data equated to a odds ratio of 50·0 (95% CI 46·0–54·4) for HIV in female sex workers compared with other women, and suggested that about half of all HIV infections (48·6%) in women in China occur in female sex workers.[1]

Chen and colleagues draw attention to several concerns with this estimate, including geospatial variations in the HIV burden in China and bias that favours publication of higher prevalence studies. As noted in the limitations section of our paper, "pooling of data comes at the risk of masking intracountry and intercountry variations in the risk status, including practices and HIV prevalence…Such masking in the variation of risk status is relevant in India and China, which have wide geographical variations in HIV prevalence and risk factors for HIV infection".[1] We wrote of this limitation in view of the wide variation of HIV prevalence in the different studies included; five of the 11 studies reported a HIV prevalence equal or close to 0%. Although assessment of the contribution of publication bias is impossible without a registry of epidemiological studies, the publication of studies with low HIV prevalence argues against a major role for publication bias.

Surveillance of female sex workers in China has increased substantially in the past few years, with 61 919 women tested in 2009 and 204 614 tested in 2011.[2] However, although testing has increased, Chen and colleagues emphasise that the highest-risk establishments are undersampled in the present surveillance system. They also draw attention to wide variation in self-reported drug use (2·8%–18·2%) in female sex workers in Honghe Prefecture in Yunnan Province. Female sex workers who report drug use in research studies are probably protected from the adverse consequences of doing so because of protection of study participants.[3] However, dual-risk female sex workers who use drugs might self-exclude themselves from the HIV surveillance system in China because of fear of the adverse consequences of the state knowing about their drug use.[4,5] Although the number of sentinel surveillance systems increased between 2003 and 2007, a recent study emphasises that repressive measures targeting female sex workers in China increased concurrently during this period, which potentially reduced access to the highest-risk female sex workers.[6] Overall, these factors probably limit the sensitivity of the national surveillance system in investigation of female sex workers at highest risk for HIV infection.

Our study focused primarily on assessment of the disproportionate burden of HIV in female sex workers through a comparison of the prevalence of HIV in female sex workers with that in reproductive-age women. In view of the fact that female sex workers in China have about a 50-times increased risk for HIV infection and bear an estimated 50% of HIV infections in women in the country, we believe that this group should continue to represent a key population for research and programmes in China. The pooled estimate presented probably overestimates the actual prevalence of HIV in Chinese female sex workers, and the national surveillance system probably underestimates this prevalence by undersampling the highest-risk women. The unknown reality probably lies somewhere between these two estimates.

We declare that we have no conflicts of interest.

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Bloodstream infections in south and southeast Asia

We read with interest the Review by Jacqueline Deen and colleagues[1] about bloodstream infections in south and southeast Asia region. We appreciate the work done by the authors in collection of valuable data for invasive bacterial infections and their resistance patterns from a region that is especially affected by the antimicrobial resistance epidemic. However, we are not convinced that their method—although sound and meticulous—represents "the best available to describe case fractions and prevalent pathogens in developing countries in south and southeast Asia, as well as patterns of antimicrobial resistance". Despite the strict criteria used to select the individual articles, the final compilation of 19 publications might not guide the reader well. For example, the compilation includes seven paediatric studies with a very strong focus on pneumonia, meningitis, or both. Data from these studies, which represent more than a third of the compiled articles, provide useful information about respiratory pathogens, but do not represent the entire range of other important pathogens in children, such as *Staphylococcus aureus*. The compilation is also affected by other biases—eg, some studies

predominantly focused on patients with HIV[2] or also included data for nosocomial resistance.[3]

Compilation of pathogen frequencies and antibiotic resistance patterns from very diverse patient groups and countries can lead to diluted information, which is inaccurate for any country or patient group. South and southeast Asia are highly diverse in terms of microbiology and antibiotic resistance. For example, among 450 prospectively collected bloodstream infection isolates from adults in Phnom Penh, Cambodia,[4] *Burkholderia pseudomallei* was the third most common pathogen after *Escherichia coli* and *Staphylococcus aureus*. *B pseudomallei* is also highly prevalent in northeast Thailand, but rare in central or southern Thailand and southern Vietnam. Similarly, important intraregional differences in resistance patterns exist, as shown by Ochiai and colleagues[5] for nalidixic acid resistance rates in *Salmonella typhi*, which ranged from 0% (Indonesia and China) to 59% (Pakistan). Therefore, we think that the aggregated figure of 5% nalidixic acid resistance among *S typhi* does not convey the most relevant information to clinicians and policy makers, since it probably underestimates the actual resistance rate in many countries in south and southeast Asia.

In our opinion, display of these data as regional maps with resistance data per country, per pathogen, and per patient category would be a better way to represent the real-life situation and inform the scientific community.

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Authors' reply

Erika Vlieghe and colleagues reiterate our points about the strengths and shortcomings of our Review on bloodstream infections in developing countries in south and southeast Asia.[1] We agree that the amalgamation of data from very different contexts is problematic, and for this reason we presented study-specific findings, classified our results by age group, and provided ranges and point estimates when appropriate.

Mapping of aetiology and resistance data per country, per pathogen, and per patient category is a very worthwhile endeavour. However, this project needs far more extensive data than are available at present, as evidenced by the total of 19 qualifying papers in our Review to describe all of south and southeast Asia. Spatial heterogeneity is only part of the challenge and is complicated further by temporal variability, both seasonal and longer term, due to economic development, environmental changes, and increased population mobility.

The ultimate goal should be a data repository, which is updated continuously with the most recent research, and has a user-friendly graphical interface to describe spatial and longitudinal trends. Initiatives such as the Malaria Atlas Project and the WorldWide Antimalarial Resistance Network aim to achieve this goal in the simpler context of malaria, but substantial challenges exist in sharing of primary research data. For bacterial infections, the need for data is greater by several orders of magnitude because of the large number of pathogens and antibiotics implicated. Our own experience in attempting to obtain the primary data needed for more detailed analyses in this and similar reviews[2] confirms these challenges.

Such a data repository could be feasible in the future. Better use of routine microbiological testing data could offer huge amounts of information from a wide range of settings that might circumvent data propriety challenges in the research community. Cheap, high-throughput diagnostic technologies will strengthen capacities in remote, under-researched areas. Expansion of national surveillance networks, WHONET software, and standardisation of protocols could all eventually provide a far more detailed and up-to-date description of aetiological and antimicrobial resistance patterns than that presently provided by the small number of disparate research studies.

As microbiology and information technologies improve and a culture of data sharing develops, such an endeavour will hopefully become a reality. Meanwhile, reviews such as ours, notwithstanding their many limitations, make the best use of the existing data.

We declare that we have no conflicts of interest.

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