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# The Impact of Emerging Infectious Diseases on Chinese Blood Safety<sup>☆</sup>



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## ABSTRACT

Emerging infectious diseases (EIDs) have always been one of the major threats to public health. Although the implementation of mandatory testing for 4 classical transfusion-transmitted infectious—human immunodeficiency virus, hepatitis B virus, hepatitis C virus, and syphilis—has reduced the transfusion risk of these pathogens, the potential threat of various EID agents and their constantly evolving variants to blood safety in China is not fully understood. This review presents 9 representative EID agents that are autochthonous and epidemic nationally or regionally in China. The epidemiologic status and distribution of these EID agents among donors and/or healthy populations are summarized. The potential risks of these EID agents to blood safety are discussed. The review also explores strategies to strengthen hemovigilance systems and studies to further evaluate the impact of EID agents on blood safety.

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## Contents

Nationwide Distribution of EID Agents . . . . .	95
Human Parvovirus B19 . . . . .	95
Malaria . . . . .	95
Hepatitis E Virus . . . . .	95
EID Agents with Distributions Concentrated in Different Regions of China . . . . .	96
Dengue Viruses (DENV) . . . . .	96
Brucella . . . . .	96
Human T-cell lymphotropic virus . . . . .	96
Severe Fever with Thrombocytopenia Syndrome Virus . . . . .	97
Leishmania . . . . .	97
Q Fever . . . . .	97
Discussion . . . . .	98
Acknowledgement . . . . .	99
References . . . . .	99

Emerging infectious diseases (EID) agents are considered as major threats to transfusion safety. The most notorious EID agent that sabotaged blood safety during 1980s was human immunodeficiency virus (HIV). It raised global concerns of EIDs and triggered organized activity to systematically prevent EID agents from threatening transfusion

safety. Nowadays, blood donations are screened for various infectious agents in developed countries or regions where EID agents have been well studied. In the United States, the blood supply is routinely screened for Human T-lymphocyte virus (HTLV). West Nile virus (WNV); *Trypanosoma cruzi* [1–3] and *Babesia spp.* [4–7] have been systematically scrutinized to evaluate the value of donor screening [8]; and Zika virus has recently emerged as an EID threat [9]. In China, however, many of the EID agents are rarely investigated among blood donor and evidence for their impact on blood safety is absent. In 2009, the American Association of Blood Banks published a catalog of pathogens relevant to blood

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safety in which 68 EID agents were listed as confirmed or suspected to be associated with transfusion transmissible infection (TTI) [10]. The threat of these EID agents to blood safety varies, due to different spreading patterns, transmission routes, epidemiologic characteristics, and endemic status; therefore, they need to be specifically evaluated in each country or area.

In China, blood donors are routinely tested for only 4 pathogens: HIV-1/2, hepatitis B virus (HBV), hepatitis C virus (HCV), and syphilis [11]. With the broad implementation of nucleic acid testing (NAT), the improvement in performance of enzyme immunoassay assays, and the more rigorous policies for donor recruitment and testing, the transfusion risks of the conventional TTIs have been largely reduced in China [11,12]. However, many of the diversely distributed EID agents still pose potential threats to blood safety, yet their risks have never been fully evaluated. Nevertheless, China has witnessed recurrent outbreaks of highly virulent EIDs including severe acute respiratory syndrome (SARS), highly pathogenic avian influenza (H5N1) and *Streptococcus suis*, a zoonotic bacterium mostly carried by pigs or pork products which causes syndromes of streptococcal toxic shock, sepsis and meningitis. [13]. For example, outbreaks of human *Streptococcus suis* infection in China were reported in Sichuan province, resulting in 66 laboratory confirmed cases and 39 deaths from mid-July to the end of August 2005 [14]. Some EID agents with asymptomatic distribution among Chinese general population, such as malaria, hepatitis E virus, and dengue virus may emerge as greater threats to Chinese blood safety and require interventions. In this review, we highlight 9 representative, autochthonous EIDs agents that are nationwide or regionally epidemic. The epidemiology of these EID agents and the investigations among blood donors and/or the general population are reviewed. The geographic distribution for EID agents that are regionally epidemic is summarized, and the prevalence of these EID agents among Chinese donors is summarized.

## Nationwide Distribution of EID Agents

### Human Parvovirus B19

Human parvovirus B19 (B19V) is a small, non-enveloped, single-strand DNA virus [15], causing various clinical manifestations such as chronic anemia, aplastic crises and arthropathies, and a variety of other syndromes among immune-compromised or immunosuppressed patients [16–19]. B19V has been confirmed to be one of the TTIs transmitted through blood or blood products [20]. The US Food and Drug Administration (FDA) and European Pharmacopeia have proposed a limit of  $1 \times 10^4$  gEq/mL for pooled-plasma in order to reduce the potential risk of transmission [21,22].

There is limited data on B19V prevalence among blood donors or the general population in China. According to several reports, the estimated prevalence rate could be as high as 3.5% in the general Chinese population [23] and 4.5% in HIV co-infected individuals [24]. In the Tibetan area, the B19V DNA positivity rate was 4.8% among the general population [23]. Among Chinese blood donors, the B19V DNA prevalence rate was 0.58%, which is much lower than that in the general population [25]. The same study also reported that different geographic locations demonstrated different prevalence rates for B19V, and that the DNA sequences in Xinjiang Province showed a different genetic lineage than in other places of China [25]. In another study, B19V DNA was detected in 54.2% (77/142) of plasma pools from 2 Chinese blood product manufacturers of intravenous immunoglobulin (IVIG), factor VIII, fibrinogen and prothrombin complex concentrates, with levels of B19V-DNA varying from  $1 \times 10^2$  gEq/mL to  $1 \times 10^7$  gEq/mL [26]. The viral load in one donation sample was  $1.09 \times 10^{10}$  gEq/mL, which was significantly higher than the threshold recommended by the US FDA and European Pharmacopeia ( $1 \times 10^4$  gEq/mL). While further investigation is necessary to determine whether B19V NAT screening should be implemented as a

routine in Chinese blood centers, the current B19V contamination in plasma products is a serious concern.

### Malaria

Malaria is caused by infection with the parasites of *Plasmodia spp.* and the current distribution covers the tropics and large parts of the subtropics [27]. Infection with *Plasmodia spp.* often resembles a common viral infection which may lead to a delay in diagnosis [28]. Malaria is considered a transfusion risk since asymptomatic immigrants who reside in and travelers who visit endemic areas might import malaria to non-endemic areas [10]. Therefore, US FDA has initiated a donor deferral policy that temporarily defers donors who travel to endemic areas. As a result, about 1% of US donors are deferred for that reason [29].

Malaria was once highly endemic in China with an estimated 30 million cases per year [30]. The Chinese government began a tremendous effort to eliminate malaria in 1955 when the National Malaria Control Program was launched [31]. The main species that causes malaria in China is *P vivax* and has been found in many regions; however, other species of *Plasmodia* have also been reported [32]. Although malaria has been well controlled in the last 2 decades, sporadic outbreaks are frequently reported [31], and malaria remains a reportable infectious disease in China [13]. Several cases of malaria transmission by transfusion were recently reported (Table 1) [33–49]. Meanwhile, the DNA of *P knowlesi* was also found in pooled plasma from a manufacturer in Guizhou [50]. However, currently Chinese blood centers do not have a policy to defer donors who have traveled to malaria endemic areas or malaria infected countries during epidemic seasons. The actual prevalence of malaria and its residual risks among voluntary blood donors is unknown. Further studies on malaria infected blood donors in China, such as a survey on the risks of infection and demographic characteristics of *Plasmodium* infected donors, are crucial to better understand the transfusion risks of malaria in China.

### Hepatitis E Virus

Hepatitis E virus (HEV) is an enterically transmitted, positive-sense, single-stranded non-enveloped RNA icosahedral virus [51]. It usually causes an acute and self-limiting infection. HEV has a worldwide distribution and substantial morbidity and mortality in some developing countries [52]. Many cases of HEV transmission by blood transfusion have been documented all over the world [53–59]. Routine screening of donors for HEV RNA was suggested by some studies [60].

In China, the anti-HEV seroprevalence is about 40% in the general population and increases with age by 1% per year [61]. Approximately 2.7% of individuals are IgM positive (indicating acute infection) and 0.3% are asymptomatic with viremia [62]. In the early 1990s, due to the frequent occurrence of illegal blood donation in central China, the anti-HEV IgG prevalence spiked to 22.7% and anti-HEV IgM prevalence was 1.8% among illegal blood donors [63]. In a recent study using test results from routine donations collected at 6 urban blood centers, investigators reported a prevalence of 32.6% for anti-HEV IgG, 0.94% for anti-HEV IgM, and 0.07% for HEV RNA among 44 816 donations. In addition, they found that prevalence rates varied by blood center locations [64]. In a comparative study [63], where samples from both qualified blood donors and donors deferred due to elevation of alanine aminotransferase (ALT) were examined, the prevalence rates of anti-HEV IgM and anti-HEV IgG in ALT-elevated donors (2.76% and 40.02%, respectively) were significantly higher than those in qualified donors (1.02% and 27.42%, respectively). Meanwhile, the prevalence of HEV antigen among the ALT-elevated donors (0.25%) was also higher than that among qualified donors (0.06%), but not at a statistically significant level. These data suggest that routine pre-screening and post-donation ALT tests can reduce, but not eliminate the potential risks of HEV infection from otherwise qualified donations in China.

**Table 1**  
Parts of the transfusion-transmitted malaria infections in China.

Malarial species	Location (province)	Number of cases	Reasons for transfusion	Outcomes	Ref
<i>P vivax</i>	Sichuan	1	Orthopedic surgery	Acute renal failure and death	[31]
<i>P vivax</i>	Sichuan	1	Orthopedic surgery, anemia	Chills and fever	[31]
<i>P falciparum</i>	Zhejiang	1	Brain trauma	Fever and headache and diarrhea	[32]
<i>P vivax</i>	Sichuan	2	Primary thrombocytopenic	Chills and fever	[33]
<i>P sp.</i>	Liaoning	1	Uterine bleeding	Fever	[34]
<i>P sp.</i>	Liaoning	1	Extrauterine pregnancy	Chills, fever and icteric sclera	[34]
<i>P sp.</i>	Liaoning	1	Splenectomy	Chills and fever	[34]
<i>P sp.</i>	Beijing	5	NA	Chills and fever	[35]
<i>P sp.</i>	Jilin	4	NA	Chills and fever	[38]
<i>P malariae</i>	Shanghai	1	Hip replacement	Fever	[42]
<i>P vivax</i>	Jiangsu	69	NA	Chills, fever and splenomegaly	[43]

## EID Agents with Distributions Concentrated in Different Regions of China

### Dengue Viruses (DENV)

DENV causes dengue fever, dengue hemorrhagic fever (DHF), and dengue shock syndrome. DENV is a life-threatening mosquito-borne disease with global spread [65]. DENV was shown to be capable of transmission by transfusion [66]. Transfusion of red blood cells which tested DENV seronegative but were RNA positive with high viral load ( $>10^7$  copies/mL) can lead to DENV infections in transfusion recipients [67]. Several countries and regions with a high prevalence of DENV have investigated DENV among blood donors and recipients to evaluate its impact on blood safety, as well as to develop a proper donor enrollment strategy to reduce the transfusion-transmission risk [68–70].

In China, early outbreaks of DHF in 1980s were reported mostly in Guangdong, Guangxi, Yunnan, Hainan, Fujian, and Zhejiang provinces located in the southeast coastal regions or border areas next to South-east Asia [71]. More than 80% of the documented DHF cases were from Guangdong province, one of the most developed provinces located in the South coastal area [72]. Since dengue fever first reemerged in Guangdong province in 1978 [73], the epidemic of DENV spread to 26 Chinese provinces by 2014 [74]. From 1990 to 2013, the epidemic status of DHF gradually changed from sporadic imported to autochthonous endemic cases [75]. In 2013, there was a large DHF outbreak from July to November in Foshan city, Guangdong province with 5173 suspected febrile cases [76]. Among them, 641 DENV infections were confirmed by laboratory testing (436 RNA positive and 205 IgM positive) [76]. The following year, the third historically largest DHF outbreak spread throughout Guangdong province (20 of 21 cities with reported cases) with 45 236 febrile cases (6024 DENV infections confirmed) resulting in 6 deaths [77]. Partly in response to the outbreaks in 2013 and 2014, the Chinese Center for Disease Control and Prevention (CDC) amended the guidelines for DHF prevention and control to strengthen the implementation of mosquito control [78]. In 2015, the DHF cases in Guangdong province dropped sharply to 739 cases by the end of September [79], reflecting the effectiveness of DENV control measures in this area. DENV sentinel monitoring by sero-surveillance has been in operation in DHF epidemic regions in China since 1990s. The DENV seroprevalence rate varied (IgG: 0.25%–14.49%; IgM: 0.56%–5.2%) in the DENV endemic areas in Guangdong [80,81], Guangxi [82], Yunnan [83,84], Hainan [85], and Fujian [86] provinces. A pilot study of DENV serology and viremia among asymptomatic donors in Guangzhou city (Guangdong province) in September and October 2014 found that the DENV IgM prevalence rate was 2.4% ( $n = 3000$ ). The study also identified one DENV RNA positive donor with viral load of 944 copies/mL [87]. Another post-outbreak serological investigation among healthy populations in Foshan city (next to Guangzhou city) found significantly higher DENV seroprevalence rates in the 4 towns that experienced DHF outbreaks in 2013 (IgG rate: 2.7%,  $n = 817$

compared with the 2 towns without autochthonous cases (IgG rate: 0.6%) [76]. A blood product with DENV RNA viremia can potentially lead to transfusion-transmitted infection. However, to date, there are no published studies on DENV transmission via transfusion in China.

### Brucella

Human brucellosis caused by *Brucella spp.* is one of the most severe zoonotic diseases worldwide [88]. Transfusion-transmitted brucellosis cases have been reported since the 1950s [89–92], and *Brucella spp.* are considered a potential risk for blood safety [10]. Human brucellosis is one of the leading threats to public health in farming areas with livestock in China [93]. More than 90% of brucellosis cases in China were found in north China and were concentrated in Inner Mongolia, Shaanxi, Heilongjiang, Jilin, and Hebei provinces [94]. A total of 141 604 brucellosis cases were confirmed in these areas. In addition, a rapidly increasing trend was observed in brucellosis incidence, from 0.92 cases per 100 000 people in 2004 to 2.62 clinical cases per 100 000 people in 2010 [94,95]. An epidemiological investigation in Inner Mongolia reported the incidence rate as high as 12.94% among people who had close contact with livestock [96].

In China, most of *Brucella* surveillance has focused on risk factors for infections [97,98], prevalence in dairy cattle [99] and local animals [100,101] with the goal of providing information for brucellosis prevention and control. The DNA prevalence rate of *Brucella* in raw whole milk samples was found to be 1.07% in 15 provinces [102]. The low-risk population in urban areas is at increasing risk of Brucellosis from contaminated milk or raw meat [103]. Limited data showed the seroprevalence rate of *Brucella* among the healthy human population to be 9.82% in endemic areas [104]. Recently, a *Brucella spp.* investigation based on enzyme immunoassay testing among blood donors in an endemic area (Kashi, Xinjiang province) showed that the reactive rate was 1% (39/3896), in which 0.64% (25/3896) samples were further confirmed by western blot (WB) testing, and the *Brucella* DNA prevalence rate was 0.39% (15/3896) [105]. Although no infection cases transmitted by transfusion have been reported, the existence of *Brucella* DNA in donors' plasma samples indicates potential risk of transfusion-transmitted brucellosis in endemic areas and warrants future investigation.

### Human T-cell lymphotropic virus

As the first retrovirus discovered in humans [106], HTLV is one of the important TTIs that may lead to various human diseases such as adult T-cell leukemia/lymphoma, myelopathy/tropical spastic paraparesis, opportunistic infections, and inflammatory disorders [107]. The implementation of mandatory testing on donors has been in effect since mid-1980s in many countries to reduce the risk of transfusion transmission.

In China, sero-surveillance of HTLV among the general population started in 1980s when an early study in Beijing and other 28 provinces found a 0.08% positive rate in 9303 samples—all connected to the endemic country Japan [108]. In 2005 and 2012, 2 nationwide investigations reported the prevalence of HTLV among blood donors to be 0.05% (n = 145 293) [109] and 0.03% (n = 122 468) [110] respectively. A meta-analysis of 40 studies among 458 525 donors in 21 provinces and regions found that the pooled estimates of HTLV-1 prevalence in Fujian and Guangdong were 9.9/10 000 (95% CI, 4.4/10 000–22.2/10 000) and 2.9/10 000 (95% CI: 1.7/10 000–4.8/10 000), respectively. Most isolates belonged to the transcontinental subgroup A whereas only 2 cases of HTLV-1 infection were found among 204 763 donors in other provinces and regions [111]. Data from these studies indicate that while HTLV prevalence is low in China, the infection has expanded from concentrated coastal regions in Fujian and Guangdong to the neighboring provinces where seroprevalence remains low (ranging from 0.02% in Shanghai and 0.12% in Jiangxi) [108,110]. Although no transfusion-transmitted HTLV infections have been reported, the surveillance of HTLV among blood donors and the evaluation of its impact on blood safety continue to be studied in China.

#### Severe Fever with Thrombocytopenia Syndrome Virus

Severe fever with thrombocytopenia syndrome virus (SFTSV), a novel tick-borne bunyavirus, was first identified in China to be the etiologic agent of severe fever with thrombocytopenia syndromes (SFTS) with initial fatality rates between 12% and 30% in 2009 [112]. SFTSV is concentrated in the mountainous rural areas in central and eastern China [112–114]. The epidemic seasons of SFTS are mainly from spring to autumn and peak in May to July [113]. Farmers are at high risk for SFTS due to more exposure to ticks [115]. The molecular characteristics, epidemiologic distribution, risk factors and clinical symptoms have been well summarized in several reviews [116,117]. By the end of 2013, SFTSV had spread from 6 provinces in 2009 [113] to 14 provinces with a growing incidence but a decreasing fatality rate [118]. The increasing epidemic of SFTS was reported and annual incidence was estimated to be 3 cases per 100 000 populations in autochthonous endemic area [118]. Meanwhile, increasing numbers of SFTS cases were reported in Japan [119–121] and South Korea [122,123]. Migratory birds are suspected to have played an important role in promoting the spread of SFTSV in East Asia [124].

Although there is no recorded transfusion-transmitted SFTS case at present, SFTSV has the potential to become a transfusion-transmitted infectious agent due to several considerations: (1) nosocomial transmissions caused by direct exposure to SFTS patients' blood have demonstrated that SFTSV is a blood-borne pathogen [125–128]. (2) The incubation period from infection to onset of the disease is one or 2 weeks on average [129], and in some cases up to thirty days [130]. Viremic asymptomatic blood donors within the incubation period may therefore potentially transmit SFTSV to recipients leading to SFTS. In a study launched by the National Heart, Lung, and Blood Institute, Johns Hopkins University, the Chinese Institute of Blood Transfusion, and 3 Chinese blood centers (one located in an endemic and 2 in non-endemic regions), antibody screening and follow-up SFTSV RNA detections were performed on 17 208 blood donor plasma samples collected between April and October 2012. The seroprevalence rates were 0.54% (80/14 752), 0.27% (3/1130) and 0.28% (3/1326) in an endemic area (Xinyang) and non-endemic regions (Mianyang and Luoyang) respectively, with no significant difference observed ( $P > .1$ ). Among 9964 donors screened by 4-sample minipool SFTSV RNA testing, 2 suspected viremic samples were detected each with a viral load less than 20 plaque-forming units (PFU)/mL [131]. Other regional SFTSV among the healthy individuals reported seroprevalence rates varying between 0.44% and 7.2% [132–134] in epidemic areas, with finding asymptomatic viremic cases. Continued investigation is needed to evaluate whether SFTSV presents a risk to transfusion recipients in China.

#### Leishmania

*Leishmania* infection is responsible for cutaneous and visceral leishmaniasis (kala-azar). *Leishmania spp.* are usually transmitted to people through the Phlebotomine sandfly [135]. The infected individual may harbor a persistent infection up to 30 years before recovery [136]. The transmissibility of *Leishmania* infection via blood has been demonstrated in animals [137,138] as well as human beings [139–142]. *Leishmania* in human red blood cells (RBCs) can survive for as long as 15 days under blood bank storage conditions [143]. It has been reported to cause cutaneous or visceral leishmaniasis in infants and immunocompromised patients [139–142]. Asymptomatic infections are usually found in healthy blood donors from endemic areas [144–148]. US military blood banks enforce permanent deferral for individuals with any history of leishmaniasis, but there is no existing regulation or standard for *Leishmania* testing in civilian donor screening [10]. During the 1950s, there were more than 500 000 documented kala-azar cases in China, mainly in rural areas in the north [149]. With the efforts of a national control program, kala-azar was almost eliminated in 1960s [150]. Currently, more than 300 cases of kala-azar are reported each year, mainly from Xinjiang Province and other provinces in Western China [150]. Recently, a retrospective study of visceral leishmaniasis by the Chinese CDC reported an increase in the number of visceral leishmaniasis cases in endemic areas between 2005 and 2010 [149], indicating that prevention and control strategies must be taken to restrain the increasing incidence and spread of leishmaniasis. Otherwise, frequent population migration, tourism, and a rapidly growing public transportation may lead to further spread of the infection and push it up on the list of transfusion-transmitted infectious diseases in China. To date, there are still no survey studies of infection among donors and no documented transfusion-transmitted cases for *Leishmania* infection in China.

#### Q Fever

Q fever is a zoonosis due to *Coxiella burnetii* infection. *C. burnetii* usually causes asymptomatic clinical manifestations such as a flu-like disease or atypical pneumonia in humans [151]; however, acute [152,153] and fatal chronic infections [154–157] have been reported. In 2007, there was a large outbreak of Q fever in the Netherlands [158]. Hogema et al initiated a surveillance of *C. burnetii* DNA and antibodies in local blood donations and found that the *C. burnetii* DNA positive rate was 0.3%, while the IgG seropositive rate was 12.2% [159]. Furthermore, 10 seroconversions were detected in donors with an incidence rate of 5.7% per year during the outbreaks from 2007 to 2009 [159]. After the great outbreaks of Q fever, Slot et al. started to investigate if chronically infected donors posed a threat to blood safety in the Netherlands. The serological results from 2490 serum samples collected in the most affected area during August 2012 to January 2013 showed that chronic *C. burnetii* infection was absent in the epidemic blood donors, which led to the donor re-entry policy that had already been initiated elsewhere in Europe [160].

In China, most *C. burnetii* infections have been observed in Tibet, Yunnan, Xinjiang and Inner Mongolia [161]. The *C. burnetii* DNA positivity rate was about 10% in ticks and 7% in humans in Western China [162]. As Q fever is mainly an airborne disease, the individuals with exposure to livestock bear a higher risk. Some epidemiological studies show that more than 50% of rural farmers had antibodies to *C. burnetii* [163,164]. Although blood donor screening of *C. burnetii* has not been initiated in China, the DNA of *C. burnetii* was found in pooled plasma from a manufacturer in Guizhou [50]. A cross-sectional study of the seroprevalence and viremia status of *C. burnetii* among blood donors, especially in nomadic herding and livestock regions, would provide a more comprehensive assessment of its impact on blood safety in China.

## Discussion

Due to its biological and geographic diversity, China will always be at high risk for various EID agents. As a populous country, a dramatic ramp-up in the number of blood donations was reported recently, with more than 21 million donations collected in 2012 at the donation index of 8.5 donations per 1000 people [165]. However, monitoring of the classical TTIs such as HIV, HBV, HCV and syphilis, as well as EID agents has only been implemented by the Chinese CDC and mostly based on sentinel investigations and clinical case report systems. The monitoring systems have demonstrated effectiveness in establishing proper guidelines for disease prevention and control based on epidemiological analysis of transmission routes and infection risk factors. The fatality rates and clinical symptoms from the documented cases are periodically summarized and analyzed to help with diagnosis and therapy of these pathogens, as well as with the development and improvement of laboratory diagnostic assays. Effort towards disease control has benefitted from the system in the face of several outbreaks of EID epidemics, such as: SARS [166], H5N1 [167], SFTSV [113], and DENV [76].

The regional spread of infection is an important aspect to consider when evaluating the transfusion risk for EID agents. Among the 9 EID agents listed above, all of them have been proven to result in pathological and autochthonous epidemics in China. B19V, HEV and *Plasmodium spp.* have nationwide distribution. Three insect-borne EID agents (DENV, SFTSV, and *Leishmania spp.*) and 2 zoonoses (*Brucella spp.* and *C burnetii*) display significant geographic diversity due to their patterns of transmission. HTLV is clustered in one coastal region. The regional distribution of 6 EID agents is shown in Fig. 1. Not surprisingly, the regional distribution of insect-borne pathogens matches that of disease vectors (mosquitos, sand-flies and ticks). DENV, a well-described mosquito-borne virus, has a global distribution in tropical and subtropical areas, the location of recent outbreaks of DHF. The infections of SFTSV, the novel tick-borne bunyavirus, were identified from SFTS patients in rural mountainous areas in central and eastern China, mainly because of the higher risk of tick exposure. In a similar way, most of the infections of zoonotic diseases (Q-fever and Brucellosis) were found in rural livestock farming areas in northern and western China. By compiling the distribution of reported clinical cases and the prevalence of EID agents in donors and/or general population, we provide estimates of the frequency of EID agents among Chinese blood donor populations. See Fig. 2. HEV and B19V are estimated to have national distribution among donors and general population in China based on previous cross-sectional studies. Spread of *Brucella spp.* depends on transmission

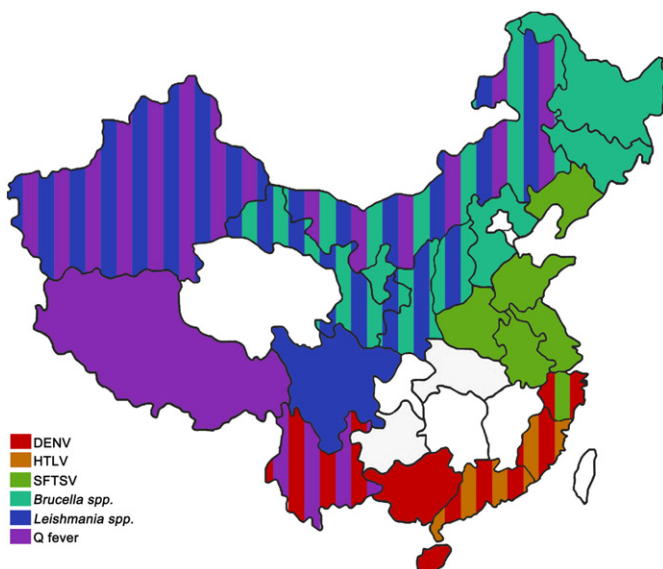


Fig. 1. The distribution of 6 major regional EID agents in China.

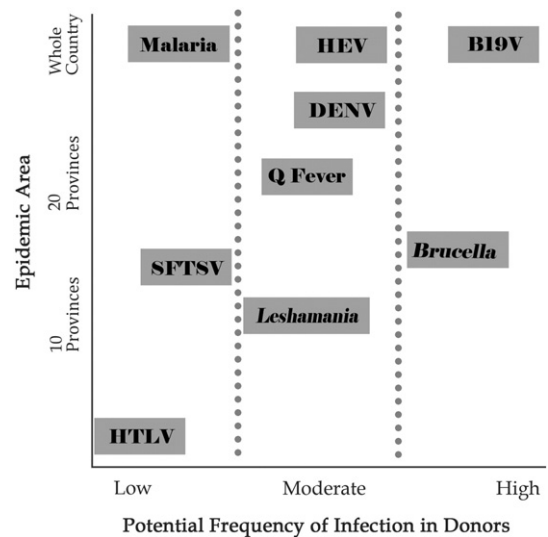


Fig. 2. The distribution and potential prevalence of EID agents in blood donors in China.

routes from contaminated milk and raw meat produced from endemic regions. Considering the current DNA prevalence rate (0.39%) of *Brucella spp.* among blood donors in endemic regions and its potential high frequency in the general donor population, this EID is a matter for concern. In the shadows of recent global outbreaks and the fast expanding trends of DHF, DENV should also be highlighted for its potential risks in endemic areas in China. The other 3 regionally concentrated EID agents: Q-fever, *Leishmania spp.*, and SFTSV are estimated to have moderate or low frequency among the blood donor population. However, ongoing surveillance on these EID agents in donors is prudent in order to provide sound evidence regarding their impact on blood safety in China.

In order to evaluate the impact of EIDs on blood safety, a practical and feasible approach is to monitor the existence of EID agents among asymptomatic blood donors and obtain direct evidence from transfusion-transmitted cases confirmed by molecular analysis. Firstly, the surveillance among blood donors through sero-markers and nucleic acid of pathogens provides data for estimating transfusion risk. Among the 9 EIDs discussed in this review, only HTLV has been continuously investigated at blood centers since 1980s. There are a few investigations and case reports on B19V, HEV and *Plasmodium spp.* among blood donors, but no systematic and continuous investigation on these EIDs. Data on SFTSV, DENV and *Brucella spp.* in China are very limited with only one documented donor surveillance study available for each agent. *C burnetii* (Q fever) and *Leishmania spp.* have not been investigated. In addition, well-organized and appropriately designed donor-recipient linkage studies may directly confirm transmission by transfusion, facilitate further evaluation of the post-transfusion outcomes, and yield more convincing evidence to support strategies for screening donors for EID agents. Although China has not performed such linkage studies, Brazil examined donor-recipient linkage for dengue virus using a large, nationally representative database [168]. This study may serve as an example to follow in order to evaluate transfusion risk of EIDs in China.

Collaborative efforts from global surveillance programs may prove useful to mitigate the transfusion risk of EIDs. Although most EID agents in China were historically imported, some agents, such as SARS and SFTSV, originated in China and are expanding to other adjacent countries. Also, non-endemic EID agents such as West Nile Virus (WNV), Chikungunya virus, variant Creutzfeldt-Jacob disease (vCJD) and Zika virus (ZIKV) should be immediately addressed due to their worldwide distribution and severity of clinical outcomes. Recently, transfusion-transmitted ZIKV has been documented [169–170]. Several cases of ZIKV infection among travelers from epidemic areas have been reported in China [171–172]. Currently immigration authorities recommend oral

declaration of infection at entry-exit inspection and quarantine of symptomatic travelers from ZIKV epidemic areas upon entry into China. Travelers from countries epidemic for vCJD are deferred from donation by health questionnaire in Chinese blood centers. However, whether WNV, Chikungunya virus and ZIKV should also be added to the deferral list remains a matter of controversy that needs evidence from further investigation.

Pathogen reduction of blood products is an alternative defense against EID agents. Several studies described effective inactivation of EID agents such as DENV [173] and WNV [174]. Currently the only pathogen reduction technology in use in China is the methylene blue-photochemical technology applied to plasma products [175]. The technology is not mandatory and only performed at a few blood centers. More efforts should be made to evaluate whether and how pathogen reduction can be used to safeguard the blood supply in China. The cost-effectiveness of screening strategies is a key factor to consider. Currently there is a lack of cost-effectiveness studies on the existing screening strategies for the 4 classical TTIs in China. Such studies are needed to enhance the development and improvement of additional EID screening strategies in blood donations. In conclusion, the threats to blood safety posed by EID agents in China require further evaluation. With the support of the substantial evidence from such studies, China can implement more effective blood screening strategies on EID agents and further reduce transfusion risk to patients.

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#### References

- Sabino EC, Lee TH, Montalvo L, Nguyen ML, Leiby DA, Carrick DM, et al. Antibody levels correlate with detection of *Trypanosoma cruzi* DNA by sensitive polymerase chain reaction assays in seropositive blood donors and possible resolution of infection over time. *Transfusion* 2013;53:1257–65.
- Benjamin RJ, Stramer SL, Leiby DA, Dodd RY, Fearon M, Castro E. *Trypanosoma cruzi* infection in North America and Spain: evidence in support of transfusion transmission. *Transfusion* 2012;52:1913–21 [quiz 2].
- Leiby DA, Herron RM, Garratty G, Herwaldt BL. *Trypanosoma cruzi* parasitemia in US blood donors with serologic evidence of infection. *J Infect Dis* 2008;198:609–13.
- Gubernot DM, Lucey CT, Lee KC, Conley GB, Holness LG, Wise RP. Babesia infection through blood transfusions: reports received by the US Food and Drug Administration, 1997–2007. *Clin Infect Dis* 2009;48:25–30.
- Leiby DA, Johnson ST, Won KY, Nace EK, Slemenda SB, Pieniazek NJ, et al. A longitudinal study of Babesia microti infection in seropositive blood donors. *Transfusion* 2014;54:2217–25.
- Leiby DA. Transfusion-transmitted Babesia spp.: bull's-eye on Babesia microti. *Clin Microbiol Rev* 2011;24:14–28.
- Johnson ST, Cable RG, Tonnetti L, Spencer B, Rios J, Leiby DA. Seroprevalence of Babesia microti in blood donors from Babesia-endemic areas of the northeastern United States: 2000 through 2007. *Transfusion* 2009;49:2574–82.
- Stramer SL. Current risks of transfusion-transmitted agents: a review. *Arch Pathol Lab Med* 2007;131:702–7.
- Musso D, Stramer SL, Busch MP. Zika virus: a new challenge for blood transfusion. *Lancet* 2016;387:1993–4.
- Stramer SL, Hollinger FB, Katz LM, Kleinman S, Metzger PS, Gregory KR, et al. Emerging infectious disease agents and their potential threat to transfusion safety. *Transfusion* 2009;49(Suppl. 2):1S–29S.
- Shan H, Wang JX, Ren FR, Zhang YZ, Zhao HY, Gao GJ, et al. Blood banking in China. *Lancet* 2002;360:1770–5.
- Shi L, Wang JX, Stevens L, Ness P, Shan H. Blood safety and availability: continuing challenges in China's blood banking system. *Transfusion* 2014;54:471–82.
- Wang L, Wang Y, Jin S, Wu Z, Chin DP, Koplan JP, et al. Emergence and control of infectious diseases in China. *Lancet* 2008;372:1598–605.
- Yu H, Jing H, Chen Z, Zheng H, Zhu X, Wang H, et al. Human Streptococcus Suis outbreak, Sichuan, China. *Emerg Infect Dis* 2006;12:914–20.
- Corcoran A, Doyle S. Advances in the biology, diagnosis and host-pathogen interactions of parvovirus B19. *J Med Microbiol* 2004;53:459–75.
- Heegaard ED, Brown KE. Human parvovirus B19. *Clin Microbiol Rev* 2002;15:485–505.
- Bremner JA, Cohen BJ. Parvovirus B19 as a cause of anemia in human immunodeficiency virus-infected patients. *J Infect Dis* 1994;169:938–40.
- Tavil B, Sanal O, Turul T, Yel L, Gurgey A, Gumruk F. Parvovirus B19-induced persistent pure red cell aplasia in a child with T-cell immunodeficiency. *Pediatr Hematol Oncol* 2009;26:63–8.
- Nocton JJ, Miller LC, Tucker LB, Schaller JG. Human parvovirus B19-associated arthritis in children. *J Pediatr* 1993;122:186–90.
- Young NS, Brown KE. Parvovirus B19. *N Engl J Med* 2004;350:586–97.
- Brown KE, Young NS, Alving BM, Barbosa LH. Parvovirus B19: implications for transfusion medicine. Summary of a workshop. *Transfusion* 2001;41:130–5.
- Tabor E, Yu MY, Hewlett I, Epstein JS. Summary of a workshop on the implementation of NAT to screen donors of blood and plasma for viruses. *Transfusion* 2000;40:1273–5.
- Tong R, Shen L, Yin W, Zhou W, Lu J, Zheng M, et al. Prevalence of human parvovirus B19, bocavirus, and PARV4 in blood samples from the general population of China and lack of a correlation between parvovirus and hepatitis B co-infection. *PLoS One* 2013;8:e64391.
- He M, Zhu J, Yin H, Ke L, Gao L, Pan Z, et al. Human immunodeficiency virus/human parvovirus B19 co-infection in blood donors and AIDS patients in Sichuan, China. *Blood Transfus* 2012;10:502–14.
- Ke L, He M, Li C, Liu Y, Gao L, Yao F, et al. The prevalence of human parvovirus B19 DNA and antibodies in blood donors from four Chinese blood centers. *Transfusion* 2011;51:1909–18.
- Zhang W, Ke L, Changqing L, Zhang Y, Li W. Parvovirus B19V DNA contamination in Chinese plasma and plasma derivatives. *J Transl Med* 2012;10:194.
- Nadjm B, Behrens RH. Malaria: an update for physicians. *Infect Dis Clin North Am* 2012;26:243–59.
- Trampuz A, Jereb M, Muzlovic I, Prabhu RM. Clinical review: severe malaria. *Crit Care* 2003;7:315–23.
- Leiby DA, Nguyen ML, Notari EP. Impact of donor deferrals for malaria on blood availability in the United States. *Transfusion* 2008;48:2222–8.
- Zhou ZJ. The malaria situation in the People's Republic of China. *Bull World Health Organ* 1981;59:931–6.
- Lu G, Zhou S, Horstick O, Wang X, Liu Y, Muller O. Malaria outbreaks in China (1990–2013): a systematic review. *Malar J* 2014;13:269.
- Bi P, Tong S, Donald K, Parton KA, Ni J. Climatic variables and transmission of malaria: a 12-year data analysis in Shuchen County, China. *Public Health Rep* 2003;118:65–71.
- Chen DJ, Wang XW. Report of five malaria infections post transfusion. *Sichuan Med* 1992;47:102.
- Chen SB. A case report of malaria infection post transfusion. *Pract Prev Med* 2015;28:87–9.
- Huang C, Wang XG, Zhao YL. Retrospective analysis of transfusion transmitted malaria-case report. *J Chin Transfus* 2015;48:538–9.
- Jing LW, Zhang FC. Three cases reports on transfusion transmitted malaria. *Liaoning Med J* 1996;28:162.
- Li W, Yi B, Wei ZY. Reports of five malaria infections post transfusion. *Mil Med J* 1995;37:395.
- Qian P, Wu FQ. 60 cases report on malaria infection post transfusion. *Moderate Level J* 1993;51:22–3.
- Ruan W, Wei YL, Yao LN. A retrospective analysis on one transfusion transmission of malaria in Zhejiang Province. *Chin Parasit J* 2014;41:54–7.
- Su XF, Yuan WJ, He YM. Four cases analysis due to transfusion transmitted malaria. *J Bai Qiu En Med School* 1995;77:64.
- Su YP, Guo XS, Ma JS. 148 cases analysis for 148 transfusion infections. *J Pract Parasit Res* 1996;56:87–91.
- Wang G, Li ZL. A case report for transfusion-transmitted malaria. *Mil Med* 2006;55:556.
- Wang HL, Liu W, Sun GQ, et al. A case report for transfusion related malaria. *J Chin Transfus* 2002;59:417.
- Wang ZY, Zhang YG, Jiang L, et al. A case report for transfusion-transmission of malaria in Shanghai. *Chin Parasit Res* 2015;23:362–6.
- Wu FQ, Qian P. Analysis on 69 clinical cases of malaria. *Moderate Level J* 1996;13:7–8.
- Wu MY, Xie YQ, Zhu SY. Retrospective analysis on malaria infection post transfusion in Chang Zhou. *Chin Parasites Res* 2012;20:110–1.
- Ying LH, Huang GP, Zhang BG. A case report for transfusion transmitted malaria. *Zhe Jiang Prev Med* 2014;41:1031–2.
- Zhao M, Yang JQ, Yang WF, et al. Three cases of malaria infections after transfusion. *Chin Pract Med* 1994;34:624.
- Zhou BQ, Xu HQ. Investigation on 94 malaria infections post transfusion. *Chin Parasit J* 1994;67:46–7.
- He M, Zhou Y, Xu M. The potential risk of emerging infectious diseases hazarded to blood safety of China: the microbiome analysis on pooled plasma from manufacturers. Report on Chinese microbiology and immunology congress; 2014. p. 2.
- Mast EE, Krawczynski K. Hepatitis E: an overview. *Annu Rev Med* 1996;47:257–66.
- Skidmore SJ. Factors in spread of hepatitis E. *Lancet* 1999;354:1049–50.
- Matsubayashi K, Kang JH, Sakata H, Takahashi K, Shindo M, Kato M, et al. A case of transfusion-transmitted hepatitis E caused by blood from a donor infected with hepatitis E virus via zoonotic food-borne route. *Transfusion* 2008;48:1368–75.
- Boxall E, Herborn A, Kochethu G, Pratt G, Adams D, Ijaz S, et al. Transfusion-transmitted hepatitis E in a 'nonhyperendemic' country. *Transfus Med* 2006;16:79–83.
- Mitsui T, Tsukamoto Y, Yamazaki C, Masuko K, Tsuda F, Takahashi M, et al. Prevalence of hepatitis E virus infection among hemodialysis patients in Japan: evidence

- for infection with a genotype 3 HEV by blood transfusion. *J Med Virol* 2004;74:563–72.
- [56] Khuroo MS, Kamili S, Yattoo GN. Hepatitis E virus infection may be transmitted through blood transfusions in an endemic area. *J Gastroenterol Hepatol* 2004;19:778–84.
- [57] Lee CK, Chau TN, Lim W, Tsoi WC, Lai ST, Lin CK. Prevention of transfusion-transmitted hepatitis E by donor-initiated self exclusion. *Transfus Med* 2005;15:133–5.
- [58] Slot E, Hogema BM, Riezebos-Brilman A, Kok TM, Molier M, Zaaier HL. Silent hepatitis E virus infection in Dutch blood donors, 2011 to 2012. *Euro Surveill* 2013;18 [pii = 20550].
- [59] Vollmer T, Diekmann J, Johne R, Eberhardt M, Knabbe C, Dreier J. Novel approach for detection of hepatitis E virus infection in German blood donors. *J Clin Microbiol* 2012;50:2708–13.
- [60] Nelson KE. Transmission of hepatitis E virus by transfusion: what is the risk? *Transfusion* 2014;54:8–10.
- [61] Li RC, Ge SX, Li YP, Zheng YJ, Nong Y, Guo QS, et al. Seroprevalence of hepatitis E virus infection, rural southern People's Republic of China. *Emerg Infect Dis* 2006;12:1682–8.
- [62] Zheng Y, Ge S, Zhang J, Guo Q, Ng MH, Wang F, et al. Swine as a principal reservoir of hepatitis E virus that infects humans in eastern China. *J Infect Dis* 2006;193:1643–9.
- [63] Cheng XF, Wen YF, Zhu M, Zhan SW, Zheng JX, Dong C, et al. Serological and molecular study of hepatitis E virus among illegal blood donors. *World J Gastroenterol* 2012;18:986–90.
- [64] Guo QS, Yan Q, Xiong JH, Ge SX, Shih JW, Ng MH, et al. Prevalence of hepatitis E virus in Chinese blood donors. *J Clin Microbiol* 2010;48:317–8.
- [65] Bhatt S, Gething PW, Brady OJ, Messina JP, Farlow AW, Moyes CL, et al. The global distribution and burden of dengue. *Nature* 2013;496:504–7.
- [66] Stramer SL, Linnen JM, Carrick JM, Foster GA, Krysztof DE, Zou S, et al. Dengue viremia in blood donors identified by RNA and detection of dengue transfusion transmission during the 2007 dengue outbreak in Puerto Rico. *Transfusion* 2012;52:1657–66.
- [67] Matos D, Tomashek KM, Perez-Padilla J, Munoz-Jordan J, Hunsperger E, Horiuchi K, et al. Probable and possible transfusion-transmitted dengue associated with NS1 antigen-negative but RNA confirmed-positive red blood cells. *Transfusion* 2015;56:215–22.
- [68] Dias LL, Amarilla AA, Poloni TR, Covas DT, Aquino VH, Figueiredo LT. Detection of dengue virus in sera of Brazilian blood donors. *Transfusion* 2012;52:1667–71.
- [69] Mohammed H, Tomashek KM, Stramer SL, Hunsperger E. Prevalence of anti-dengue immunoglobulin G antibodies among American Red Cross blood donors in Puerto Rico, 2006. *Transfusion* 2012;52:1652–6.
- [70] Banu S, Hu W, Guo Y, Naish S, Tong S. Dynamic spatiotemporal trends of dengue transmission in the Asia-Pacific region, 1955–2004. *PLoS One* 2014;9:e89440.
- [71] Wu JY, Lun ZR, James AA, Chen XG. Dengue fever in mainland China. *Am J Trop Med Hyg* 2010;83:664–71.
- [72] Qi X, Wang Y, Li Y, Meng Y, Chen Q, Ma J, et al. The effects of socioeconomic and environmental factors on the incidence of dengue fever in the Pearl River Delta, China, 2013. *PLoS Negl Trop Dis* 2015;9:e0004159.
- [73] Zhao HLLQ, Shen G. Epidemiology of the dengue outbreak in Shiwanzhen, Nanhai County, Guangdong Province. *Chin Med J* 1981;61:466–9.
- [74] Lai S, Huang Z, Zhou H, Anders KL, Perkins TA, Yin W, et al. The changing epidemiology of dengue in China, 1990–2014: a descriptive analysis of 25 years of nationwide surveillance data. *BMC Med* 2015;13:100.
- [75] Jin X, Lee M, Shu J. Dengue fever in China: an emerging problem demands attention. *Emerg Microbes Infect* 2015;4:e3.
- [76] Wang T, Wang M, Shu B, Chen XQ, Luo L, Wang JY, et al. Evaluation of inapparent dengue infections during an outbreak in southern China. *PLoS Negl Trop Dis* 2015;9:e0003677.
- [77] Sun J, Wu, Zhou H, Zhang H, Guan D, He X, et al. The epidemiological characteristics and genetic diversity of dengue virus during the third largest historical outbreak of dengue in Guangdong, China, in 2014. *J Infect* 2016;72:80–90.
- [78] Aquino LC, Hicks CA, Scalon MC, Lima MG, Lemos Mdos S, Paludo GR, et al. Prevalence and phylogenetic analysis of haemoplasmas from cats infected with multiple species. *J Microbiol Methods* 2014;107:189–96.
- [79] Kmush BL, Nelson KE, Labrique AB. Risk factors for hepatitis E virus infection and disease. *Expert Rev Anti Infect Ther* 2015;13:41–53.
- [80] Cao YJ, Xu LY, Jing Y, Cao QL, Geng Q, Yang B, et al. Sero-surveillance on dengue virus in Guangzhou, 2011–2013. *South China J Prev Med* 2015;41:364–6.
- [81] Zhou JW, Lin LD. Surveillance on mosquito vectors of dengue fever and dengue virus in Longgang district of Shenzhen city, 2009–2011. *Chin J Public Health* 2012;28:1628–30.
- [82] Zhou KC, Tan MM, Mo Y, Bi Y, Yong F. Sentinel dengue virus sero-surveillance in Guangxi. *Appl Prev Med* 2013;19:236–7.
- [83] Yu AL, Yang Y, Yan YH, Zhou HZ, Nan H. Investigation of the prevalence of dengue fever in port of Menglian, Yunnan province. *J Pathog Biol* 2015;10:442–5.
- [84] Wei YJ, Li DC. Survey of prevalence of dengue fever and management of infections in Dehong prefecture bordering Myanmar. *China Trop Med* 2010;10:144–8.
- [85] Ming JY, Yin SL, Zeng XJ. Sero-epidemiological survey and analysis on dengue fever in Hainan province. *China Trop Med* 2007;7:2007–8.
- [86] Lin XK, Tai SL. The analysis on epidemic risk of dengue fever at Putian port. *Port Health Control* 2014;19:33–7.
- [87] Rong X, Huang JT, Jing XH, et al. Serum epidemiological investigation of dengue virus infection in blood donors from Guangzhou. *J Trop Med* 2015;15:1014–6.
- [88] Franco MP, Mulder M, Gilman RH, Smits HL. Human brucellosis. *Lancet Infect Dis* 2007;7:775–86.
- [89] Watts RE, Boley LE, Greig WA. Sulfamethazine and blood transfusion in experimental treatment of bovine brucellosis. *Am J Vet Res* 1950;11:304–7.
- [90] Wood EE. Brucellosis as a hazard of blood transfusion. *Br Med J* 1955;1:27–8.
- [91] Xie NM, Huang J, Wang LP, Lang SH, Jiang XD, Gao Y. Electron microscopic observations of *Brucella canis* isolated in China. *Wei Sheng Wu Xue Bao* 1988;28:371–4.
- [92] Doganay M, Aygen B, Esel D. Brucellosis due to blood transfusion. *J Hosp Infect* 2001;49:151–2.
- [93] Zhang X, Wang Z, Mu G, Wang T. Brucellosis control in Northeast China: a long way to go. *Public Health* 2015;129:1132–4.
- [94] Ding F, Zhang W, Wang L, Hu W, Soares Magalhaes RJ, Sun H, et al. Epidemiologic features of severe fever with thrombocytopenia syndrome in China, 2011–2012. *Clin Infect Dis* 2013;56:1682–3.
- [95] Zhang J, Yin F, Zhang T, Yang C, Zhang X, Feng Z, et al. Spatial analysis on human brucellosis incidence in mainland China: 2004–2010. *BMJ Open* 2014;4:e004470.
- [96] Bai KZ, Zhao XX. The epidemiology study on brucellosis at Wulanchabu, Inner Mongolia, 2010. *Mod Anim Husband* 2011;24:55–6.
- [97] Cui B. The epidemic situation and prevention countermeasures of brucellosis in China. *Zhonghua Yi Xue Za Zhi* 2014;48:1035–8.
- [98] Jia P, Joyner A. Human brucellosis occurrences in Inner Mongolia, China: a spatio-temporal distribution and ecological niche modeling approach. *BMC Infect Dis* 2015;15:36.
- [99] Zhang J, Sun GQ, Sun XD, Hou Q, Li M, Huang B, et al. Prediction and control of brucellosis transmission of dairy cattle in Zhejiang Province, China. *PLoS One* 2014;9:e108592.
- [100] Liang XL, Qin HL, Bai ZY, et al. Seroprevalence of *Brucella* infection in yaks (*Bos grunniens*) on the Qinghai-Tibet plateau of China. *Trop Anim Health Prod* 2011;43:305–6.
- [101] Sun J, Tang Y, Ling F, Chang Y, Ye X, Shi W, et al. Genetic susceptibility is one of the determinants for severe fever with thrombocytopenia syndrome virus infection and fatal outcome: an epidemiological investigation. *PLoS One* 2015;10:e0132968.
- [102] Ning P, Guo M, Guo K, Xu L, Ren M, Cheng Y, et al. Identification and effect decomposition of risk factors for *Brucella* contamination of raw whole milk in China. *PLoS One* 2013;8:e68230.
- [103] Chen S, Zhang H, Liu X, Wang W, Hou S, Li T, et al. Increasing threat of brucellosis to low-risk persons in urban settings. *China Emerg Infect Dis* 2014;20:126–30.
- [104] Bai J, Kun ZX. The epidemic investigation on brucellosis at Wulanchabu city, Inner Mongolia. *Mod Anim Husband* 2011;31:134–6.
- [105] Wang W, Liao Q, Wu X, Hou S, Wang Y, Wu J, et al. Potential risk of blood transfusion-transmitted brucellosis in an endemic area of China. *Transfusion* 2015;55:586–92.
- [106] Poesz BJ, Russett FW, Gazdar AF, Bunn PA, Minna JD, Gallo RC. Detection and isolation of type C retrovirus particles from fresh and cultured lymphocytes of a patient with cutaneous T-cell lymphoma. *Proc Natl Acad Sci U S A* 1980;77:7415–9.
- [107] Marano G, Vaglio S, Pupella S, Facco G, Catalano L, Piccinini V, et al. Human T-lymphotropic virus and transfusion safety: does one size fit all? *Transfusion* 2015;56:249–60.
- [108] Cao F, Ji Y, Huang R, Lin S. Prevalence of antibodies to HTLV-I/II in blood donors and risk populations in South China. *Vox Sang* 1998;75:154.
- [109] Wang Y, Li X, Song A, Zhang C, Chen Y, Chen C, et al. Prevalence and partial sequence analysis of human T cell lymphotropic virus type I in China. *J Med Virol* 2005;76:613–8.
- [110] Du J, Chen C, Gao J, Xie J, Rong X, Xu X, et al. History and update of HTLV infection in China. *Virus Res* 2014;191:134–7.
- [111] Shen Y, Su B, Wu J, Qin Y, Jin L, Miao L, et al. The prevalence of transmitted HIV drug resistance among MSM in Anhui province, China. *AIDS Res Ther* 2014;11:19.
- [112] Zhang X, Liu Y, Zhao L, Li B, Yu H, Wen H, et al. An emerging hemorrhagic fever in China caused by a novel bunyavirus SFTSV. *Sci China Life Sci* 2013;56:697–700.
- [113] Yu XJ, Liang MF, Zhang SY, Liu Y, Li JD, Sun YL, et al. Fever with thrombocytopenia associated with a novel bunyavirus in China. *N Engl J Med* 2011;364:1523–32.
- [114] Ding L. Fever with thrombocytopenia associated with a novel bunyavirus in China. *Chin J Exp Clin Virol* 2011;25:81–4.
- [115] Xiong WY, Feng ZJ, Matsui T, Foxwell AR. Risk assessment of human infection with a novel bunyavirus in China. *West Pac Surveill Response J* 2012;3:61–6.
- [116] Xie YT, Lai DH, Liu GY, Zhou JL, Lun ZR. Severe fever with thrombocytopenia syndrome in China. *Lancet Infect Dis* 2015;15:145.
- [117] Liu S, Chai C, Wang C, Amer S, Lv H, He H, et al. Systematic review of severe fever with thrombocytopenia syndrome: virology, epidemiology, and clinical characteristics. *Rev Med Virol* 2014;24:90–102.
- [118] Liu K, Zhou H, Sun RX, Yao HW, Li Y, Wang LP, et al. A national assessment of the epidemiology of severe fever with thrombocytopenia syndrome, China. *Sci Rep* 2015;5:9679.
- [119] Yoshikawa T, Shimajima M, Fukushi S, Tani H, Fukuma A, Taniguchi S, et al. Phylogenetic and geographic relationships of severe fever with thrombocytopenia syndrome virus in China, South Korea, and Japan. *J Infect Dis* 2015;212:889–98.
- [120] Shimajima M, Fukushi S, Tani H, Taniguchi S, Fukuma A, Saijo M. Combination effects of ribavirin and interferons on severe fever with thrombocytopenia syndrome virus infection. *Virology* 2015;52:181.
- [121] Shimajima M, Fukushi S, Tani H, Yoshikawa T, Morikawa S, Saijo M. Severe fever with thrombocytopenia syndrome in Japan. *Uirusu* 2013;63:7–12.
- [122] Shin J, Kwon D, Youn SK, Park JH. Characteristics and factors associated with death among patients hospitalized for severe fever with thrombocytopenia syndrome, South Korea, 2013. *Emerg Infect Dis* 2015;21:1704–10.
- [123] Kim WY, Choi W, Park SW, Wang EB, Lee WJ, Jee Y, et al. Nosocomial transmission of severe fever with thrombocytopenia syndrome in Korea. *Clin Infect Dis* 2015;60:1681–3.



- [124] Yun Y, Heo ST, Kim G, Hewson R, Kim H, Park D, et al. Phylogenetic analysis of severe fever with thrombocytopenia syndrome virus in South Korea and migratory bird routes between China, South Korea, and Japan. *Am J Trop Med Hyg* 2015;93:468–74.
- [125] Zhang L, Liu Y, Ni D, Li Q, Yu Y, Yu XJ, et al. Nosocomial transmission of human granulocytic anaplasmosis in China. *JAMA* 2008;300:2263–70.
- [126] Bao CJ, Guo XL, Qi X, Hu JL, Zhou MH, Varma JK, et al. A family cluster of infections by a newly recognized bunyavirus in eastern China, 2007: further evidence of person-to-person transmission. *Clin Infect Dis* 2011;53:1208–14.
- [127] Gai Z, Liang M, Zhang Y, Zhang S, Jin C, Wang SW, et al. Person-to-person transmission of severe fever with thrombocytopenia syndrome bunyavirus through blood contact. *Clin Infect Dis* 2012;54:249–52.
- [128] Liu Y, Li Q, Hu W, Wu J, Wang Y, Mei L, et al. Person-to-person transmission of severe fever with thrombocytopenia syndrome virus. *Vector Borne Zoonotic Dis* 2012;12:156–60.
- [129] Dinu LP, Ionescu RT, Tomescu AI. A rank-based sequence aligner with applications in phylogenetic analysis. *PLoS One* 2014;9:e104006.
- [130] Chen HZ, Liang WF. The epidemic survey on first case with novel severe fever with thrombocytopenia bunyavirus in Zhe Jiang province. *J Int Epidemiol Infect Dis* 2011;38:360.
- [131] Zeng P, Ma L, Gao Z, Wang J, Liu J, Huang X, et al. A study of seroprevalence and rates of asymptomatic viremia of severe fever with thrombocytopenia syndrome virus among Chinese blood donors. *Transfusion* 2015;55:965–71.
- [132] Liang S, Bao C, Zhou M, Hu J, Tang F, Guo X, et al. Seroprevalence and risk factors for severe fever with thrombocytopenia syndrome virus infection in Jiangsu Province, China, 2011. *Am J Trop Med Hyg* 2014;90:256–9.
- [133] Zhao L, Zhai S, Wen H, Cui F, Chi Y, Wang L, et al. Severe fever with thrombocytopenia syndrome virus, Shandong Province, China. *Emerg Infect Dis* 2012;18:963–5.
- [134] Zhang L, Sun J, Yan J, Lv H, Chai C, Sun Y, et al. Antibodies against severe fever with thrombocytopenia syndrome virus in healthy persons, China, 2013. *Emerg Infect Dis* 2014;20:1355–7.
- [135] Roberts LJ, Handman E, Foote SJ. Science, medicine, and the future: leishmaniasis. *BMJ* 2000;321:801–4.
- [136] Guevara P, Ramirez JL, Rojas E, Scorza JV, Gonzalez N, Anez N. *Leishmania braziliensis* in blood 30 years after cure. *Lancet* 1993;341:1341.
- [137] Giger U, Oakley DA, Owens SD, Schantz P. *Leishmania donovani* transmission by packed RBC transfusion to anemic dogs in the United States. *Transfusion* 2002;42:381–3.
- [138] Owens SD, Oakley DA, Marryott K, Hatchett W, Walton R, Nolan TJ, et al. Transmission of visceral leishmaniasis through blood transfusions from infected English foxhounds to anemic dogs. *J Am Vet Med Assoc* 2001;219:1076–83.
- [139] Andre R, Brumpt L, Dreyfus B, Passelecq A, Jacob S. Cutaneous leishmaniasis, cutaneous-ganglionic leishmaniasis, and transfusional kala-azar. *Bull Mem Soc Med Hop Paris* 1957;73:854–60.
- [140] Cohen C, Corazza F, De Mol P, Brasseur D. Leishmaniasis acquired in Belgium. *Lancet* 1991;338:128.
- [141] Mauny I, Blanchot I, Degeilh B, Dabadie A, Guiguen C, Roussey M. Visceral leishmaniasis in an infant in Brittany: discussion on the modes of transmission out endemic zones. *Pediatric* 1993;48:237–9.
- [142] Cummins D, Amin S, Halil O, Chiodini PL, Hewitt PE, Radley-Smith R. Visceral leishmaniasis after cardiac surgery. *Arch Dis Child* 1995;72:235–6.
- [143] Grogil M, Daugirda JL, Hoover DL, Magill AJ, Berman JD. Survivability and infectivity of viscerotropic *Leishmania tropica* from operation desert storm participants in human blood products maintained under blood bank conditions. *Am J Trop Med Hyg* 1993;49:308–15.
- [144] Riera C, Fisa R, Lopez-Chejade P, Serra T, Girona E, Jimenez M, et al. Asymptomatic infection by *Leishmania infantum* in blood donors from the Balearic Islands (Spain). *Transfusion* 2008;48:1383–9.
- [145] Riera C, Fisa R, Udina M, Gallego M, Portus M. Detection of *Leishmania infantum* cryptic infection in asymptomatic blood donors living in an endemic area (Eivissa, Balearic Islands, Spain) by different diagnostic methods. *Trans R Soc Trop Med Hyg* 2004;98:102–10.
- [146] Scarlata F, Vitale F, Saporito L, Reale S, Vecchi VL, Giordano S, et al. Asymptomatic *Leishmania infantum*/chagasi infection in blood donors of western Sicily. *Trans R Soc Trop Med Hyg* 2008;102:394–6.
- [147] Colomba C, Saporito L, Polara VF, Barone T, Corrao A, Titone L. Serological screening for *Leishmania infantum* in asymptomatic blood donors living in an endemic area (Sicily, Italy). *Transfus Apher Sci* 2005;33:311–4.
- [148] le Fichoux Y, Quaranta JF, Aufeuvre JP, Lelievre A, Marty P, Suffia I, et al. Occurrence of *Leishmania infantum* parasitemia in asymptomatic blood donors living in an area of endemicity in southern France. *J Clin Microbiol* 1999;37:1953–7.
- [149] Wang JY, Cui G, Chen HT, Zhou XN, Gao CH, Yang YT. Current epidemiological profile and features of visceral leishmaniasis in people's Republic of China. *Parasit Vectors* 2012;5:31.
- [150] Li T, He S, Zhao H, Zhao G, Zhu XQ. Major trends in human parasitic diseases in China. *Trends Parasitol* 2010;26:264–70.
- [151] Maurin M, Raoult D. Q fever. *Clin Microbiol Rev* 1999;12:518–53.
- [152] Kagawa FT, Wehner JH, Mohindra V. Q fever as a biological weapon. *Semin Respir Infect* 2003;18:183–95.
- [153] Madariaga MG, Rezaei K, Trenholme GM, Weinstein RA. Q fever: a biological weapon in your backyard. *Lancet Infect Dis* 2003;3:709–21.
- [154] Raoult D, Levy PY, Harle JR, Etienne J, Massip P, Goldstein F, et al. Chronic Q fever: diagnosis and follow-up. *Ann N Y Acad Sci* 1990;590:51–60.
- [155] Raoult D. Host factors in the severity of Q fever. *Ann N Y Acad Sci* 1990;590:33–8.
- [156] Raoult D, Levy PY, Dupont HT, Chicheportiche C, Tamalet C, Gastaut JA, et al. Q fever and HIV infection. *AIDS* 1993;7:81–6.
- [157] Ayres JG, Flint N, Smith EG, Tunnicliffe WS, Fletcher TJ, Hammond K, et al. Post-infection fatigue syndrome following Q fever. *QJM* 1998;91:105–23.
- [158] van der Hoek W, Dijkstra F, Schimmer B, Schneeberger PM, Vellema P, Wijkman C, et al. Q fever in the Netherlands: an update on the epidemiology and control measures. *Euro Surveill* 2010;15 [pii = 19520].
- [159] Hogema BM, Slot E, Molier M, Schneeberger PM, Hermans MH, van Hanne E, et al. *Coxiella burnetii* infection among blood donors during the 2009 Q-fever outbreak in the Netherlands. *Transfusion* 2012;52:144–50.
- [160] Slot E, Hogema BM, Molier M, Zaaier HL. Screening of blood donors for chronic *Coxiella burnetii* infection after large Q fever outbreaks. *Transfusion* 2014;54:2867–70.
- [161] Feng XY, Wu M, Luo M. Progress of Q-fever epidemiological research in China. *Med Anim Prev* 2010;32:219–20.
- [162] Zhang F, Wu ZJ. Molecular epidemiology investigation for Q-fever in northeast of China. *J Chin Pathol* 2011;22 [183–185 + 235].
- [163] Zhang YG, Shi YH, Liu H. Sero-investigation of Q-fever among different population and livestock in Anhui Province. *Anhui Prev Med* 2010;21 [87–88 + 98].
- [164] Zhu XY, Wei JC, Zhang HJ, Yu DZ. Q-fever detection on antibody of one causal fever. *J Chin Diagn* 2008;22:1130–1.
- [165] Yin YH, Li CQ, Liu Z. Blood donation in China: sustaining efforts and challenges in achieving safety and availability. *Transfusion* 2015;55:2523–30.
- [166] Zhong NS, Zheng BJ, Li YM, Poon, Xie ZH, Chan KH, et al. Epidemiology and cause of severe acute respiratory syndrome (SARS) in Guangdong, People's Republic of China, in February, 2003. *Lancet* 2003;362:1353–8.
- [167] Wang H, Feng Z, Shu Y, Yu H, Zhou L, Zu R, et al. Probable limited person-to-person transmission of highly pathogenic avian influenza A (H5N1) virus in China. *Lancet* 2008;371:1427–34.
- [168] Sabino EC, Loureiro P, Lopes ME, Capuani L, McClure C, Chowdhury D, et al. Transfusion-transmitted dengue and associated clinical symptoms during the 2012 epidemic in Brazil. *J Infect Dis* 2016;213:694–702.
- [169] Motta IJ, Spencer BR, Cordeiro da Silva SG, Arruda MB, Dobbins JA, Gonzaga YB, et al. Evidence for transmission of Zika virus by platelet transfusion. *N Engl J Med* 2016;375:1101–3.
- [170] Vasquez AM, Sapiano MR, Basavaraju SV, Kuehnert MJ, Rivera-Garcia B. Survey of blood collection centers and implementation of guidance for prevention of transfusion-transmitted Zika virus infection—Puerto Rico, 2016. *Am J Transplant* 2016;16:2487–90.
- [171] Zhong YB, Liu XQ, Deng YC, Xu PH, Zhong GR, Zhang W. First case of laboratory-confirmed Zika virus infection imported into China. *Chin Med J (Engl)* 2016;129:2013–4.
- [172] Zhang J, Jin X, Zhu Z, Huang L, Liang S, Xu Y, et al. Early detection of Zika virus infection among travellers from areas of ongoing transmission in China. *J Travel Med* 2016;23 [pii = taw047].
- [173] Xie YW, Chan PK, Szeto CK, Kwok SY, Chu IM, Chu SS, et al. Clearance of dengue virus in the plasma-derived therapeutic proteins. *Transfusion* 2008;48:1342–7.
- [174] Kreil TR, Berting A, Kistner O, Kindermann J. West Nile virus and the safety of plasma derivatives: verification of high safety margins, and the validity of predictions based on model virus data. *Transfusion* 2003;43:1023–8.
- [175] Chunhui Y, Guohui B, Hong Y, Xiaopu X, Zherong B, Mingyuan W, et al. Quantitative evaluation of plasma after methylene blue and white light treatment in four Chinese blood centers. *Transfus Apher Sci* 2013;49:631–9.