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DEMOGRAPHIC AND EVOLUTIONARY HISTORIES OF MALARIA PARASITES DERIVED FROM LONG-TAILED MACAQUES

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Macaques are natural hosts for five Plasmodium species: P. knowlesi, P. cynomolgi, P. coatneyi, P. inui, and P. fieldi. The demographic and evolutionary histories of P. knowlesi, assessed by analysis of the P. knowlesi mitochondrial genome sequences, revealed that P. knowlesi is derived from an ancestral parasite population and underwent population expansion approximately 30,000-40,000 years ago. In order to test the hypothesis that the population expansion of P. knowlesi was due to an expansion in the macaque hosts rather than the human population, the mitochondrial genomes (approximately 6 kb) of other Plasmodium in macaques were sequenced from 33 macaque blood samples. For each sample, the full length mitochondrial genome was PCR amplified, cloned and sequenced. A series of 16 forward and reverse walk-in primers was established for sequencing. Phylogenetic tree topologies constructed using 24 P. inui-like sequences exhibit the formation of a separate sister clade of the P. inui-like sequences compared to the P. inui referral sequences with two other sequences that were phylogenetically distinct from Plasmodium sequences. Significant negative values for Tajima’s D (-2.53540), Fu and Li’s D (-3.8306) and Fu and Li’s F (-4.06115) statistics provide evidence for an expansion of the P. inui-like parasite population. The indication of population expansion is further evident from the unimodal shape of the pairwise mismatch distribution, supported by a low Harpending’s raggedness index (r = 0.007, P = 0.76). The signature of population expansion for the P. inui-like sequences appears to be similar to that for P. knowlesi, thereby supporting the hypothesis.

S 6.6

ANTIBIOTIC SUSCEPTIBILITY OF ENTEROCOCCUS SPP. IN PIGS

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Enterococcus spp. does not cause major infection in pigs but multidrug resistant Enterococcus in pigs is an emerging issue. The use of Enterococcus spp. as probiotics in pigs remains controversial. The objective of this study was to determine the antimicrobial susceptibility of Enterococcus spp. isolated from pigs in selected swine farms in Peninsular Malaysia. Isolation was done by standard culture method from 110 pigs from 5 farms located in Peninsular. Kirby-Bauer disk diffusion method was used to determine the antibiotic resistance of the isolates towards ampicillin, vancomycin, chloramphenicol, tetracycline, cefotaxim, gentamicin, erythromycin, linzolid, penicillin, and telocplanin. A total of 143 Enterococcus spp. were isolated. Majority of the strains were susceptible to ampicillin and penicillin. 42% of the strains were non-susceptible to the antibiotic. 40.8% of the strains were non-susceptible to high-level gentamycin (120 μg) and more than 50% of the strains were non-susceptible to chloramphenicol, tetracycline, cefotaxim, gentamicin, and erythromycin. Based on the results, a trend can be observed where the antibiotic susceptibility of bacteria can be influenced by the level of farm hygiene practices. Although not statistically significant, similar findings suggested that enterococci from swine should be regarded with caution because they can be reservoirs for antimicrobial resistance.