Azole-Resistant Aspergillus fumigatus, Iran

To the Editor: Aspergillus fumigatus causes a variety of diseases in humans. The drugs recommended for treatment of Aspergillus diseases are the mold-active azole antifungal drugs (1). However, a wide range of mutations in A. fumigatus confer azole resistance, which commonly involves modifications in the cyp51A gene (2), the target for azole antifungal drugs.

Azole resistance is thought to be selected for as a result of patient therapy or exposure toazole compounds in the environment; resistance in clinical A. fumigatus isolates has been increasingly reported in several European countries, Asia, and the United States (3–7). The most frequently reported resistance mechanism is a 34-bp tandem repeat (TR34) in combination with a substitution at codon 98 (TR34/L98H) (4); this mechanism is believed to have been selected for through environmental exposure to azole fungicides.

Because routine in vitro susceptibility testing of clinical Aspergillus isolates is not common in many centers worldwide, the prevalence of azole resistance might be underestimated. We investigated the prevalence of azole resistance in clinical A. fumigatus isolates stored for 6 years (2003–2009) at Tehran University Mycology Reference Centre and Islamic Azad University, Ardabil Branch, Iran.

We investigated 124 clinical A. fumigatus isolates obtained from patients with Aspergillus diseases (online Technical Appendix Table 1, wwwnc.cdc.gov/EID/article/19/5/13-0075-Technical Appendix Table 1, wwwnc.cdc.gov/EID/article/19/5/13-0075-Technical Appendix Table 2) (3–7). In the study reported here, prevalence of azole resistance in clinical A. fumigatus isolates obtained from patients in Iran was 3.2%; most isolates exhibited the TR34/L98H resistance mechanism. The fact that the first TR34/L98H isolate was found relatively early, in 2005, underscores the possibility that prevalence

References

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of azole resistance might be underestimated in many countries because in vitro susceptibility testing of *A. fumigatus* is not routinely performed.

Microsatellite genotypic analysis of *A. fumigatus* isolates from the Netherlands and various European countries showed that the genetic diversity of TR<sub>34</sub>/L98H isolates is lower than that of wild-type controls (8). It has been suggested that TR<sub>34</sub>/L98H isolates might have a common ancestor that developed locally and subsequently migrated across Europe. In contrast, genotyping of TR<sub>34</sub>/L98H originating from India suggested a different dynamic; all environmental and clinical TR<sub>34</sub>/L98H isolates from India shared the same multilocus microsatellite genotype not found in any other analyzed samples, from within India or from the Netherlands, France, Germany, or the People’s Republic of China (9). The molecular epidemiology of the TR<sub>34</sub>/L98H isolates from Iran suggests that they cluster apart from the European isolates, indicating that migration from Europe to Iran, or vice versa, is unlikely. Genotyping of more TR<sub>34</sub>/L98H isolates from the Middle East and comparison with those from India would enhance understanding of the origin and geographic spread of TR<sub>34</sub>/L98H.

Our study indicates that TR<sub>34</sub>/L98H was in Iran in 2005; this finding adds to the growing list of regions where acquired resistance in *A. fumigatus* of environmental origin is documented. From a global perspective, fungicide use is second highest in the Asia–Pacific regions (24%), preceded only by western Europe (37%) (10).

For a bettering understand of the scale of this emerging public health problem and for insight into the dynamics of geographic migration, surveys of fungal culture collections for TR<sub>34</sub>/L98H and molecular typing studies are warranted. These data would be useful not only for clinical management of *Aspergillus* diseases but also for enabling policy makers to develop strategies that prevent resistance selection by the environmental route.

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**References**


appeared to be responsible for abortions in small ruminants and for clinical disease in humans (2,3). However, little is known about the outbreak genotype and the prevalence of C. burnetii in possible additional reservoirs for human Q fever (i.e., cats, dogs, horses, sheep, and cattle) in the Netherlands.

We aimed to search for possible additional reservoirs for human Q fever in the Netherlands. Placentas from 15 cats, 54 dogs, and 31 horses were collected in 2011 at 5 veterinary practices. Placentas were collected by targeted sampling at breeding facilities and during parturition with veterinary assistance. In addition, 27 ovine, 11 caprine, 16 porcine, 8 equine, and 139 bovine placentas (originating from aborting animals from throughout the Netherlands that were submitted in 2011 to investigate the abortion cause) were included in the study. Samples were stored at −20°C before testing.

DNA was extracted from the allantochorion of the placenta and analyzed as described (2). Samples with sufficient DNA load (cycle threshold [C] value <32) were typed by using 2 multilocus variable-number-tandem-repeat analyses (MLVA) genotyping methods (MLVA-12 and MLVA-6), and the multispacer sequence typing method (3–5). Two C. burnetii strains from the Netherlands representing the outbreak genotype (X09003262, 3345937) and the Nine Mile RSA 493 were included as reference. For prevalence calculations, the Netherlands was divided in a southern part, comprising the Q fever hot spot area of no more than 25% of the population, and a northern part. Until now, horses had been discussed as a risk factor in the Q fever outbreak in the Netherlands (8).

Prevalence data from sheep and cattle suggest that C. burnetii is present in placentas in 25% of the abortion cases in these species. Presence of the outbreak genotype of C. burnetii in sheep has been observed (2,5), indicating sheep are a reservoir for Q fever.
Technical Appendix

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

<table>
<thead>
<tr>
<th>Year of isolation</th>
<th>Wild type</th>
<th>Resistant, TR34/L98H</th>
<th>Resistant, non-TR34/L98H</th>
</tr>
</thead>
<tbody>
<tr>
<td>2003</td>
<td>11</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>2004</td>
<td>18</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>2005</td>
<td>11</td>
<td>1</td>
<td>–</td>
</tr>
<tr>
<td>2006</td>
<td>17</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>2007</td>
<td>19</td>
<td>2</td>
<td>1</td>
</tr>
<tr>
<td>2008</td>
<td>20</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>2009</td>
<td>24</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Total</td>
<td>120</td>
<td>3</td>
<td>1</td>
</tr>
</tbody>
</table>

Technical Appendix Table 2. First reports of multiple-triazole-resistant *Aspergillus fumigatus* isolate(s) carrying the TR34/L98H mutations in the CYP51A gene, by country

<table>
<thead>
<tr>
<th>Region/Country</th>
<th>First reported TR34/L98H <em>A. fumigatus</em> isolate(s)</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Europe</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Netherlands</td>
<td>1998</td>
<td>Snelders et al. 2008 (1)</td>
</tr>
<tr>
<td>UK</td>
<td>1999</td>
<td>Howard et al. 2009 (2)</td>
</tr>
<tr>
<td>Norway</td>
<td>2001</td>
<td>Snelders et al. 2008 (1)</td>
</tr>
<tr>
<td>Spain</td>
<td>2002/2003</td>
<td>Mellado et al. 2012 (3)</td>
</tr>
<tr>
<td>Denmark</td>
<td>2007</td>
<td>Mortensen et al. 2011 (4)</td>
</tr>
<tr>
<td>Belgium</td>
<td>2008</td>
<td>Lagrou et al. 2008 (5)</td>
</tr>
<tr>
<td>France</td>
<td>2010/2011</td>
<td>Burgel et al. 2012 (6), Moro et al. 2012 (7)</td>
</tr>
<tr>
<td>Germany</td>
<td>2012</td>
<td>Rath et al. 2012 (8)</td>
</tr>
<tr>
<td>Asia</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Iran</td>
<td>2005</td>
<td>Present study</td>
</tr>
<tr>
<td>India</td>
<td>2008</td>
<td>Chowdhary et al. 2012 (9,10)</td>
</tr>
<tr>
<td>China</td>
<td>2008/2009</td>
<td>Lockhart et al. 2011 (11)</td>
</tr>
</tbody>
</table>
Technical Appendix Figure. Minimum spanning tree comparing genotypic relatedness of clinical azole-resistant *Aspergillus fumigatus* isolates carrying TR34/L98H alteration in the *CYP51A* 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 TR34/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 TR34/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 >4 microsatellite marker differences between genotypes.

References


11. Lockhart SR, Frade JP, Etienne KA, Pfaffer MA, Diekema DJ, Balajee SA. Azole resistance in 
*Aspergillus fumigatus* isolates from the ARTEMIS global surveillance study is primarily due to 