Conclusions Pakistani infants were smaller in all measurements but had a tendency to greater central obesity (as indicated by subscapular skinfold thickness). Differences do not appear to differ markedly across generations. This suggests that differences may be genetically driven or are affected by epigenetic or persisting behaviour characteristics.

P1-546 MALARIA INFECTION IN PREGNANCY AS A RISK FACTOR FOR LOW BIRTH WEIGHT IN THE DISTRICT OF BANGKA BELITUNG, INDONESIA, 2010

doi:10.1136/jech.2011.142976h.33

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Background Malaria is a major health problem in Indonesia. The District of Bangka is one of 338 malaria endemic areas with a clinical malaria rate of 51.87% and positive malaria rate of 9.46% in 2008. In malaria endemic areas pregnant mothers are the major group at risk for malaria infection. Malaria infection during pregnancy contributes to maternal morbidity and low birth weight (LBW) infants (<2500 g) caused either by preterm birth or intrauterine growth restriction (IUGR), factors that become the greatest risk factors for infant morbidity and mortality.
Methods This was a case-control study where the population are infants, namely LBW infants (<2500 g) as a case and normal birth weight infants (2500–4000 g) as a control within the period of 2008–2009. There were 174 subjects in total, comprising 58 cases and 116 controls. Data analysis used univariable, bivariable (χ^2) and multivariable (logistic regression) techniques.
Results There was a significant association between malaria infection in pregnant mothers and the incidence of LBW infants (crude OR =2.90; 95% CI 1.38 to 6.10), and after adjustment or controlled simultaneously for external variables, the influence of malaria infection remained (adjusted OR =2.97; 95% CI 1.37 to 6.39). Pregnant mothers with malaria infection had a risk 2.9 times greater for delivering LBW infants than normal birth weight infants. All external variables had no influence on malaria infection in pregnant mothers and the incidence of LBW infants.
Conclusion Pregnant mothers who delivered infants with LBW were more likely to be infected with malaria than pregnant mothers who delivered infants with normal birth weight.

P1-547 ASSOCIATION OF DNA METHYLATION WITH METAL EXPOSURE AMONG HEALTHY KOREAN POPULATION

doi:10.1136/jech.2011.142976h.34

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Introduction DNA methylation is regarded as a well-defined epigenetic mechanism and involved in biological processes including ageing and cancer. The purpose of this study is to find whether DNA methylation is associated with lifestyle and environmental factors in healthy population residing in an industrialised zone in Korea.
Methods A total of 758 subjects (324 males and 434 females) were included in this study. Global DNA methylation level by lifestyle factors and environmental pollutants was measured in peripheral blood leukocyte.
Results Global DNA methylation levels (expressed as PMR values) of men were varied with age, while no change was seen in women. No association between lifestyle and biochemical factors (smoking, homocysteine, leptin, albumin and BMI) with global DNA methylation was observed. The relationship between metal such as mercury, cadmium and arsenic and DNA methylation was analysed. Arsenic only had positive association with DNA methylation level in male group. Global DNA methylation pattern among family members was analysed to find familial aggregation. Significant associations of Mother with offspring, offspring with offspring were found. Correlation between sibling pairs was also increased in young age group, suggesting that DNA methylation patterns determined not only by genetic factors but environmental factors.
Conclusion DNA methylation levels of men were varied with age, while those of women were consistent throughout the age group. Positive association was shown in urinary arsenic only in adult male. DNA methylation level can be regulated by environmental stressor, but the association between each environmental factor and global DNA methylation was not strong.

P1-548 RISK FACTORS FOR AN OUTBREAK OF CHIKUNGUNYA FEVER IN WEST BORNEO, INDONESIA, 2010

doi:10.1136/jech.2011.142976h.35

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Background Chikungunya fever is a vector-borne disease with high morbidity rates, prolonged polyarthritis in some cases and it cause substantial socioeconomic impact. On 4 January 2010, an outbreak of Chikungunya fever was reported in West Borneo in Indonesia. The total number of cases was 65 with no fatalities. An analytical study was undertaken to determine the risk factors for the outbreak.
Method This was an observational study with case control design. Cases were those with major clinical symptoms of Chikungunya fever, such as fever, arthalgia, myalgia, rash and headache. Controls were neighbours of cases who did not have clinical symptoms of the disease. The study used bivariate and multivariate analyses with χ^2 and logistic regression. OR was used to determine risk factors. Some patient's blood was tested to confirm the diagnosis.
Results From the bivariate analyses, risk factors were farming in the forest (p value <0.05, OR=10.14, 95% CI 3.84 to 26.76); not using mosquito repellent devices (p=0.001, OR=4.70, CI 1.75 to 12.60); not eradicating mosquito nests (p=0.007, OR=3.18, CI 1.33 to 7.61); and hanging clothes (p=0.015, OR=2.814, CI 1.206 to 6.566). The multivariate analyses showed that farming farming in the forest was an independent risk factor for infection (Exp.(B): 9.122, p<0.05). Laboratory examination of blood samples confirmed that two out of four cases were positive for Chikungunya fever.
Conclusions Farming in the forest was a risk factor for infection. This was the basis for health promotion and prevention of future cases of Chikungunya fever in West Borneo.

P1-549 THE ROLE OF PSYCHOSOCIAL FACTORS IN SLEEP DURATION IN ELDERS AND ITS EFFECT ON ALL-CAUSE MORTALITY: THE KRAKOW STUDY

doi:10.1136/jech.2011.142976h.36

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Introduction Epidemiological studies performed in the last decades confirmed the significant role of sleep as an independent predictor of survival in older age.
Objective The aim of the study was to assess the role of the social position, self-reported functional status, self-rated health, and a

J Epidemiol Community Health: first published as 10.1136/jech.2011.142976h.35 on 5 August 2011. Downloaded from http://jech.bmj.com/ on April 18, 2024 by guest. Protected by copyright.