service-related reasons, which is consistent with previously reported data and of concern given that malaria can be a life-threatening illness (4). Nonetheless, a surprisingly low proportion of persons who traveled for business or service-related reasons received pretravel medical advice, used malaria prophylaxis, and received influenza vaccination. Public health agencies should work closely with organizations sending personnel abroad to improve their use of health precautions during travel. Furthermore, although most persons who traveled to visit friends or relatives received pretravel medical advice, few used malaria prophylaxis. The reason for this discrepancy deserves further evaluation.

Public health agencies should also work closely with communities whose members are likely to visit friends or relatives abroad and with medical providers caring for these communities to increase the use of travel health precautions, particularly when exceptional circumstances apply as during the EVD outbreak. Increasing the use of health precautions among persons traveling to an area for which active monitoring is recommended could directly benefit the travelers and improve the specificity of active monitoring by reducing the occurrence of malaria, influenza, and other preventable travel-associated illnesses.

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We thank all persons who underwent active monitoring for their cooperation, DOHMH staff involved with Ebola active monitoring, and Douglas H. Esposito and Emily S. Jentes for providing recommendations.

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References
reported in Lebanon. However in 2013 alone, 1,033 new cases were reported, of which 96.6% occurred among the displaced Syrian refugee populations. Similarly in Turkey, nonendemic parasite strains \( L. \text{major} \) and \( L. \text{donovani} \) were introduced by incoming refugees.

Many of the temporary refugee settlements are predisposed to increased risk because of malnutrition, poor housing, absence of clean water, and inadequate sanitation. The combination of favorable climate, abundant sand fly populations, displaced refugees, and deficient medical facilities and services has created an environment conducive to cutaneous leishmaniasis reemergence. For example, refugee settlements in Nizip in southern Turkey have reported several hundred cases.

Using current datasets published in English and Arabic, we mapped cutaneous leishmaniasis prevalence within Syria and its neighboring countries. Our results demonstrate that cutaneous leishmaniasis prevalence coincides with the presence of refugee camps (Figure, panel A), which is plausible given the strong association between disease outbreaks and refugee settlements. The deterioration of Syrian health systems, including the cessation of countrywide vector control programs, has created an ideal environment for disease outbreaks. Likewise, the sand fly vectors are widely distributed throughout the Middle East; expansive \( \text{Ph. papatasi} \) and \( \text{Ph. sergenti} \) sand fly populations exist in Syria and Iraq. The presence of these vectors in regions of instability can create new cutaneous leishmaniasis foci, which might have debilitating, and often stigmatizing, consequences for residents and deployed military personnel. In addition, the distribution of \( \text{Leishmania} \) spp. overlaps with sand fly habitats (Figure, panel B) and disease reservoirs. Consequently, the movement of large refugee populations...
into regions that are ill-equipped to manage imported cutaneous leishmaniasis has resulted in outbreaks in Turkey and Lebanon (5,6).

Our findings emphasize the importance of contemporaneous disease tracking to identify human populations at highest disease risk. To ameliorate the current cutaneous leishmaniasis crisis, particularly during the winter when cases start to appear, accurate disease monitoring and strategic training of persons based within refugee camps (medical staff, aid workers, volunteers, and military personnel) needs to be prioritized. Moreover, clinicians and other medical personnel residing in refugee-hosting countries must be suitably trained to diagnose cutaneous leishmaniasis because other local diseases (e.g., sarcoidosis and cutaneous tuberculosis) can have similar manifestations. Along with vector and rodent control, new cutaneous leishmaniasis outbreaks should be managed by prompt diagnosis and treatment, which are even more pertinent given that _L. tropica_–associated cutaneous leishmaniasis typically is resistant to several treatment regimens. In summary, the coexistence of sand fly populations and _Leishmania_ spp. within refugee camps, together with the considerable influx of persons who already have cutaneous leishmaniasis, create a dangerous cocktail that can lead to an outbreak unprecedented in modern times.

References


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**Phylogeny of Zika Virus in Western Hemisphere, 2015**

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To the Editor: _Zika_ virus belongs to the genus _Flavivirus_, family _Flaviviridae_, and is transmitted by _Aedes_ spp. mosquitoes. Clinical signs and symptoms of human infection include fever, headache, malaise, maculopapular rash, and conjunctivitis.

_Zika_ virus was first isolated in 1947 from the blood of a febrile sentinel rhesus monkey during a study of yellow fever in the _Zika_ Forest of Uganda (1). During the next 20 years, _Zika_ virus isolates were obtained primarily from East and West Africa during arbovirus surveillance studies in the absence of epidemics. During those 20 years, cases of _Zika_ virus infection were detected sporadically; however, given the clinical similarity of _Zika_ and dengue virus infections and the extensive cross-reactivity of _Zika_ virus antibodies with dengue viruses, it is possible that _Zika_ virus was associated with epidemics that were incorrectly attributed to dengue viruses. Beginning in 2007, substantial _Zika_ virus outbreaks were reported first in Yap Island ( Federated States of Micronesia), then in French Polynesia, and then in other Pacific Islands (2–4).

Genetic studies have revealed that _Zika_ virus has evolved into 3 distinct genotypes: West African (Nigerian cluster), East African (MR766 prototype cluster), and Asian. It has been postulated that the virus originated in East Africa and then spread into both West Africa and Asia ≈50–100 years ago (5). In early 2015, cases of _Zika_ virus infection were detected in Rio Grande State, northern