harbors a complex community with the dominances of *Elizabethkingia* (26.1%), *Acidovorax* (10.5%) and *Enterobacteriaceae* (10.8%). In newly emerged adults, flora composition becomes simpler, dominated by *Elizabethkingia* (55.9%), *Staphylococcus* (8%), *Enterobacteriaceae* (7.5%) and *Leucobacter* (6.9%). At least 7 out 20 (35%) genera that were present in pupa did not rise in the adult, likely being cleaned up by the sterilization process during the metamorphosis. *Finegoldia, Serretia* and *Pantoea* seem to be newly established in the adult. Bloodmeal reduces the diversity of gut microbiota. After blood feeding, 6 out 17 (35.3%) genera disappeared. *Elizabethkingia* and *Enterobacteriaceae* dominate the community, accounting for up to 77% of the total tags. The diversity of gut communities reduced with operational taxonomic unit (OUT) dropping from 110 to 36. Richness of the communities was estimated by ACE and Chao implemented by the software Mothur. By picturing gut communities we have gone one step further towards a better understanding the mosquito gut ecosystem.

1297

SYMPATRIC *PLASMODIUM FALCIPARUM - ANOPHELES GAMBIAE* POPULATIONS PRODUCE LOWER INFECTION INTENSITIES IN AFRICA

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Both *Plasmodium falciparum* and *Anopheles gambiae* show great diversity in Africa, in their own genetic makeup and malaria infection phenotypes. The genetics of the individual mosquito and parasite are known to play a role in determining the outcome of infection, but whether differences in infection phenotype vary between populations remains to be investigated. Here we conducted experimental infections using two recently established *An. gambiae* colonies from Cameroon and Burkina Faso and wild *P. falciparum* corresponding to their sympatric and allopatric populations. Infection phenotype was determined in terms of oocyst prevalence and intensity for at least nine infections for each vector-parasite combination and compared between infection types. We show that the mosquito colony used (sympatric or allopatric to the parasite) has no significant effect on infection prevalence, however has strong effects on infection intensity. Sympatric infections produced 25% fewer oocysts per midgut than allopatric infections, while prevalence was not affected by sympatric/allopatric interactions. The reduction in oocyst numbers in sympatric couples may benefit both the vector and parasite. It has been proposed that increasing the number of parasites ingested by a mosquito reduces its survival. If this is the case then a lower infection intensity, without affecting prevalence, would increase the fitness of infected mosquitoes while at the same time increasing the parasites chance of being transmitted. If the fitness costs are confirmed, this suggests local adaptation of the vector to the parasite and parasite to the vector, which has strong implications for malaria transmission dynamics.

1298

THE EVOLUTIONARY CONSEQUENCES OF HOST SPECIES CHOICE FOR AFRICAN MALARIA VECTORS: COULD UNTREATED BED NETS SELECT FOR A HOST SHIFT?

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The host preference of malaria vectors is one of the key determinants of global transmission patterns. Here we conducted an experimental investigation of the major African malaria vectors Anopheles gambiae s.s and An. arabiensis to test whether their preference for humans over other commonly available animal hosts can be explained by the fitness benefits they derive from them, and whether the use of common interventions such as bednets can reduce the advantage of anthrophily to the point where selection for a host species shift could be generated. Experiments were conducted in which one host of either cow, human (exposed or protected by untreated net), dog, goat or chicken was placed inside an experimental hut set within a unique Semi-Field System (SFS) at Ifakara Health Institute in Tanzania. Groups of 200 insectary-reared An. gambiae s.s or An. arabiensis were released into the chamber at dusk and left overnight with the host. The next morning mosquitoes were recaptured and their blood feeding success and subsequent fecundity and survival measured (6 replicates of each host and vector species combination).

Whereas Anopheles arabiensis had a significantly greater feeding success on its naturally preferred bovid hosts, the more anthrophilic An. gambiae s.s. took considerably bigger blood meals and had greater survival after feeding on human than animal blood. The use of a bednet failed to completely prevent biting by either vector, but did reduce the expected fitness benefits from human hosts. By modeling the combined effect of all host species impacts on vector fitness, a mosquito life-history model predicted the lifetime egg production of An. arabiensis to be considerably higher on their naturally preferred bovids than all other host types. However, the lifetime reproductive success of the naturally anthrophilic An. gambiae s.s. was not predicted to be higher on humans than any other host species. Further study is required to identify the nature of selection favouring anthrophily in this vector, and possibilities for reducing it through vector control and/or environmental management.

1299

QUANTIFYING AND ANALYZING DANCE OF *ANOPHELES GAMBIAE* IN MATING SWARMS

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We describe a technological breakthrough achieved through interdisciplinary collaboration that allows us to track individual swarming *Anopheles gambiae* males and females from stereoscopic video footage obtained from the field in Mali, Africa in August 2009. Mating behaviors of malaria vectors in nature are rarely described or studied, and even more rarely quantified. The actual movement of individual members of a mating swarm of mosquitoes over time has never before been measured. The principal reason this stage of the life history remains unexplored is that direct observation and quantification of mating in a swarm is very difficult due to the small size of mosquitoes, their relatively fast rate of movement and their habit of aggregating under conditions of low light. Despite our lack of knowledge in this area, determinants of male mating success in

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