

Supplementary material

Brief Reports

Geographically structured genotypes and resistance clustering in *Aspergillus fumigatus*

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Supplementary Table 1. Geographic distribution and number of distinct sequence types (STs) of *Aspergillus fumigatus* isolates

Location	Isolates count	Number of distinct STs
Australia	2	2
Austria	2	2
Brazil	1	1
Canada	2	2
China	43	9
France	10	8
Germany	256	176
Japan	1	1 ^a
Korea	155	131
Netherlands	1	1
New Zealand	2	2
Peru	1	1
Russia	1	1
Space	2	2 ^b
Spain	5	5
United Kingdom	7	6
USA	7	6
Total	498	356(343) ^c

^a JCM 10253 is registered in Japan (NCBI), but was originally isolated from a human lung in the USA (listed as “animal” in the database).

^b Strains IF1SW-F4 and ISSFT-021 were isolated from the International Space Station; isolation and analysis were conducted by NASA.

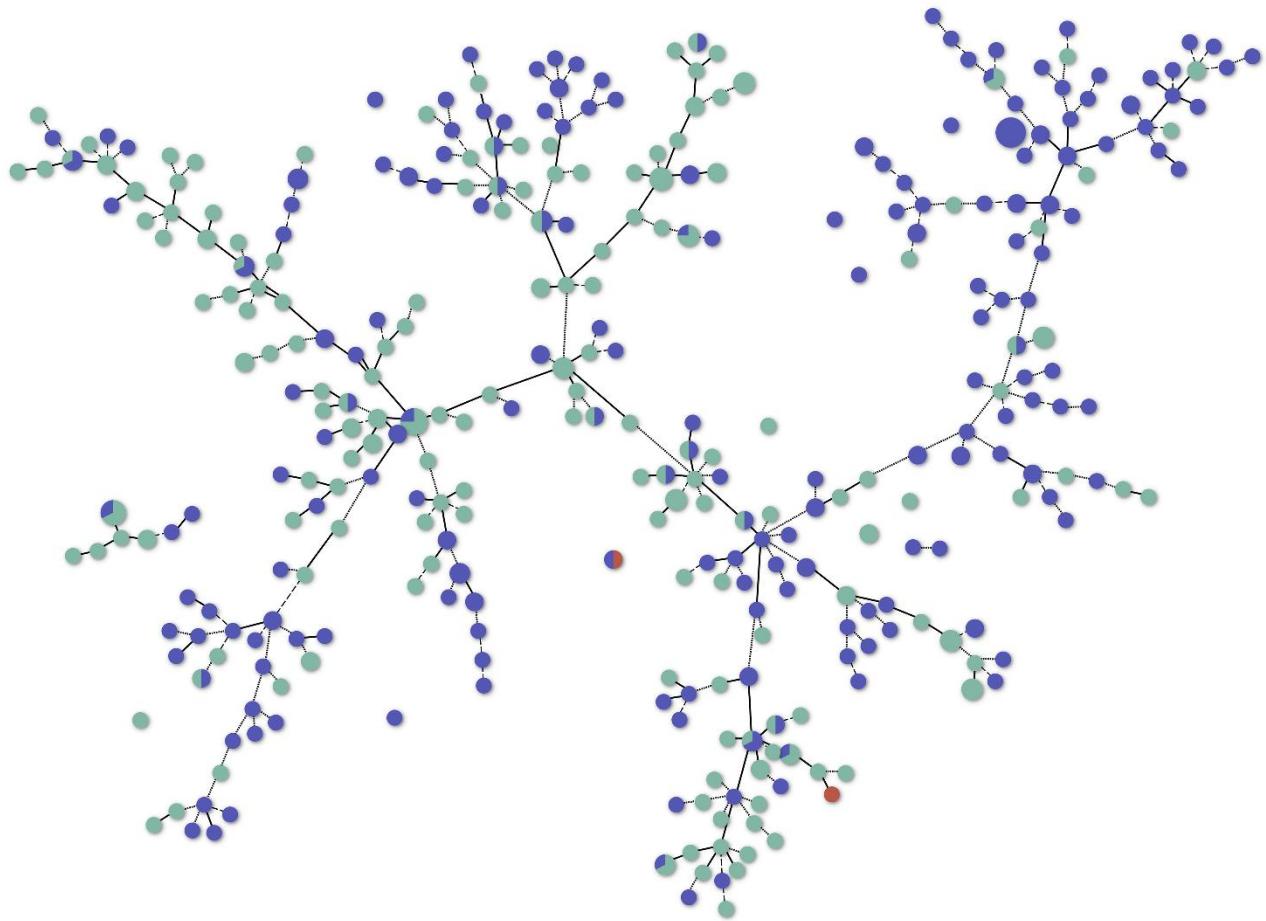
^c Aggregating ST types by country yields 356 STs; however, 13 STs are shared between countries, resulting in a total of 343 distinct STs.

Supplementary Table 2. Geographic and genotypic distribution of *cyp51A* tandem-repeat mutations among azole-resistant *Aspergillus fumigatus* isolates.

Strain	ST	Genotype	Location	Collection	Date	Azole resistance
F214	102	10-2-3-5-1-4-2-4-4-2	Korea	Clinical	2020-07-24	TR34
F623	106	10-2-3-5-2-5-3-11-7-3	Korea	Clinical	2022-03-08	TR34
F669	109	10-2-3-7-3-4-2-8-3-3	Korea	Clinical	2022-06-28	TR46
F430	117	10-4-3-5-2-5-4-11-3-3	Korea	Clinical	2021-07-15	TR34
F461	123	10-6-3-7-3-4-2-7-3-3	Korea	Clinical	2021-08-16	TR46
F296	128	11-2-5-5-1-4-3-12-4-3	Korea	Clinical	2020-12-18	TR34
NRZ-2017-381	132	10-2-3-6-1-3-2-9-2-1	Germany	Clinical	2017-01-01	TR34
NRZ-2017-214	133	8-2-3-3-3-3-2-10-3-2	Germany	Clinical	2017-01-01	TR46
NRZ-2018-529	152	7-5-3-5-3-5-2-9-4-2	Germany	Clinical	2018-01-01	TR34
NRZ-2017-362	155	8-6-3-3-3-3-2-6-3-2	Germany	Clinical	2017-01-01	TR34
NRZ-2018-539	266	7-5-3-5-3-5-2-9-4-2	Germany	Clinical	2018-01-01	TR46
NRZ-2018-290	280	8-3-3-6-1-3-2-9-3-2	Germany	Clinical	2018-01-01	TR34
CNM-CM8714	290	8-2-3-5-1-4-2-6-4-2	Spain	Clinical		TR34
C-1-67s-1	303	12-3-3-5-3-0-2-9-3-1	Germany	Environmental	2016-07-05	TR34
I-1-12-1	303	12-2-3-5-3-3-3-5-3-1	Germany	Environmental	2016-05-20	TR34
NRZ-2016-121	303	12-4-4-6-1-0-2-11-3-1	Germany	Clinical	2016-01-01	TR34
C-1-6s-2	319	9-6-3-5-3-3-3-2-3-1	Germany	Environmental	2016-04-08	TR34
A-3-46s-1	322	8-5-3-5-3-3-5-6-4-2	Germany	Environmental	2016-07-13	TR34
NRZ-2014-065	337	8-9-3-3-3-3-3-9-3-2	Germany	Clinical	2014-01-01	TR46
CNM-CM8057	339	8-2-3-6-1-4-2-6-3-2	Spain	Clinical		TR46
E-1-48-2	341	8-4-3-6-1-5-3-6-1-2	Germany	Environmental	2016-04-12	TR34

Abbreviations: MLVA, multilocus variable-number tandem-repeat analysis; ST, sequence type; TR,

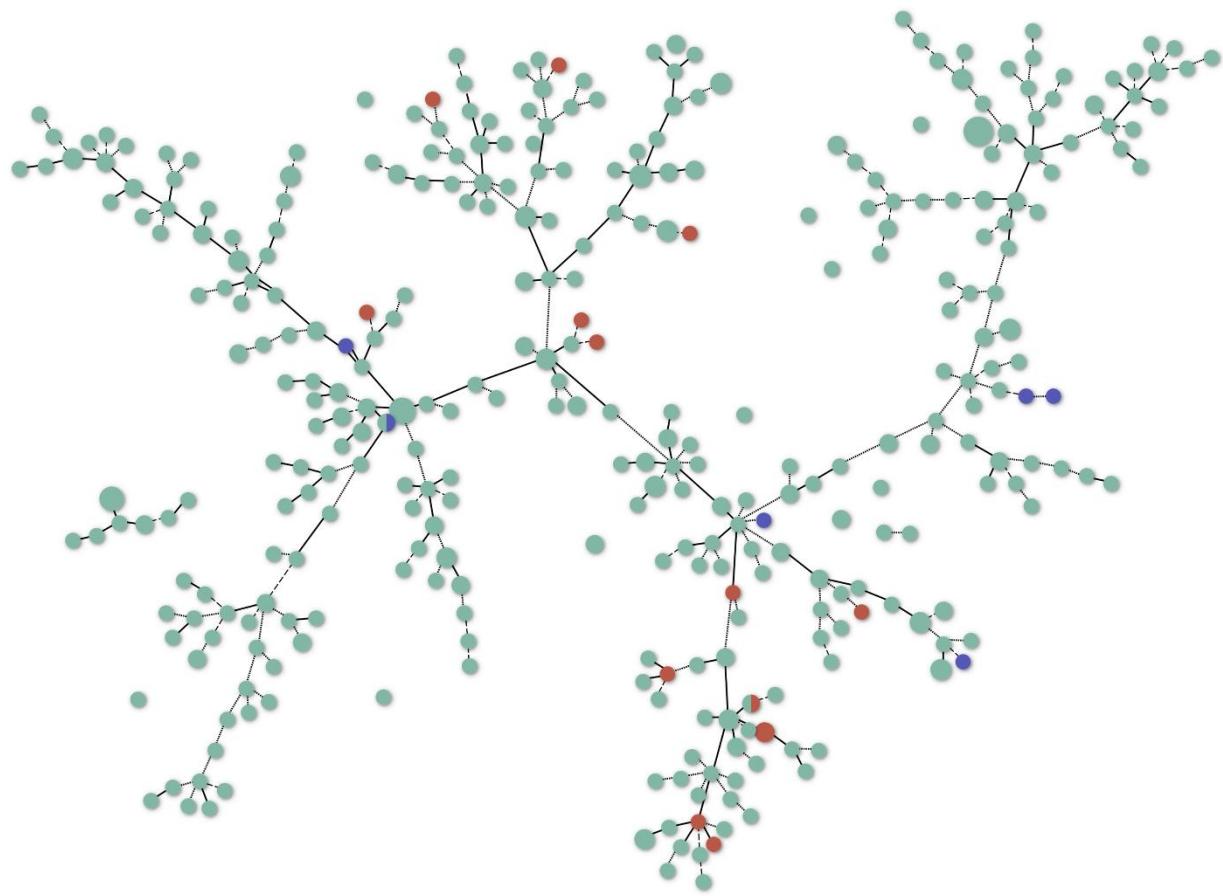
tandem-repeat.



● collection : Clinical (n = 267, 53.61%) ● collection : Environmental (n = 229, 45.98%) ● collection : Animal (n = 2, 0.40%)

Supplementary Fig. 1 Minimum spanning tree (MST) of 498 *Aspergillus fumigatus* isolates, color-coded by source of isolation

The MST was generated based on multilocus variable-number tandem-repeat profiles. Each node represents a unique sequence type, with node size proportional to the number of isolates. Nodes are colored by source: clinical (blue), environmental (green), and animal (red). Isolates from different sources were broadly intermixed across all clusters, with no evidence of source-specific segregation.



● azole resistance : WT (n = 477, 95.78%) ● azole resistance : TR34 (n = 15, 3.01%) ● azole resistance : TR46 (n = 6, 1.2%)

Supplementary Fig. 2 Minimum spanning tree (MST) of 498 *Aspergillus fumigatus* isolates highlighting *cyp51A* tandem-repeat (TR) mutations associated with azole resistance

The MST was constructed from multilocus variable-number tandem-repeat profiles. Each node represents a unique sequence type (ST), with size proportional to the number of isolates. Nodes are colored by *cyp51A* genotype: wild-type (green), TR34 (red), and TR46 (blue). Among 18 resistance-associated STs, 13 (72%) clustered within Cluster 3 (predominantly European), while the remaining STs were located in Clusters 1 and 4 (East Asian origin), indicating regional aggregation of resistance genotypes.