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Azole-resistant *Aspergillus fumigatus*, Iran

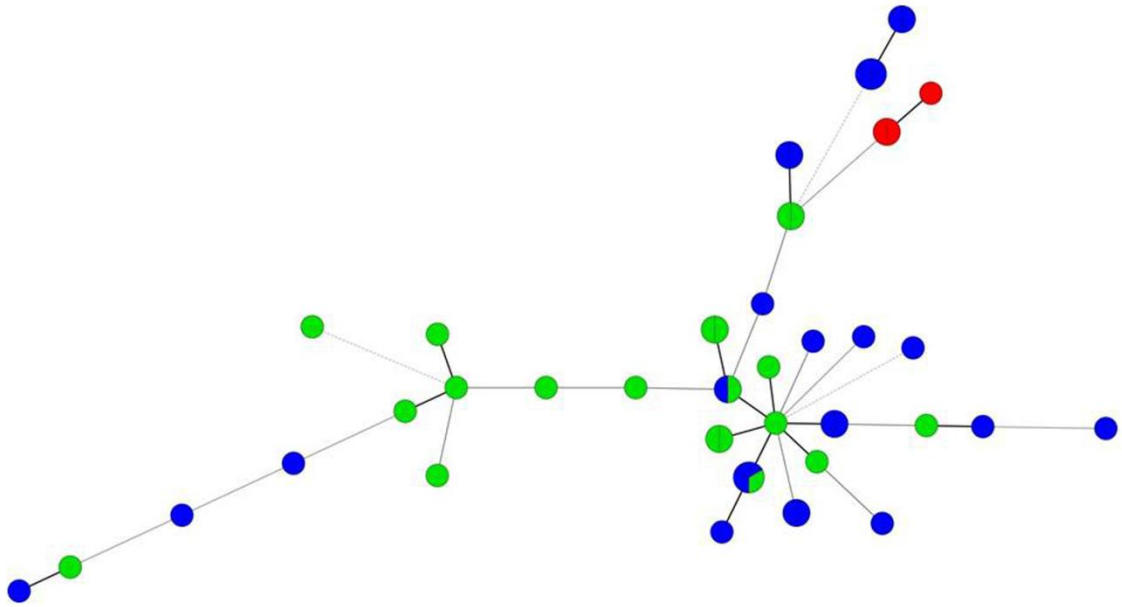
Technical Appendix

Technical Appendix Table 1. Distribution of azole-resistant and azole-susceptible *Aspergillus fumigatus* isolates, Iran, 2003–2009

	No. isolates with each phenotype and resistance mechanism		
Year of isolation	Wild type	Resistant, TR_{34}/L98H	Resistant, non-TR_{34}/L98H
2003	11	–	–
2004	18	–	–
2005	11	1	–
2006	17	–	–
2007	19	2	1
2008	20	–	–
2009	24	–	–
Total	120	3	1

Technical Appendix Table 2. First reports of multiple-triazole-resistant *Aspergillus fumigatus* isolate(s) carrying the TR_{34}/L98H mutations in the *CYP*51A gene, by country

Region/Country		First reported TR_{34}/L98H *A.fumigatus* isolate(s)	Reference
Europe	Netherlands	1998	Snelders et al. 2008 (*1*)
	UK	1999	Howard et al. 2009 (*2*)
	Norway	2001	Snelders et al. 2008 (*1*)
	Spain	2002/2003	Mellado et al. 2012 (*3*)
	Denmark	2007	Mortensen et al. 2011 (*4*)
	Belgium	2008	Lagrou et al. 2008 (*5*)
	France	2010/2011	Burgel et al. 2012 (*6*), Morio et al. 2012 (*7*)
	Germany	2012	Rath et al. 2012 (*8*)
Asia	Iran	2005	Present study
	India	2008	Chowdhary et al. 2012 (*9*,*10*)
	China	2008/2009	Lockhart et al. 2011 (*11*)



Technical Appendix Figure. Minimum spanning tree comparing genotypic relatedness of clinical azole-resistant *Aspergillus fumigatus* isolates carrying TR_{34}/L98H alteration in the *CYP*51A gene from Iran with those reported from European countries. Microsatellite typing of 6 STR loci demonstrated identical patterns for two of the three azole-resistant isolates from Iran, but the TR_{34}/L98H isolates from Iran did not cluster with those from the Netherlands and other European countries, indicating no close genetic relatedness. Each circle corresponds to a unique genotype, and each color indicates the origin of azole-resistant TR_{34}/L98H isolates: red, Iran (n = 3); green, the Netherlands (n = 20); blue, other European countries (n = 24). The size of the circle corresponds to the number of isolates with that genotype. Connecting lines correspond to the number of different microsatellite loci between the genotypes: solid thick and thin branches indicate 1 and 2 microsatellite marker differences, respectively; dashed branches indicate 3 microsatellite marker difference; dotted branches indicate $\geq$4 microsatellite marker differences between genotypes.

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