tuberculosis than those living in the most deprived areas (multivariate incidence rate ratio 0·74, 95% CI 0·62–0·89; p=0·002). Second, delayed access (≥1 year) to primary medical care services after migration was associated with an increased risk of active tuberculosis (2·96, 2·59–3·38; p<0·0001).[8] Third, migrants who were not tested for active tuberculosis were more likely to develop the disease than those who were tested (1·49, 1·33–1·67; p<0·0001). Testing for latent tuberculosis infection was done in 2451 migrants, with 421 (17%) positive tests and no subsequent diagnoses of active tuberculosis.

Berrocal-Almanza and colleagues' findings add to the body of evidence that testing for active tuberculosis in migrants before entry to a country with a low incidence of tuberculosis might be associated with a reduced risk of active tuberculosis diagnosis following migration,[9] despite the low yield of this intervention (<0·4% of new-entrant migrants[2]). The study provides preliminary evidence with respect to the effectiveness of latent tuberculosis infection testing, but additional data are needed because only a small number of participants in the study underwent testing for latent tuberculosis. The results are important for drawing attention to social determinants of tuberculosis risk, including social and material deprivation and health-care access. Berrocal-Almanza and colleagues argue that improving migrants' access to primary medical care would probably improve tuberculosis control in the UK. This concept is plausible because delayed diagnosis is common, and comorbidities that are prevalent in migrants, such as diabetes,[10] are associated with tuberculosis risk and treatment outcomes. The present findings imply that people who are not tested for tuberculosis, are not registered in primary care, and live in deprived circumstances might be a particularly high-risk group that future research should aim to include.

It is important to consider the perspectives of people who live as migrants and to recognise the financial, legal, organisational, and social barriers to accessing health care that they experience.[11] The results remind us of Virchow's remark that "medicine is a social science, and politics nothing but medicine at a larger scale".[12] Tuberculosis control not only requires the detection of infections and delivery of antimicrobial treatment—it also requires establishing conditions in which people can protect and preserve their health.

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Increased mortality in survivors of Ebola virus disease

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Long-term sequelae of Ebola virus disease—including myalgia, arthralgia, ocular diseases, and mental confusion—have come to light in survivors of the 2014–16 Ebola outbreak in west Africa. The frequency and duration of these sequelae, which are collectively referred to as post-Ebola virus disease syndrome, have since been reported.[1] However, information about subsequent mortality in survivors of Ebola is scarce.

Anecdotal reports and one previous study[2] have documented the unexpected death of survivors of Ebola virus disease after viral clearance and discharge from Ebola treatment units, suggesting that the acute phase of the disease can lead to protracted death in some survivors, but no systematic investigations of increased mortality in survivors have previously been published.

In *The Lancet Infectious Diseases*, Mory Keita and colleagues[3] report mortality in survivors of Ebola virus disease in Guinea, who were followed up for a mean of 21·2 months after discharge from Ebola treatment units. Within a year of discharge, mortality in survivors of Ebola virus diseases was five times higher than that in the aged-matched general population (age-standardised mortality ratio 5·2 [95% CI 4·0–6·8]). Unfortunately, limited data were available for the precise time and cause of death after discharge from Ebola treatment units.

Understanding the cause of delayed mortality associated with Ebola virus disease is essential to the development of optimal countermeasures. In Keita and colleagues' study,[3] 37 (64%) of the 59 late deaths were tentatively attributed to kidney failure on the basis of the symptoms of deceased people as described by family members. Because autopsies were not done, additional causes of death cannot be ruled out. The authors noted that survivors with longer stays in Ebola treatment units during acute infection had an increased risk of mortality during the year after discharge compared with those with shorter stays, suggesting that initial disease severity could be associated with late mortality.[3] Further investigations are needed to understand the role of severe damage to major organs (eg, kidneys, liver, lungs) that occurs during the acute phase of disease in patients who survive Ebola virus disease.

Additional factors could also contribute to these unexpected late deaths. Ebola virus can persist in immune privileged sites, including semen, where it has been isolated more than a year after infection.[4–6] Viral persistence in the CNS was associated with severe meningitis in two survivors of Ebola virus disease, suggesting that Ebola relapses can contribute to late deaths.[6,7] Finally, the prolonged aberrant immune activation that has been documented in survivors of Ebola virus disease could also be implicated.[8]

Keita and colleagues' study is the first of its kind to show a significant increase in mortality in survivors of Ebola virus disease after discharge from Ebola treatment units. Reductions in life expectancy have previously been reported in elderly survivors of sepsis and pneumococcal diseases, suggesting that delayed death could be a common feature of severe acute disseminated diseases.[9–11] The results of Keita and colleagues' study suggest that long-term follow up could be necessary in survivors of other viral haemorrhagic fevers, including Marburg, Crimean-Congo, Lassa, and Nipah haemorrhagic fever viruses. If, as Keita and colleagues report, most delayed death occurs within a year of initial viral clearance, 2-year follow-up studies should be sufficient to measure important decreases in life expectancy. The low frequency of late deaths (2·6–5·2%) in survivors of Ebola virus disease suggests that large cohorts will be needed to detect any substantial reductions in the life expectancy of survivors of viral haemorrhagic fevers.[2,3] Additionally, robust, segregated data for life expectancies within affected countries and regions that account for discrepancies between urban and rural populations are needed to identify variations in mortality.

Increased mortality in survivors of Ebola virus disease is a new reality added to a harsh infectious disease that, however, could be mitigated. Indeed, the high case fatality associated with Ebola virus infection, together with the long-term sequelae and late mortality associated with the infection, highlight the importance of preventive and early therapeutic clinical interventions against severe acute infections. Such measures should include immunisation of at-risk individuals, early treatment of patients, and education and social intervention within affected communities.

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Scarlet fever changes its spots

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Historically, the human pathogen *Streptococcus pyogenes* (group A streptococcus) was a major cause of death as a result of sepsis and fatal epidemics of scarlet fever.[1] Despite a decline in the incidence and severity of these toxin-mediated diseases over the past century in high-income countries, group A streptococcus is still among the top ten infectious causes of human mortality, with more than 500 000 deaths annually.[2] In addition to the persistently high disease burden in low-resource nations, an unprecedented global resurgence of scarlet fever and severe invasive group A streptococcal infections has been seen in the past few decades. However, there is continuing scientific uncertainty surrounding specific factors that might have led to the re-emergence of these diseases.

Group A streptococcus is classified into more than 200 *emm* types.[3] Since the mid-1980s, a hypervirulent serotype *emm*1 group A streptococcus clone has been frequently isolated from severe forms of invasive group A streptococcal disease.[4] The ongoing outbreak of scarlet fever in the UK, first reported in 2014, is polyclonal in nature and not caused by a single epidemic strain of group A streptococcus.[5,6] This scarlet fever outbreak is associated with multiple distinct *emm* types, with *emm3, emm12*, *emm1*, and *emm4* being the most prevalent. In *The Lancet Infectious Diseases*, Nicola Lynskey and colleagues[7] report on the rapid emergence of a new dominant group A streptococcus *emm1* lineage in the UK ($M1_{UK}$) during the 2014–16 scarlet fever seasonal surges, accounting for a synchronous rise in the incidence of invasive infections. Comparative genomic and phylogenetic analysis of upper respiratory tract (isolates from 2009–16) and invasive (2013–16) *emm1* group A streptococcus isolates from the UK showed that the $M1_{UK}$ lineage—which appears to have evolved in the UK as early as 2010—is genotypically distinct from other pandemic *emm1* isolates and is characterised by 27 lineage-defining mutations in regulatory and metabolic genes. These conserved and lineage-specific mutations are associated with significantly increased expression of streptococcal pyrogenic exotoxin A (SpeA)—a phage-encoded superantigen that is crucial for the establishment of nasopharyngeal infection[8] and has played an important role in the epidemic spread of *emm1* strains since the 1980s.[4] Lynskey and colleagues' findings, therefore, provide a plausible explanation for the increased capacity of $M1_{UK}$ to cause toxin-mediated scarlet fever and invasive infections in the UK. Given that intermediate members of the $M1_{UK}$ lineage were also identified in countries outside the UK, there is major concern as to whether similar pathogenic changes might occur elsewhere.

Public Health England reported an alarming rise in scarlet fever notifications across the UK in 2018, with a doubling in numbers of reported cases compared with the start of the outbreak in 2014. Mainland China and Hong Kong also have an ongoing outbreak of scarlet fever, with about 500 000 reported cases since 2011.[9] Similar to the UK, case numbers have been increasing in east Asia in the past 2 years; however, the driving force responsible for the enhanced pathogenicity of group A streptococcus in this region is yet to be understood. In contrast to the UK, acquisition of novel prophages harbouring new combinations of toxin genes (encoding the superantigens streptococcal superantigen A and streptococcal pyrogenic exotoxin C, and the DNase Spd1) and antimicrobial resistance genes were closely associated with the emergence and expansion of scarlet fever-associated *emm12* and *emm1* lineages in mainland China and Hong Kong.[9,10]

Comparative population analyses of scarlet fever *emm1* genomes from east Asia and the UK support