related predictors, had better predictive ability compared to models based on either climate or habitat-derived variables alone. Importantly, even though climate per se matters for the distribution, the impact of humans on habitat plays a crucial role in determining the distribution of the intermediate host snails in Africa.

O.6.8.1.002
Mapping and modeling *Dirofilaria* infections in Europe

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Climatic changes, together with an increase in the movement of dogs across Europe, have caused an increase in the geographical range of *Dirofilaria immitis* and *D. repens* infections. A Geographic Information System based on thermal regimen was constructed to identify areas potentially suitable for *Dirofilaria* transmission in Europe. These models are based on evidence that: (i) there is a threshold of 14°C below which *Dirofilaria* development will not proceed in mosquitoes; (ii) there is a requirement of 130 growing degree-days for larvae to reach infectivity, and; (iii) there is a maximum life expectancy of 30 days for a mosquito vector. The output of these models predicted that the summer temperatures (with peaks in August) are sufficient to facilitate extrinsic incubation of *Dirofilaria* even at high latitudes. Recently, an additional model was constructed to verify the influence of temperature in the course of three decades (1980–1989, 1990–1999 and 2000–2012) on the risk of infection by *Dirofilaria* in Italy. The results showed an expected increasing trend of temperatures, an increase of the *Dirofilaria* generation numbers into the mosquitoes and a significant extension of the infection risk from 5–6 months (1980–1989) to 6.5 months (1990–1999), up to more than 7 months (2000–2012). These findings show that geospatial tools are very useful for mapping, monitoring, forecasting and surveillance of both heartworm and subcutaneous dirofilariosis.

O.6.8.1.003
Epidemiological and spatiotemporal features of acute schistosomiasis in the People's Republic of China

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BACKGROUND Despite significant reduction during the past 50 years, data suggest that schistosomiasis has re-emerged in China recently. Therefore, the national control program revised its strategy in 2004.
METHODS Surveillance data on acute schistosomiasis and outbreaks were extracted from the National Diseases Reporting Information System (NDRIS) from 2005 to 2012. The data was diagrammatized and analyzed using SPSSv17.0. The spatiotemporal cluster features were described using a discrete Poison model in SatScan V9.1.1, and ArcGIS 9.3.

RESULTS A total of 1047 cases were extracted from the NDRIS. 989 (94.5%) cases were reported from the lake and marshland regions (Hunan, Hubei, Jiangxi, Anhui and Jiangsu province), only 55 (5.3%) in the mountainous regions (Sichuan, Yunnan province) and 3 (0.3%) were imported from other countries. The number of annual cases declined significantly from 2005 to 2012 by 97.7%. Most cases were school-age children, farmers and fishermen. Only five outbreaks were reported in Hubei Province and one in Sichuan Province in 2005, and none in subsequent years. Totally, 85 cases were recorded as infected in other provinces. The cases clustered from June to November and a total of nine clusters were detected with a higher risk in the lake and marshland regions of Hunan, Hubei, Jiangxi, Anhui and Sihchuan provinces.
CONCLUSIONS Decreasing numbers of cases from 2005 to 2012, indicate that the revised control strategy has played a role in reducing the prevalence of schistosomiasis. However, potential risk of infection and/or re-emergence remains in the lakes and marshland regions.

6.10 Role of natural IgM binding in parasitic diseases

O.6.10.001
The role of non-specific IgM binding to a *Plasmodium falciparum* protein PfEMP1 which mediates rosetting

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INTRODUCTION The pathogenicity of *Plasmodium falciparum*, which is responsible for most malaria-related severe morbidity and essentially all the mortality, is related to the capacity of *P. falciparum* -infected erythrocytes (IEs) to adhere to vascular host receptors. This adhesion is mediated by members of the PfEMP1 family of clonally variant *P. falciparum* erythrocyte membrane proteins. Expression of the relatively conserved PfEMP1 protein VAR2CSA mediates IE adhesion to placental CSA. It has been proposed that acquisition of protective immunity to VAR2CSA is delayed by its affinity for non-specific IgM, which could interfere with specific IgG recognition of the antigen. In addition to VAR2CSA, a number of PfEMP1 proteins that mediate rosetting also bind non-specific IgM. We therefore speculated that non-specific IgM binding to rosetting isolates serves the same immune-evasive purpose as in the case of VAR2CSA.
MATERIALS AND METHODS We used recombinant proteins representing individual domains and the entire extracellular part of the rosetting PfEMP1 protein, HB3var06 to study this hypothesis.
RESULTS AND CONCLUSIONS We could map the IgM binding region to the C-terminal part of the molecule, which corresponds well to the location of the binding site for non-specific IgM binding in VAR2CSA. However, SAXS analysis showed that full-length HB3var06 has an elongated tertiary structure rather than the globular conformation of VAR2CSA. We used domain-specific antisera to study the impact of this structural difference on the ability of non-specific IgM to interfere with binding of