conducted by infecting both colonies with dengue type 1 virus. Mosquitoes were dissected on day 2, 4, 8, 12 and 16 post infection to obtain salivary glands, midguts and ovaries. After extraction, presence of Wolbachia were determine using PCR and dengue virus load were determined using qPCR. **Results**: *Wolbachia* infected colonies had higher fecundity and egg viability compared to *Wolbachia* uninfected colony. Female lifespan for infected colony were slightly higher whereas male lifespan was significantly higher for *Wolbachia* uninfected colony. Virus titre load was the highest on day 12 for all three organs. Uninfected colony had higher viral amount on day 12 for salivary glands and midgut. The viral load in the ovaries were different at all intervals between *Wolbachia* infected and uninfected colonies.

Conclusion: *Wolbachia* infected colonies had higher fecundity, longevity and egg viability compared to *Wolbachia* uninfected colonies but male lifespan were higher in *Wolbachia* uninfected colonies. Differences were noticeable in viral load pattern between *Wolbachia* infected and uninfected colonies for dengue type 1.

OS 8-2

THE EPIDEMIOLOGY OF HUMAN Q FEVER AND THE ASSOCIATION BETWEEN HUMAN Q FEVER AND ANIMALS IN TAIWAN, 2004 TO 2012

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Purpose: The aim of this study is to investigate the epidemiology of human Q fever (QF) and the association between human QF and animals.
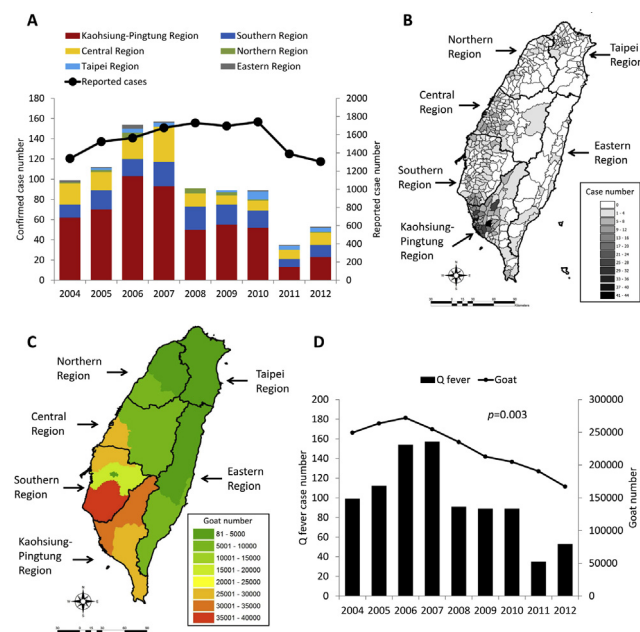
Methods: Three nationwide databanks were investigated, included 879 confirmed cases of QF from 2004—2012, goat and cattle data from 2004—2012, and 8313 reported cases of QF from Centers for Disease Control, Taiwan (Taiwan CDC) from October 2007 to 2012. The distribution of Q fever cases and animals were illustrated by geographic information system software.

Results: QF cases increased from 2004 to 2007, but dramatically declined in 2008 and 2011 (Figure A), and the trend was significantly correlated with the number of goat rather than cattle (Figure C and D). The cases (76.7%) mainly distributed in southern Taiwan, particularly in Kaohsiung-Pingtung region (59.3%) (Figure B). They were prevalent from March to September (76.1%), between age 30—69 year-old (82.7%), and in male (90.2%). Among the reported case of QF, 1116 (13.4%) cases had confirmed diseases including QF

(364, 4.4%), QF and murine typhus (MT) (2, 0.02%), QF and scrub typhus (ST) (7, 0.1%), QF and leptospirosis (LP) (4, 0.05%), MT (147, 1.8%), ST (419, 5.0%), ST and LP (8, 0.1%), and LP (165, 2.0%), and 7197 (86.6%) cases were unknown disease. Only 16.7% and 0.9% QF case had risky occupations and contact with goat, respectively.

Conclusions: In Taiwan, the case number of QF fluctuated and correlated with goat number, but the contact rate of goat was low. Other zoonoses and co-infection with other zoonoses should be considered in clinically suspected QF case.

OS 8-3

CORRELATION BETWEEN GUT MICROBIOTA COMPOSITION AND PARASITIC INFECTION OF PRE-ADOLESCENCE IN MALAYSIA

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Purpose: Gut microbiota plays an important role in mammalian host metabolism and physiological functions including energy metabolism and nutrient absorption. These functions are pivotal in the rapid growth phase of adolescence. Recent publications suggested a potential correlation between parasitic infection and gut microbiota composition. To assess the relationship, we compared the bacterial richness and composition of faeces obtained from rural pre-adolescence (aged 6-12) of three distinct ethnic groups in Malaysia, namely the Malays, Chinese and the Orang Asli (indigenous). The three groups exhibited varying level of helminthic infection, with the highest positive rate detected from the Orang Asli (100%), and lowest from the Chinese (~6%).

Methods: Parasitic identification was conducted using formalin-ether concentration technique while the gut microbiota composition and distribution was elucidated using two complementary molecular assessment tools including TRFLP and 454 NGS.

Results: Our results showed that the gut microbiota composition was correlated with the presence of parasitic infection. An increased in the overall bacterial diversity and elevated *Ruminococcaceae* was observed in Orang Asli (infected) as opposed to the Chinese and Malays. The results was supported by the predicted metagenome profiles which showed a significant increase in gene pathways related to bacterial proliferation and colonization in the former.
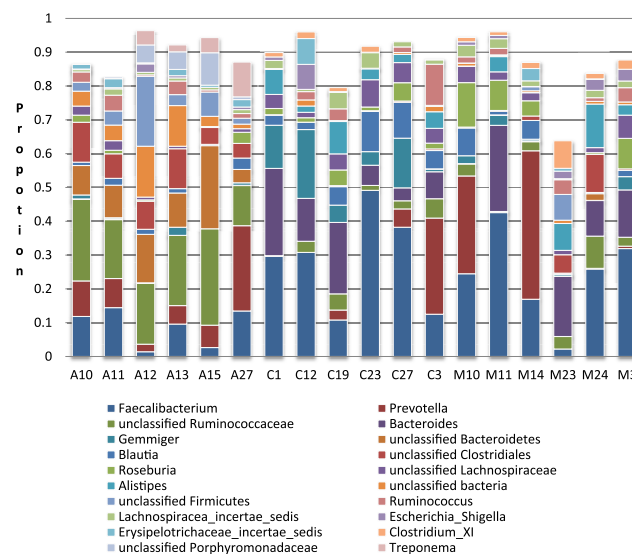

Fig 1   Top 20 bacterial genera detected from the faecal sample. A = Orang Asli, C = Chinese, M = Malays