virus subtypes not circulating in humans should be cautiously managed. We fully agree with this assertion, because this is also the primary message of our work.

We also agree that, in humans, serological determination after outbreaks of avian influenza may be very difficult. In this regard, our article had emphasized that serum samples were considered to be positive for antibodies to the H7 subtype of avian influenza virus only if, on the basis of at least 2 different serological techniques including the microneutralization assay, they had repeatedly given unequivocally positive results.

We used multiple serological tests to exclude the possibility of nonspecific cross-reactions with antibodies to human influenza viruses. Although definitive evidence for active infection would include detection of either virus or viral RNA at the time of exposure or illness, the recent increasing evidence that the number of cases of transmission of avian influenza virus to humans is higher than what had previously been observed makes serological data very important and useful; when properly evaluated, these data may provide retrospective information on the circulation of avian influenza viruses in the human population, as has been demonstrated in previous reports [2, 3].

Skowronski et al. also highlight the inability of mild, conjunctival infections to induce a systemic antibody response. In this regard, it should be emphasized that, in the case of the outbreaks of the H7N7 subtype of avian influenza virus in The Netherlands, ~50% of persons who had handled infected poultry were found to be seropositive, as were most of the virologically positive individuals, as has recently been reported by Enserink et al. [4] and Meijer et al. [5]. Although the outbreaks in The Netherlands were caused by a highly pathogenic avian influenza virus of subtype H7N7, the reported cases of human infection were always associated with mild conjunctivitis and influenza-like illness, except in 1 case [6]. Evidence of systemic antibody response to mild conjunctivitis has also been reported in association with other viruses infecting human conjunctiva—for example, adenoviruses—some of which have been shown to bind specifically to $\alpha$2,3-linked sialic-acid receptors present in the cells of the human conjunctival epithelium [7, 8].

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## Coinfection with *Borrelia burgdorferi* and *Babesia microti:* Bad or Worse?

**To the Editor**—In their recent study, Coleman et al. concluded that coinfection with *Borrelia burgdorferi,* the etiological agent of Lyme disease, and *Babesia microti,* the etiological agent of human babesiosis, does not increase the severity of either disease in mice [1]. This conclusion contradicts previous observations that coinfection with *B. burgdorferi* and *B. microti* causes increased disease severity in both mice [2, 3] and humans [4–6]. However, 2 significant design flaws in Coleman et al.'s study render its conclusions suspect.

First, Coleman et al. used a strain of *B. microti* that was "isolated from *P. leucopus* and adapted to growth in laboratory mice" and that was "maintained by blood passage in C3H/HeN mice" (p. 1635). The resultant mouse-adapted strain of *B. microti* may have been attenuated relative to wild-type strains and may have been less virulent when given in combination with *B. burgdorferi.* In contrast, the MN1 strain of *B. microti,* which was originally isolated from a human patient and was subsequently inoculated into golden Syrian hamsters prior to cryopreservation, was used in the study by Moro et al. [3]. In combination with *B. burgdorferi*, this nonadapted *B. microti* strain would be more likely to cause significant murine complications, as was seen in Moro et al.'s study. Thus, the attenuated strain of *B. microti* used by Coleman et al. may have biased the outcome of the study against more-severe coinfection.

Second, Coleman et al. failed to measure cytokine levels or symptoms of arthritis in their coinfected BALB/c mice, whereas the study by Moro et al. clearly showed increased arthritis severity and altered cytokine levels when coinfection was induced in mice of this strain. The discrepancy suggests that Coleman et al. may

have examined the wrong parameters in their mice and may have missed significant markers of disease severity in those that were coinfected, again casting doubt on the conclusions of their study.

In summary, previous studies have shown that coinfection with *B. burgdorferi* and *B. microti* increases disease severity in animals and humans [7]. In light of its methodological flaws, the study by Coleman et al. fails to alter this conclusion.

**Raphael B. Stricker, Joseph J. Burrascano, Nick S. Harris, Richard Horowitz, Lorraine Johnson, Patricia V. Smith, and Steven E. Phillips**

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## Reply to Stricker et al.

**To the Editor**—In response to the concerns of Stricker et al. [1], allow us to point out that, regardless of whether a *Babesia microti* strain is derived from a human patient or from *Peromyscus leucopus*, all isolations are first made in hamsters, because *B. microti* do not initially grow well in mice. Furthermore, the *B. microti* strain used in our study [2] was not attenuated—given the high parasitemia and marked hemolysis observed, we would hardly call it that. In fact, we provided ample parasitological and hematological data indicating that our *B. microti* strain causes a very severe course of infection in mice. Finally, we did not measure cytokine levels because we did not observe an increase in the severity of arthritis in the coinfected mice we examined.

**James L. Coleman[1,2] and Jorge L. Benach[2]**

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## Poverty and the Spread of Bloodborne Disease in Central China

The editorial commentary by Dodd [1] provides a useful framework for understanding the epidemiological aspects of infection with HIV, hepatitis C virus (HCV), and other bloodborne pathogens in central China. However, 2 points need to be made about the larger social determinants of HIV and HCV spread in rural China, to place these epidemiological aspects in the proper context. First, central China's HIV and HCV epidemics that began during the 1990s were and continue to be inextricably linked to poverty. Poor farmers in central China could earn more money during the 1990s by selling blood than by tilling land, and so they often supplemented their income by commercially donating plasma [2, 3]. Larger parts of rural central China were heavily affected by these bloodborne HIV and HCV epidemics, compared with urban eastern China, precisely because of the widespread poverty [4]. The HIV and HCV epidemics during the 1990s rendered infected rural farmers helpless and, thus, magnified the shortcomings of the post–Maoist era health care system, which, through decentralization and privatization, had widened the gap between health care delivery to China's rural western poor and that to wealthier eastern urban residents [5].

Second, although the scientific community reported the spread of HIV in commercial blood donors in central China as early as 1995 [3], an adequate response by central Chinese provincial officials, such as the initiation of safe blood-collection procedures and treatment for the thousands of rural farmers who were infected with HIV via an unsafe blood supply, lagged behind [6]. The Chinese government did react to these early warning signs of an unsafe blood supply by establishing regulations in 1995 to ban all unofficial collection of plasma and whole blood [7]. Along with increased financial support, such legislative measures have substantially improved China's blood-collection system. However, insufficient political will coupled with China's vast size and variable public health knowledge among both its citizens and its officials have hindered strict enforcement of these blood-donation laws. For example, despite a 1998 law mandating that all blood used for clinical purposes must be collected from voluntary donors [8], as of 2004, 15% of China's blood sup-