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SYSTEMATIC REVIEW
Seroprevalence of IgG antibodies to SARS-coronavirus in asymptomatic or subclinical population groups

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SUMMARY

We systematically reviewed the current understanding of human population immunity against SARS-CoV in different groups, settings and geography. Our meta-analysis, which included all identified studies except those on wild animal handlers, yielded an overall seroprevalence of 0·10% [95% confidence interval (CI) 0·02–0·18]. Health-care workers and others who had close contact with SARS patients had a slightly higher degree of seroconversion (0·23%, 95% CI 0·02–0·45) compared to healthy blood donors, others from the general community or non-SARS patients recruited from the health-care setting (0·16%, 95% CI 0–0·37). When analysed by the two broad classes of testing procedures, it is clear that serial confirmatory test protocols resulted in a much lower estimate (0·050%, 95% CI 0–0·15) than single test protocols (0·20%, 95% CI 0·06–0·34). Potential epidemiological and laboratory pitfalls are also discussed as they may give rise to false or inconsistent results in measuring the seroprevalence of IgG antibodies to SARS-CoV.

INTRODUCTION

Major outstanding questions about severe acute respiratory syndrome (SARS) remain in order to complete the agent–vector–host epidemiological triangle (Fig. 1). Is there a significant human reservoir of SARS-coronavirus (CoV) from either the 2003 epidemic or perhaps through previous but undetected circulation of the virus? Were there a limited number of susceptibles within the population before the outbreak that made community infection control easier to achieve [1]?

Studies based on hospitalized cases have suggested that the overall transmissibility of SARS is relatively low compared to other pathogens, as indicated by the basic reproductive number of ~3 [2]. However, such studies could not take into account possible episodes of mild or moderate illness which did not require in-patient medical care and, therefore, could not address whether subclinical community spread played an important role in the 2003 epidemic. If this is the case, the population might now have developed sufficient herd immunity to protect against another large outbreak. Key to understanding these issues is the

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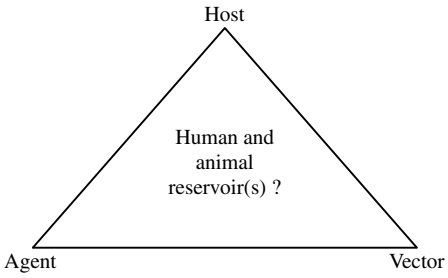

Fig. 1. Agent–vector–host triangle of infectious diseases.

systematic study of the seroepidemiology of SARS-CoV in different population groups.

Epidemiological and laboratory methods for the study of seroprevalence

The study of population immunity and prevalence of past infection is typically based on systematic random sampling from the general population with appropriate stratification, or on different groups with *a priori* varying degrees of risk for infection.

Systematic adherence to the basic epidemiological principles of unbiased, random sampling is important. The sampling frame and size must be defined clearly and in the case of special surveys the response and participation rate is also important. Together, these components determine the validity and precision of the estimates of seroprevalence ratios. The numerator of the ratio includes those who test positive based on a series of pre-defined immunological tests, each with a particular threshold of serological titre to immunoglobulin (Ig) G antibodies against the agent under consideration, indicating the number of people in the sample who had been infected at some stage of their life. Because SARS is a newly emergent human disease, this also represents the extent of asymptomatic spread since the first reported human case in November 2002 in Guangdong [3]. The appropriate laboratory tests for serological diagnosis vary depending on the agent. Moreover, the sequence of different tests is important as it changes the Bayesian pre-test probability of a positive result and thus, the overall sensitivity and specificity of the particular testing protocol. Serial testing, where only positive samples on the initial test proceed to the next test, generally increases specificity but decreases sensitivity, while parallel testing where different tests are performed simultaneously has the opposite effect. For SARS-CoV, the most widely adopted methods for detection of antibodies are indirect immunofluorescence assays (IFA) and enzyme-linked immunosorbent assays (ELISA) with cell-culture extracts from which positive screens are confirmed using standard virological neutralization tests [4]. Alternative approaches have been suggested such as ELISA-based antibody detection tests using recombinant antigens with positive screens confirmed by Western blots that use two different antigenic proteins (nucleocapsid protein and spike polypeptide) of SARS-CoV [5]. It is difficult, especially for newly emerging diseases such as SARS, to decide initially which set of laboratory techniques are optimal for antibody serosurveys. A careful comparison of these different methods against established gold standards is essential, using benchmark indices including sensitivity, specificity, the area under the receiver operating characteristic curve and likelihood ratios [6]. In addition, cross-reactivity of these assays to related microbial agents must be considered in order to achieve specificity and reduce false positives to a minimum.

Serosurveys for SARS-CoV IgG antibodies

To identify relevant serosurveys for SARS-CoV antibodies, we searched MEDLINE for articles published between January 2003 and July 2004 using combinations of the MeSH terms 'SARS virus', 'severe acute respiratory syndrome', 'seroepidemiologic studies' and/or 'antibodies', and keywords 'serosurvey' and/or 'seroprevalence'. We also searched relevant publications and websites of the World Health Organization (WHO), US Centers for Disease Control and Prevention (CDC) and other similar national or regional agencies of SARS-affected places to identify studies that were potentially not included in MEDLINE. We searched the bibliographies of identified studies manually and consulted with experts in the field to try and locate other reports not found through our main search strategy.

Our inclusion criteria were broad and required only reporting of seroprevalence (i.e. both numerator and denominator data) of SARS-CoV in individuals who were never diagnosed with SARS as defined by the WHO [7]. We did not place any limits on epidemiological study design, laboratory methods or language of publication. Data were abstracted from the original source publication by two independent, blinded research assistants. Potential disagreements were settled by a third researcher after independent review.

A total of 16 studies, from five SARS-affected regions (Beijing, Guangzhou, Hong Kong, Singapore

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and Toronto), were identified [4, 5, 8–21] (Table) There is wide variation in the reported seroprevalence of antibodies against SARS-CoV which is strongly associated with the characteristics of the subjects tested (indicating *a priori* risk of infection) and the laboratory methods employed to determine seroconversion.

With the exception of handlers of wild animals and market workers, the degree of asymptomatic infection was $<3\%$ for all studies (Table). We combined the results of these studies, stratified by subgroups indicating the *a priori* risk of infection with the timing of specimen collection classified as pre- *vs*. post-SARS epidemic (Fig. 2), and by laboratory testing protocols (Fig. 3). The 95% confidence intervals (CI) for the seroprevalence estimates in each study were computed using exact binomial CIs. The META program [22] was employed to calculate weighting associated with individual studies. In calculating the standard errors, if a study had no seropositive cases (i.e. a zero numerator), a count value of 0·1 was used instead according to the usual convention, to avoid the problem of zero-count cells while minimizing the potential to inflate precision of the underlying study. The method of DerSimonian & Laird [23] was used to test for heterogeneity across studies which was significant ($P<0{\cdot}001$) for both sets of meta-analyses presented in Figures 2 and 3. Therefore, a random-effects model was assumed in computing the weights of the study and variances of the combined estimates. The 95% CIs for the combined estimates were calculated by normal approximation.

Our meta-analysis, which included all identified studies except those on handlers of wild animals due to the presumed zoonotic origin of SARS-CoV and the very different associated risk of infection (Fig. 3), yielded an overall seroprevalence of 0·10% (95% CI 0·02–0·18). Figure 2 shows that the summary seroprevalence estimates of the different strata follow the same gradient of *a priori* risk levels, the one exception being a study of stored serum from healthy Hong Kong adults in 2001 [21]. The two Chinese studies [8, 19] in the wild animal markets of Guangzhou indicated that 14·86% (95% CI 12·77–16·94) of the workers had prior exposure to SARS-CoV although none had apparently shown significant symptoms compatible with the clinical description of SARS. Health-care workers and others who had close contact with SARS patients generally had a slightly higher degree of seroconversion (0·23%, 95% CI 0·02–0·45) compared to healthy blood donors, others from the general community or non-SARS patients recruited from the health-care setting (0·16%, 95% CI 0–0·37). The two studies on stored serum collected prior to the 2003 epidemic [5, 21] gave very different estimates although we note that the latter actually tested against both human and animal SARS-CoV strains. When analysed by the two broad classes of testing procedures, it is clear that serial confirmatory test protocols resulted in a much lower estimate (0·050%, 95% CI 0–0·15) than single test protocols (0·20%, 95% CI 0·06–0·34).

Although there are considerable variations in the seropositive estimates reported, it is clear that seroconversion is extremely rare among health-care workers, close contacts of SARS patients who did not develop the disease and members of the general population, including healthy individuals and non-SARS patients. This property of SARS-CoV, perhaps reflecting the evolutionary fitness of the virus, is in stark contrast to other common respiratory agents, most notably influenza where the usual 'iceberg' concept of disease applies [24]. Instead the pattern of SARS infection in the community can paradoxically be represented as an inverted iceberg (Fig. 4).

The extent of seroconversion in asymptomatic individuals with a history of intense exposure to those infected with SARS, including health-care workers and close contacts of cases, should provide the upper seropositivity limit in the general population. The overall finding of the near absence of transmission resulting in asymptomatic infection and seroconversion in these high-risk groups from different countries and settings indicates that the prevailing SARS-CoV strains almost always led to clinically apparent disease. Whereas some SARS patients might have been initially admitted in order to reduce transmission to family members, virtually all (perhaps with some exceptions in children) [25] had severe disease requiring in-patient treatment, so we can infer that the 2003 epidemic infection with SARS-CoV inevitably caused severe disease requiring hospitalization.

While the results of this meta-analysis suggest that SARS-CoV was a new virus in humans with neither a close precursor nor an antigenically related virus that would have induced at least a small degree of cross-reactivity on serological testing, the study by Zheng and colleagues [21] on the stored serum of 938 healthy Hong Kong adults from a hepatitis B serosurvey in 2001 detected a positive antibody response against human SARS-CoV or animal SARS-CoV-like virus in 1·81% (95% CI 1·06–2·89) of the sample by IFA

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Table. *Serosurveys for SARS-CoV antibodies*

Study	Location	Laboratory methods	Time of specimen collection	Subjects	Seroprevalence (95% exact binomial confidence interval)
CDC [8]	Guangzhou, China	ELISA	May 2003	508 wild animal traders	12·99% (10·19–16·23)
				137 hospital workers	2·92% (0·80–7·31)
				63 public health officials	1·59% (0·04–8·53)
				84 adults recruited from a clinic	1·19% (0·03–6·46)
Chan et al. [9]	Hong Kong	IFA	March–May 2003	674 health-care workers in a tertiary care hospital that admitted SARS patients	0% (0–0·44)
Chan et al. [10]	Hong Kong	Screened by ELISA; confirmed by IFA and Western blot	2003 (post-SARS epidemic)	12020 volunteers from the general population	0·0083% (0·00021–0·046)
Chow et al. [11]	Singapore	Screened by ELISA; confirmed by neutralization tests	2003 (post-SARS epidemic)	84 asymptomatic health-care workers at a tertiary care hospital that admitted SARS patients	0% (0–3·50)
Gold et al. [12]	Toronto, Canada	Screened by IFA; confirmed by Western blot and neutralization tests	July–September 2003	767 asymptomatic health-care workers at four hospitals that admitted SARS patients	1·04% (0·45–2·04)
Ho et al. [13]	Singapore	Screened by ELISA and dot-blot immunoassay; confirmed by IFA and neutralization tests	2003 (paired serum samples collected during the peak of the local epidemic and on average 31 days later)	304 asymptomatic health-care workers at a tertiary care hospital that admitted SARS patients*	0% (0–0·98)
Leung et al. [4]	Hong Kong	Screened by ELISA; confirmed by IFA and neutralization tests	October–December 2003	1068 close contacts of SARS cases	0·19% (0·02–0·67)
Li et al. [14]	Guangzhou, China	ELISA	2003 (post-SARS epidemic)	103 contacts of SARS cases	0% (0–2·87)
Li et al. [15]	Guangzhou, China	IFA and ELISA	2003 (post-SARS epidemic)	1060 healthy children	0% (0–0·28)
Liu et al. [16]	Beijing, China	ELISA	2003 (post-SARS epidemic)	197 non-SARS hospital outpatients and in-patients $\leqslant$14 years	2·03% (0·56–5·12)
				156 healthy primary school children	1·92% (0·40–5·52)
				453 non-SARS hospital outpatients and in-patients $\geqslant$18 years	0·22% (0·01–1·22)
				502 adult blood donors	0·20% (0·01–1·10)
Seto et al. [17]	Hong Kong	Screened by ELISA; confirmed by neutralization tests	2003 (post-SARS epidemic)	875 health-care workers	0·11% (0·0029–0·64)
Wang et al. [18]	Beijing, China	ELISA	2003 (post-SARS epidemic)	1127 health-care workers	2·57% (1·73–3·67)

Woo et al. [5]	Hong Kong	Screened by ELISA; confirmed by two separate Western blots	2000	149 blood donors	0% (0–1·99)
			March–May 2003	106 SARS cases	100% (97·21–100)
			March–May 2003	400 blood donors	0·75% (0·15–2·18)
			May 2003	131 non-pneumonic paediatric patients	0·76% (0·02–4·18)
			May 2003	264 non-pneumonic adult patients	0% (0–1·13)
			May 2003	33 asymptomatic health-care workers	0% (0–8·68)
Xu et al. [19]	Guangzhou, China	ELISA	May–June 2003	635 wild animal traders	16·69% (13·87–19·83)
Yu et al. [20]	Hong Kong	Screened by ELISA; confirmed by IFA	June–July 2003	574 general practitioners in the community	0% (0–0·52)
Zheng et al. [21]	Hong Kong	Screened by IFA; confirmed by neutralization tests Positive results defined as reactivity to *either* human SARS-CoV *or* animal SARS-CoV-like virus	May 2001	938 healthy adults randomly recruited in a telephone survey on hepatitis B	1·81% (1·06–2·89)

ELISA, Enzyme-linked immunosorbent assay; IFA, immunoflorescence assay.

* An additional 62 mildly symptomatic health-care workers (some admitted and others treated as outpatients) were also included in the study, two of whom tested positive yielding a seroprevalence of 3·23% (95% CI 0·39–11·2).

and was confirmed using neutralization tests. The researchers speculated that the virus that affected these healthy seropositive individuals was antigenically closer to the isolated animal SARS-CoV-like virus [26] than human SARS-CoV, and that this might account for the asymptomatic presentation of the infected individuals who seroconverted if the early animal strains of SARS-CoV-like virus were of low pathogenicity to humans. Some suggest that zoonotic transmission from animal to human was likely to be infrequent especially given the absence of markets of wild animals and restaurants in Hong Kong. Therefore, there was little opportunity for evolutionary selective pressures to facilitate interspecies infection of the human host in Hong Kong. Moreover, the acquisition by the virus of characteristics that enhance virulence in humans was likely to be immature. Human-to-human spread was probably highly inefficient as the virus might not have adapted in its new host. Together, these reasons were postulated to explain why only a few persons became infected and why they were likely to have been asymptomatic 2 years before the 2003 epidemic.

However, we hesitate in subscribing to this line of reasoning. First, it is important to clarify that this hypothesis is different to the presumed asymptomatic infection observed in Guangdong animal traders, especially in those who handled masked palm civets with an overall seropositivity rate of 72·7% (95% CI 49·8–89·3) [8]. Frequent zoonotic challenges in this group probably gave rise to the high asymptomatic seroconversion rate at a time when the SARS-CoV animal strains had not yet evolved into a highly pathogenic variant. Over time, sustained human exposure to the presumed animal reservoir(s) of SARS-CoV in wild animal farms and markets of southern China eventually resulted in multiple introductions of a moderately transmissible [2, 27] form of the virus into the human population [3, 28, 29] that led to the massive global outbreak. Second, it would be helpful to know how the antibody responses in 17 out of 938 subjects who seroconverted [21] were apportioned between human *vs.* animal SARS-CoV strains respectively. Third, and most importantly, if animal-to-human transmission was present in 2001 that led to a 1 in 55 chance of being asymptomatically infected in the general population, why has this observation not been repeated in other serosurveys since? We suggest that this outlier seroprevalence estimate will remain unexplained until the study is replicated on other stored blood samples in Hong Kong and elsewhere.

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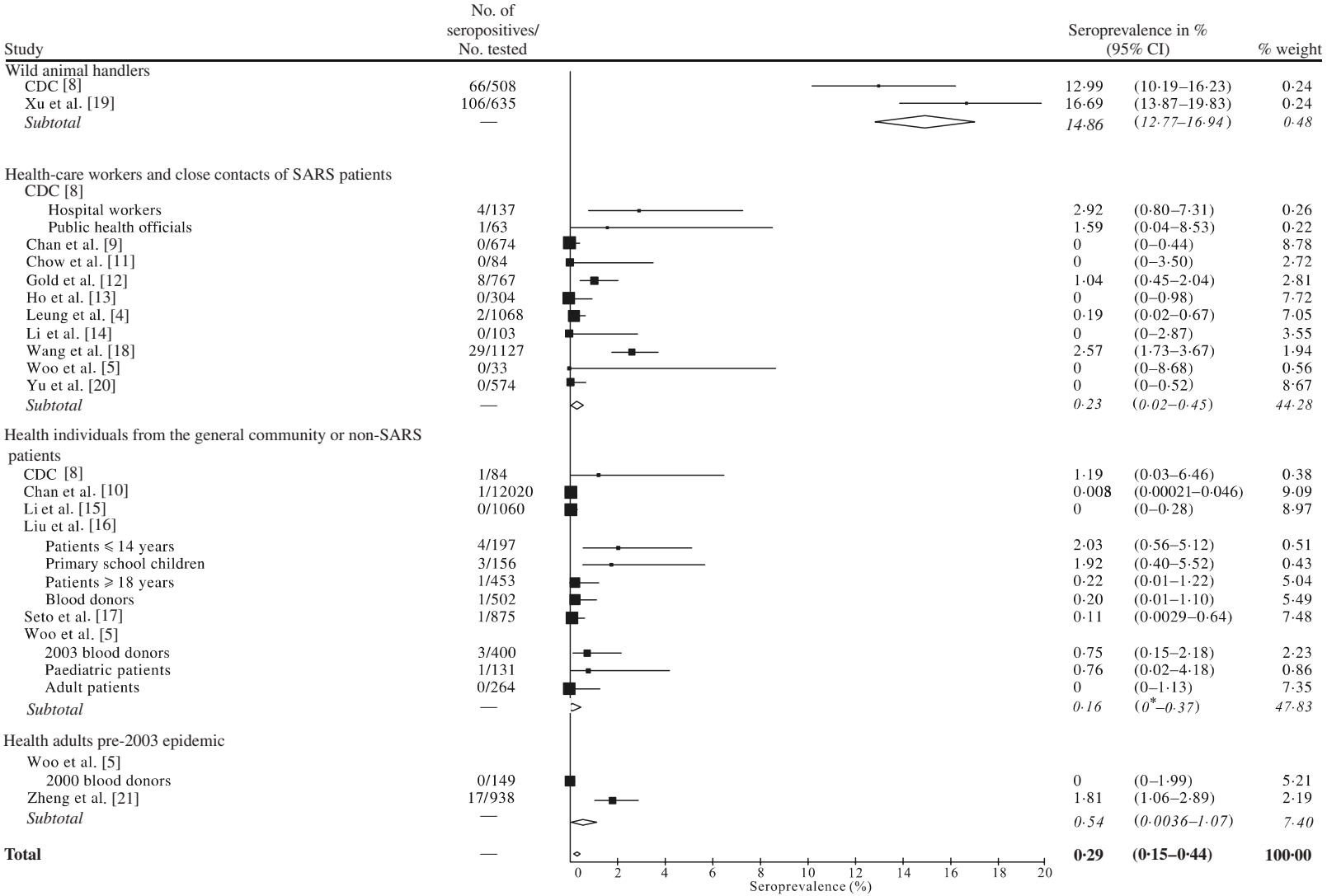

Fig. 2. Forest plots of seroprevalence estimates stratified by *a priori* risk of infection under a random-effects model. The seroprevalence for individual studies is shown as solid squares scaled according to weighting by using the inverse variance method. Error bars indicate 95% CIs. The combined seroprevlence estimates are shown as diamonds that span the 95% CI (* truncated at zero).

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Study	No. of seropositives/ No. tested	Seroprevalence in % (95% CI)		% weight
Serial confirmatory test protocols against human SARS-CoV				
Chan et al. [10]	1/12020	0·0083	(0·00021–0·046)	14·56
Chow et al. [11]	0/84	0	(0–3.50)	1·14
Gold et al. [12]	8/767	1·04	(0·45–2·04)	1·19
Ho et al. [13]	0/304	0	(0–0·98)	7·67
Leung et al. [4]	2/1068	0·19	(0·02–0·67)	5·93
Li et al. [15]	0/1060	0	(0–0·28)	13·63
Woo et al. [5]				
2000 blood donors	0/149	0	(0–1·99)	3·06
2003 blood donors	3/400	0·75	(0·15–2·18)	0·88
Paediatric patients	1/131	0·76	(0·02–4·18)	0·30
Adult patients	0/264	0	(0–1·13)	6·64
Health-care workers	0/33	0	(0–8·68)	0·19
Yu et al. [20]	0/574	0	(0–0·52)	11·67
Subtotal	—	*0·05*	*(0*–0·15)*	*66·86*
Single test protocols or testing against both human and animal SARS-CoV				
CDC [8]				
Hospital workers	4/137	2·92	(0·80–7·31)	0·08
Public health officials	1/63	1·59	(0·04–8·53)	0·07
Adults from a clinic	1/84	1·19	(0·03–6·46)	0·12
Chan et al. [9]	0/674	0	(0–0·44)	12·36
Li et al. [14]	0/103	0	(0–2·87)	1·64
Liu et al. [16]				
Patients ⩽ 14 years	4/197	2·03	(0·56–5·12)	0·17
Primary school children	3/156	1·92	(0·40–5·52)	0·14
Patients ⩾ 18 years	1/453	0·22	(0·01–1·22)	2·88
Blood donors	1/502	0·20	(0·01–1·10)	3·39
Seto et al. [17]	1/875	0·11	(0·0029–0·64)	10·67
Wang et al. [18]	29/1127	2·57	(1·73–3·67)	0·74
Zheng et al. [21]	17/938	1·81	(1·06–2·89)	0·86
Subtotal	—	*0·20*	*(0·06–0·34)*	*33·14*
Total	—	**0.10**	**(0·02–0·18)**	**100·00**

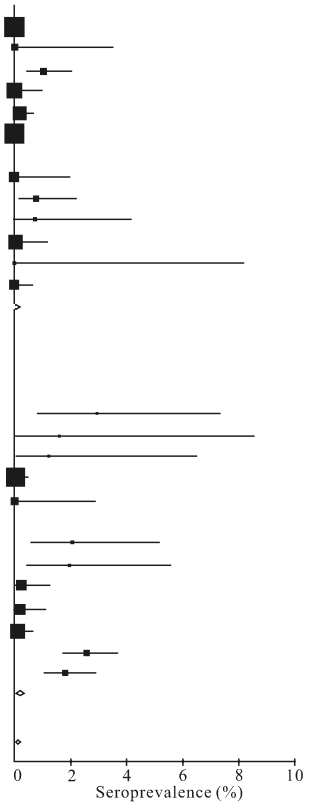

Fig. 3. Forest plots of seroprevalence estimates (excluding wild animal handlers) stratified by laboratory test strategies under a random-effects model. The seroprevalence for individual studies is shown as solid squares scaled according to weighting by using the inverse variance method. Error bars indicate 95 % CIs. The combined seroprevalence estimates are shown as diamonds that span the 95 % CI (* truncated at zero).

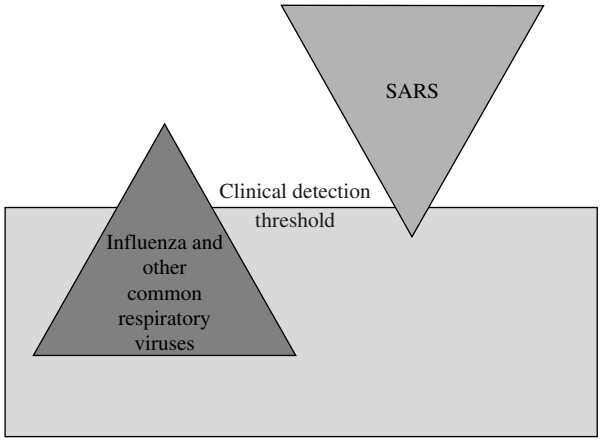

Fig. 4. Iceberg concept of disease – the SARS paradox.

In addition, there remains much uncertainty as to why two surveys by Woo and colleagues [5] and Gold et al. [12] produced much higher seroprevalence estimates than other studies that also adopted a serial confirmatory testing procedure. We believe that the difference can still be due to false positivity on laboratory testing given the test kit validation procedure adopted by Woo et al. [5] although there is insufficient detail in Gold et al.'s abstract to further appraise the laboratory analysis. In evaluating ELISA for the detection of antibody to nucleocapsid protein, Woo et al. reported a sensitivity of 94·3% and a specificity of 95·3% for IgG antibody by testing specimens from 149 healthy blood donors and 106 SARS patients. Based on subjecting the seven samples out of 149 which gave positive ELISA results to Western-blot testing, they concluded that the specificity of the IgG antibody test was 100%. No other description or information, however, was provided on how the Western-blot assay was evaluated. A larger size of samples from another appropriate source, including potentially interfering samples, would be necessary to confirm the specificity of diagnostic assays. Even with a serial testing algorithm, a small change in specificity may affect the positive predictive value to a great extent, especially when the prevalence of infection here is so low.

Pitfalls, caveats and lessons learned

The first lesson to be drawn concerns sampling methods. With the exception of two studies [4, 10], none of the other serosurveys fully specified the sampling frame, recruitment strategy or response rate. There was also scant attention paid to examining the representativeness of sampled subjects [30].

The second lesson concerns the issue of survival in health-care workers and close contacts. Both groups were clearly exposed, whether protected or not, to a significant infectious source, either through direct contact with SARS patients for whom they cared or with whom they lived in the same household, or via a common environmental point source such as the sewage pipes and bathroom ventilation system in the case of Amoy Gardens in Hong Kong [31]. The fact that they remained asymptomatic or uninfected perhaps implies a systematically different host biology to those who fell sick with the disease. Whether such potential human leukocyte antigen (HLA) allelic differences, that have been suggested to be differentially associated with the clinical severity of SARS, also extend to susceptibility and more specifically to asymptomatic infection has yet been resolved [32]. It would not be surprising if this were the case given previous experience where HLA variations were associated with susceptibility or resistance to malaria, tuberculosis, leprosy, HIV, hepatitis virus persistence and human coronavirus OC-43 infection [33–35]. In this case, the seroprevalence estimates as reported would have been biased either upwards or downwards depending on the effect of the particular HLA polymorphisms.

The third lesson concerns laboratory methods including the use of serial testing procedures and confirmation of screening test results. Our findings indicate that seroprevalence estimates tended to be considerably higher in studies that used only single test protocols compared to those that applied a series of confirmatory tests subsequent to a positive screen. Specificities for the ELISA test against SARS-CoV have been reported to be between 94·3% and 98·5% [4, 36, 37] whereas sensitivities achieved 100% at least 1 month since the acute onset of illness [4, 27]. Given the very low absolute levels of seroprevalence to be detected (i.e. $<3\%$ as in the Table), a false-positive ratio of between 1·5% and 5·7% introduces an unacceptably high level of uncertainty in the point estimate.

A related fourth lesson concerns the potential for cross-reactivity between SARS-CoV and other coronaviruses, including the four known human coronaviruses, i.e. OC-229E and OC-43 that cause the common cold and the newly discovered NL63 [38] and HKU1 [39]. NL63 is a group 1 human coronavirus and has been isolated from children and adults with respiratory tract infections as well as immunocompromised adults [40], leading some to propose

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that it is a 'global and seasonal pathogen of both children and adults associated with severe lower respiratory tract illness' [41]. HCoV-HKU1 is a novel group 2 coronavirus associated with pneumonia recently isolated from two cases in Hong Kong, although its population prevalence has yet to be documented. While this issue remains a potential consideration and various reports have thus far failed to provide conclusive empirical evidence either for [42–44] or against [37] the idea, it is nonetheless important when considering the extent of seroconversion in the population and the laboratory methods employed to reduce this potential bias to a minimum. SARS-CoV is neither a host-range mutant of a known coronavirus nor a recombinant between known coronaviruses but a distinct virus probably with a distant common ancestor to the group 2 bovine and murine coronaviruses [45, 46]. The close similarity between the SARS-CoV open reading frame (ORF) 1b and other coronaviruses [47, 48] as well as the fact that the nucleocapsid or N protein shares common antigenic epitopes with that of antigenic group 1 animal coronaviruses [43] reinforces the need for a cautionary approach in interpreting laboratory results [49–51]. In further support of this, 22 samples out of 33 ELISA-screen positives in the study by Woo et al. [5] reacted against the N protein but turned out to be negative when tested against the spike (S) protein [37]. Indeed, Woo and co-workers [44] recently showed that four out of 31 HCoV-OC43 and OC-229E samples cross-reacted on SARS-CoV ELISA testing. Although none of these four samples were found to contain a specific antibody in the recombinant SARS-CoV spike polypeptide-based Western blot assay, the gold standard to avoid this potential pitfall of cross-reactivity in SARS-CoV antibody detection probably remains the neutralization assay as the final confirmation in the serial testing protocol.

Our findings support the global consensus, from previously available clinical data, that there were very few, if any, confirmed cases of transmission from asymptomatic individuals. It remains possible, although unlikely given the results of published studies reviewed here [4, 10, 15, 16], that the pattern of infection is different in some children and adolescents. Nevertheless, results from an as yet unpublished serosurvey in children from the Amoy Gardens cluster (the largest superspreading event in Hong Kong) may yield new information on this issue.

For population-based studies of communicable disease transmission to provide valid and reliable results we have demonstrated that it is essential that standardized protocols and methods are used to obtain and investigate the sampled subjects. Such an approach would lead to a more rapid development of the evidence base needed to inform public health decision-making in communicable disease control.

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REFERENCES

1. **Breiman RF, Evans MR, Preiser W, et al.** Role of China in the quest to define and control severe acute respiratory syndrome. Emerg Infect Dis 2003; **9**: 1037–1041.
2. **Riley S, Fraser C, Donnelly CA, et al.** Transmission dynamics of the etiological agent of severe acute respiratory syndrome (SARS) in Hong Kong: the impact of public health interventions. Science 2003; **300**: 1961–1966.
3. **Zhong NS, Zheng BJ, Li YM, et al.** Epidemiology and cause of severe acute respiratory syndrome (SARS) in Guangdong, People's Republic of China, in February, 2003. Lancet 2003; **362**: 1353–1358.
4. **Leung GM, Chung PH, Tsang T, et al.** SARS-CoV antibody prevalence in all Hong Kong patient contacts. Emerg Infect Dis 2004; **10**: 1653–1656.
5. **Woo PC, Lau SK, Tsoi HW, et al.** Relative rates of non-pneumonic SARS coronavirus infection and SARS coronavirus pneumonia. Lancet 2004; **363**: 841–845.
6. **Hunink M, Glasziou P, Siegel J, et al.** Decision making in health and medicine: integrating evidence and values. Cambridge: Cambridge University Press: 2001.
7. **WHO.** Consensus document on the epidemiology of severe acute respiratory syndrome (SARS), 2003 (http://www.who.int/csr/sars/en/WHOconsensus.pdf). World Health Organisation. Accessed 29 June 2004.
8. **Centers for Disease Control and Prevention.** Prevalence of IgG antibody to SARS-associated coronavirus in animal traders – Guangdong Province, China, 2003. Morb Mortal Wkly Rep 2003; **52**: 986–987.

https://doi.org/10.1017/S0950268805004826 Published online by Cambridge University Press

9. **Chan PK, Ip M, Ng KC, et al.** Severe acute respiratory syndrome-associated coronavirus infection. Emerg Infect Dis 2003; **9**: 1453–1454.
10. **Chan FKL, Ching JYL, Wong WE, et al.** A population-based study of the seroprevalence of asymptomatic SARS-associated coronavirus infection in Hong Kong. Hospital Authority Convention 2004 – Hong Kong SARS Forum Special Issue on SARS Abstracts; 2004, p. 85.
11. **Chow PK, Ooi EE, Tan HK, et al.** Healthcare worker seroconversion in SARS outbreak. Emerg Infect Dis 2004; **10**: 249–250.
12. **Gold WL, Mederski B, Rose D, et al.** Prevalence of asymptomatic (AS) infection by Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV) in exposed healthcare workers (HCW). Abstracts from the 2003 Interscience Conference on Antimicrobial Agents and Chemotherapy (ICAAC).
13. **Ho KY, Singh KS, Habib AG, et al.** Mild illness associated with severe acute respiratory syndrome coronavirus infection: lessons from a prospective sero-epidemiologic study of health-care workers in a teaching hospital in Singapore. J Infect Dis 2004; **189**: 642–647.
14. **Li G, Chen X, Xu A.** Profile of specific antibodies to the SARS-associated coronavirus. N Engl J Med 2003; **349**: 508–509.
15. **Li LH, Shi YL, Li P, et al.** Detection and analysis of SARS coronavirus-specific antibodies in sera from non-SARS children. Di Yi Jun Yi Da Xue Xue Bao 2003; **23**: 1085–1087.
16. **Liu YN, Fan BX, Fang XQ, Yu BX, Chen LA.** The quantitative detection of anti-coronavirus antibody titer in medical personnel closely contacted with severe acute respiratory syndrome patients. Zhonghua Jie He He Hu Xi Za Zhi 2003; **26**: 583–585.
17. **Seto WH, Ng TK, Lai ST, Yam L, Lw KI, Chan JCK.** Sero-surveillance of healthcare workers in clinical areas with SARS patients. Hospital Authority Convention 2004 – Hong Kong SARS Forum Special Issue on SARS Abstracts, 2004: 84.
18. **Wang ZH, Nong Y, Lin JT, et al.** Covert infection of severe acute respiratory syndrome in health-care professionals and its relation to the workload and the type of work. Zhonghua Jie He He Hu Xi Za Zhi 2004; **27**: 151–154.
19. **Xu HF, Wang M, Zhang ZB, et al.** An epidemiologic investigation on infection with severe acute respiratory syndrome coronavirus in wild animals traders in Guangzhou. Zhonghua Yu Fang Yi Xue Za Zhi 2004; **38**: 81–83.
20. **Yu WC, Tsang TH, Tong WL, et al.** Prevalence of subclinical infection by the SARS coronavirus among general practitioners in Hong Kong. Scand J Infect Dis 2004; **36**: 287–290.
21. **Zheng BJ, Wong KH, Zhou J, et al.** SARS-related virus predating SARS outbreak, Hong Kong. Emerg Infect Dis 2004; **10**: 176–178.
22. **Sharp S, Sterne J.** Corrections to the meta-analysis command. Stata Tech Bull 1998; **STB-43**: 84.
23. **DerSimonian R, Laird N.** Meta-analysis in clinical trials (1986). Control Clin Trials 1986; **7**: 177–188.
24. **Last JM.** The iceberg.'Completing the clinical picture' in general practice. Lancet 1963; **2**: 28–31.
25. **Hon KL, Leung CW, Cheng WT, et al.** Clinical presentations and outcome of severe acute respiratory syndrome in children. Lancet 2003; **361**: 1701–1703.
26. **Guan Y, Zheng BJ, He YQ, et al.** Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China. Science 2003; **302**: 276–278.
27. **Lipsitch M, Cohen T, Cooper B, et al.** Transmission dynamics and control of severe acute respiratory syndrome. Science 2003; **300**: 1966–1970.
28. **Chinese SARS Molecular Epidemiology Consortium.** Molecular evolution of the SARS coronavirus during the course of the SARS epidemic in China. Science 2004; **303**: 1666–1669.
29. **Yeh SH, Wang HY, Tsai CY, et al.** Characterization of severe acute respiratory syndrome coronavirus genomes in Taiwan: molecular epidemiology and genome evolution. Proc Natl Acad Sci USA 2004; **101**: 2542–2547.
30. **Young M.** Prevalence of non-pneumonic infections with SARS-correlated virus. Lancet 2004; **363**: 1826.
31. **Yu IT, Li Y, Wong TW, et al.** Evidence of airborne transmission of the severe acute respiratory syndrome virus. N Engl J Med 2004; **350**: 1731–1739.
32. **Lin M, Tseng HK, Trejaut JA, et al.** Association of HLA class I with severe acute respiratory syndrome coronavirus infection. BMC Med Genet 2003; **4**: 9.
33. **Hill AVS.** The immunogenetics of human infectious disease. Annu Rev Immunol 1998; **16**: 593–617.
34. **Liu C, Carrington M, Kaslow RA, et al.** Association of polymorphisms in human leukocyte antigen class I and transporter associated with antigen processing genes with resistance to human immunodeficiency virus type 1 infection. J Infect Dis 2003; **187**: 1404–1410.
35. **Collins AR.** Human coronavirus OC43 interacts with major histocompatibility complex class I molecules at the cell surface to establish infection. Immunol Invest 1994; **23**: 313–321.
36. **Woo PC, Lau SK, Wong BH, et al.** Detection of specific antibodies to severe acute respiratory syndrome (SARS) coronavirus nucleocapsid protein for serodiagnosis of SARS coronavirus pneumonia. J Clin Microbiol 2004; **42**: 2306–2309.
37. **Che XY, Qiu LW, Pan YX, et al.** Sensitive and specific monoclonal antibody-based capture enzyme immunoassay for detection of nucleocapsid antigen in sera from patients with severe acute respiratory syndrome. J Clin Microbiol 2004; **42**: 2629–2635.
38. **van der Hoek L, Pyrc K, Jebbink MF, et al.** Identification of a new human coronavirus. Nat Med 2004; **10**: 368–373.
39. **Woo PC, Lau SK, Chu CM, et al.** Characterization and complete genome sequence of a novel coronavirus, coronavirus HKU1, from patients with pneumonia. J Virol 2005; **79**: 884–895.

https://doi.org/10.1017/S0950268805004826 Published online by Cambridge University Press

40. **Ebihara T, Endo R, Ma X, Ishiguro N, Kikuta H.** Detection of human coronavirus NL63 in young children with bronchiolitis. J Med Virol 2005; **75**: 463–465.
41. **Arden KE, Nissen MD, Sloots TP, Mackay IM.** New human coronavirus, HCoV-NL63, associated with severe lower respiratory tract disease in Australia. J Med Virol 2005; **75**: 455–462.
42. **Ksiazek TG, Erdman D, Goldsmith CS, et al.** A novel coronavirus associated with severe acute respiratory syndrome. N Engl J Med 2003; **348**: 1953–1966.
43. **Sun ZF, Meng XJ.** Antigenic cross-reactivity between the nucleocapsid protein of severe acute respiratory syndrome (SARS) coronavirus and polyclonal antisera of antigenic group I animal coronaviruses: implication for SARS diagnosis. J Clin Microbiol 2004; **42**: 2351–2352.
44. **Woo PC, Lau SK, Wong BH, et al.** False-positive results in a recombinant severe acute respiratory syndrome-associated coronavirus (SARS-CoV) nucleocapsid enzyme-linked immunosorbent assay due to HCoV-OC43 and HCoV-229E rectified by Western blotting with recombinant SARS-CoV spike polypeptide. J Clin Microbiol 2004; **42**: 5885–5888.
45. **Holmes KV, Enjuanes L.** Virology. The SARS coronavirus: a postgenomic era. Science 2003; **300**: 1377–1378.
46. **Snijder EJ, Bredenbeek PJ, Dobbe JC, et al.** Unique and conserved features of genome and proteome of SARS-coronavirus, an early split-off from the coronavirus group 2 lineage. J Mol Biol 2003; **331**: 991–1004.
47. **Rota PA, Oberste MS, Monroe SS, et al.** Characterization of a novel coronavirus associated with severe acute respiratory syndrome. Science 2003; **300**: 1394–1399.
48. **Marra MA, Jones SJ, Astell CR, et al.** The genome sequence of the SARS-associated coronavirus. Science 2003; **300**: 1399–1404.
49. **Yip CW, Hon CC, Zeng F, Chow KYC, Leung FCC.** Prevalence of non-pneumonic infections with SARS-correlated virus. Lancet 2004; **363**: 1825.
50. **Zhou YH.** Prevalence of non-pneumonic infections with SARS-correlated virus. Lancet 2004; **363**: 1825–1826.
51. **Theron M.** Prevalence of non-pneumonic infections with SARS-correlated virus. Lancet 2004; **363**: 1825.

https://doi.org/10.1017/S0950268805004826 Published online by Cambridge University Press