 | 13 | 34 | 2 to 6 | 43 | 44.2 | 0.3014 | 0.9880 |
| 4156 | QUB-4156 | 56 | 13 | 34 | 2 to 6 | 43 | 44.2 | 0.1729 | 0.9880 |
| 2401 | Mtub30 | 56 | 13 | 34 | 2 to 6 | 43 | 44.2 | 0.0513 | 0.9880 |
|  |  |  |  | SIT53/T1 |  |  |  |  |  |
| 3690 | Mtub39 |  |  |  |  |  |  | 0.7375 | 0.7376 |
| 4052 | QUB-26 | 15 | 11 | 48 | 2 to 15 | 4 | 92.3 | 0.6305 | 0.8824 |
| 2163b | QUB-11b | 23 | 9 | 38 | 2 to 8 | 14 | 73.1 | 0.6041 | 0.9397 |
| 2165 | ETR-A | 27 | 13 | 38 | 2 to 6 | 14 | 73.1 | 0.5618 | 0.9661 |
| 802 | MIRU40 | 29 | 12 | 35 | 2 to 6 | 17 | 67.3 | 0.3115 | 0.9691 |
| 2996 | MIRU26 | 31 | 11 | 32 | 2 to 6 | 20 | 61.5 | 0.2805 | 0.9713 |
| 960 | MIRU10 | 33 | 10 | 29 | 2 to 6 | 23 | 55.8 | 0.2745 | 0.9736 |
| 1644 | MIRU16 | 33 | 10 | 29 | 2 to 6 | 23 | 55.8 | 0.2149 | 0.9736 |
| 424 | Mtub04 | 35 | 10 | 27 | 2 to 6 | 25 | 51.9 | 0.2149 | 0.9774 |
| 4156 | QUB-4156 | 35 | 10 | 27 | 2 to 6 | 25 | 51.9 | 0.1478 | 0.9774 |
| 2401 | Mtub30 | 35 | 10 | 27 | 2 to 6 | 25 | 51.9 | 0.0754 | 0.9774 |
| 1955 | Mtub21 | 35 | 10 | 27 | 2 to 6 | 25 | 51.9 | 0.0385 | 0.9774 |

a SIT: Spoligotyping International Type number.

b : MIRU-VNTR: Mycobacterial Interspersed Repetitive Unit–Variable Number Tandem Repeat.

c : HGDI: Hunter–Gaston Diversity Index.

**Table 4.** Summary of *M. tuberculosis* lineage/clade distributions from previous studies in Egypt and other EMR† and North African countries

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  | Country of isolation (%) |  |  |  |  |  |  |
|  |  | Egypt |  | Sudan |  | Saudi Arabia |  | Syria |  | Iraq |  | Tunisia |  | Morocco |
| Lineages/Clades\* | Current study2015 | Cookseyet al(2002)[12] | Abbadiet al(2009)[13] | Helalet al(2009)[14] |  | Sharafet al(2011)[26] |  | Al-Hajoj et al (2007)[27] | Varghese et al(2013)[28] |  | Bedrossianet al(2013) [29] |  | Merza and Salih(2012) [30] |  | Namouchi et al(2008) [31] |  | Lahlouet al(2012)[17] |
|  |  | N= 230 | N= 67 | N= 44 | N= 151 |  | N= 235 |  | N= 1,505 | N= 322 |  | N= 96 |  | N= 53 |  | N= 378 |  | N= 592 |
| Lineage 1 | Manu | 0 | 0 | 0 | 27.2 |  | 0 |  | 2.7 | 0 |  | 0 |  | 0 |  | 0 |  | 0 |
| Lineage 3 | CAS | 7 | 13.6 | 9 | 4 |  | 50.7 |  | 22.5 | 21.1 |  | 10.4 |  | 24 |  | 0 |  | 0 |
| Lineage 4 | T | 44.4 | 34.8 | 50 | 53.6 |  | 8.2 |  | 19.5 | 0 |  | 47.8 |  | 30 |  | 16.4 |  | 20.1 |
|  | Haarlem | 10.9 | 1.5 | 4.5 | 2 |  | 3 |  | 7.5 | 10.6 |  | 13.4 |  | 18 |  | 40.2 |  | 22.6 |
|  | LAM | 13. 5 | 15.2 | 18.2 | 4.6 |  | 2.2 |  | 7.2 | 7.5 |  | 22.8 |  | 0 |  | 28.3 |  | 43.7 |
|  | S | 7.4 | 6.1 | 4.5 | 1.3 |  | 0.4 |  | 0 | 2.45 |  | 0 |  | 14 |  | 0 |  | 3.8 |

† Eastern Mediterranean Region.

N: number of isolates

\*Lineages classifications based on [9], [11] and [23].

**Table 5** Comparison of data from the HGDI analysis based on 12 MIRU-VNTR loci used in the present study with those reported by other researchers in MTB strains belonging to SIT53/T1 a.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
|  |  |  |  |  |  |  |  |
| MIRU-VNTR / HGDI b, c | Egypt2015N = 52 | Italy Rindi*et al*(2014)[19]N = 13 | Zambia Mulenga*et al* (2010)[20] N = 16 | South Africa　　　　Stavrum*et al*(2009)[21]N = 13 | Brazil Vasconcellos*et al*(2014)[22]N = 26 | Coˆ te d’IvoireOuassa*et al*(2012)[33]N = 74 |  |
|  | 3690 | Mtub39 | 0.7375 | 0.7051 | 0.5809 | 0.8333 | 0.7169 | 0.0270 |  |
|  | 4052 | QUB-26 | 0.6305 | 0.5385 | 0.6912 | 0.7179 | 0.8338 | 0.0796 |  |
|  | 2163b | QUB-11b | 0.6041 | 0.7308 | 0.4853 | 0.7692 | 0.8031 | 0.1292 |  |
|  | 2165 | ETR-A | 0.5618 | 0.5128 | 0.5294 | 0.3846 | 0.5815 | 0.0270 |  |
|  | 802 | MIRU40 | 0.3115 | 0.7308 | 0.75 | 0.6795 | 0.8092 | 0.4838 |  |
| MIRU-VNTR | 2996 | MIRU26 | 0.2805 | 0.7564 | 0.3235 | 0.5385 | 0.6092 | 0.0796 |  |
|  | 960 | MIRU10 | 0.2745 | 0.5897 | 0.5 | 0.6026 | 0.7969 | 0.0270 |  |
|  | 1644 | MIRU16 | 0.2149 | 0.8205 | 0.5294 | 0.5385 | 0.6246 | 0 |  |
|  | 424 | Mtub04 | 0.2149 | 0.7308 | 0.2279 | 0.5 | 0.6831 | 0.2217 |  |
|  | 4156 | QUB-4156 | 0.1478 | 0.1538 | 0.3824 | 0.4103 | 0.6092 | 0.0270 |  |
|  | 2401 | Mtub30 | 0.0754 | 0 | 0.4706 | 0.3846 | 0.7108 | 0.2455 |  |
|  | 1955 | Mtub21 | 0.0385 | 0.1538 | 0.4853 | 0.5256 | 0.6769 | 0.1292 |  |

a SIT: Spoligotyping International Type number.

b MIRU-VNTR:Mycobacterial Interspersed Repetitive Unit–Variable Number Tandem Repeat.

c HGDI: Hunter–Gaston Diversity Index.

N: number of isolates