**Results**

MRR estimates the length of time a mosquito remains alive and is still in the area available for recapture, meaning that estimates of lifespan using this data are likely biased downwards. In dissections of females, the majority of ovarioles have fewer dilations than the number of gonotrophic cycles an individual has experienced, also meaning that estimates derived from these data likely understand true physiological age (Hugo et al., 2008). It is unclear which of these methods leads to lower estimates but in both cases we term our estimates lower bounds on lifespan, which we shall refer to as LBL.

**Lifespan estimates from MRR**

*Variation in LBL across MRR studies*

To begin, we estimated LBL independently for each of the 230 available MRR time-series (Figure 1; Methods). The estimates varied substantially both within and among species, though a majority were less than ten days (187 of 230 time-series estimates, based on posterior mean). In comparison, mosquito longevity in laboratory conditions is typically found to exceed 30 days (e.g. - SEVERAL REFS POINTING TO ESTIMATE AND SPECIES). Overall the MRR estimates ranged from 1.1 days from a study of *Anopheles* *subpictus s.l.*  (an Asian malaria vector) to 26.9 days from a study of the temperate species *Aedes simpsoni s.l.* (an African yellow fever vector). It is likely that the very short longevity estimates (three days or less) reflect dispersalout of the recapture zone or a violation of the assumptions of our analyses, and we thus advise caution in their interpretation (see Discussion). There are multiple data sets for the most important vector species such as *Anopheles gambiae s.l.* (malaria)*, Aedes aegypti* and *albopictus* (yellow fever, dengue and zika viruses) and *Culex tarsalis* (West Nile Fever, Western Encephalitis) all of which show considerable variation. For example, there are 54 estimates of LBL for *Ae. aegypti* which range from 2.5 days to 42.1 days with a mean of 11.4 days and coeﬃcient of variation of 0.6 (all estimates are posterior means). To help make sense of the variation both within and among species, we next consider the following four potentially confounding factors: (i) mosquito sex, (ii) whether or not the mosquitoes are fed before release, (iii) the spatial extent of the recapture zone, and (iv) the average temperature during the MRR study.

*Mosquito sex*

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*Feeding before release*

The MRR data includes information on whether mosquitoes were pre-fed with sugar (41 time series), blood (71), both (4) or alternatively unfed (116), and we pooled the female-specific time-series into these 3/4 [BEN – SEE PREVIOUS COMMENT] categories to investigate his factor. We did not find any significant effects of female pre-feeding (fig. S4). There were insuﬃcient studies including males that were both fed and unfed with sugar prior to release to make a meaningful comparison.

*The spatial extent of the recapture zone*

Following a release of marked mosquitoes, the rate of their recapture typically reduces in time because some mosquitoes die, and also because some disperse out of the recapture area. These factors are indistinguishable in recapture data which is why our estimates are lower bounds on lifespan. If dispersal out of the recapture area commonly reduces the LBL below the true lifespan then we should expect a positive correlation between the spatial extent of the recapture zone and LBL. We found no such pattern (Fig. S2), although there was a positive correlation between LBL and trap density (Fig. S3).

*Ambient temperature*

affects

*Species and genus-specific variation in LBL*

We computed species (or species complex) and genus specific estimates to subsume the variation within these taxonomic groupings. To ensure fair comparison, we used only female MRR time-series where the females were not blood or sugar fed before release (Figure 2). These criteria precluded only a minority of the available data (xx of yy time-series). There were also differences in longevity at the genera level, with *Culex* estimated to have the shortest longevity (2.9 days) and *Aedes* the longest (8.1 days). *Anopheles* were estimated to live on average 6.8 days while the average across all the available data covering the three genera was 6.0 days. The diﬀerences between genera were significant (ANOVA on median LBL controlling for sex and pre-release feeding: F2,229 = 12.4, *p* <0.01; Kruskal Wallace: *, p <* 0*.*01). *K* -fold cross validation suggests that after the eﬀect of genus is accounted for the incorporation of a species term provides little predictive power (Fig. S1; in part explained by the latter model over-fitting the data where there are few time series per species).

**Number of gonotrophic cycles estimates from dissection**

Dissection allows the number of completed gonotrophic cycles to be counted and from this the mean number of cycles before death was estimated. Across the 131 studies, 95% of the individual time series estimates were less than 3 gonotrophic cycles (Fig. S7) and, overall, the mean number of cycles completed in a lifetime was 1.3 (posterior mean; Fig. 4; Table S2). The estimated greatest number of cycles was for *Anopheles sergentii* (3.0 cycles; posterior mean) which is adapted to desert conditions (it is known as the “oasis vector” of malaria) and may have evolved greater longevity. The important African malaria vector *A. gambiae* *s.l.* was estimated to be the second longest living (2.4 cycles; posterior mean).The smallest estimated mean number of gonotrophic cycles was for *Anopheles* *bellator* (0.6 cycles; posterior mean) which transmits malaria in Brazil’s AtlanticForest. There were significant diﬀerences in estimated lifetime gonotrophic cycles amongst species (ANOVA: F24,106 =2.2, *p* <0.01; the non-parametric Kruskal-Wallace: , *p*<0.01).

The estimated lifetime gonotrophic cycles for the diﬀerent genera were *Anopheles,* 1.6; *Culex,* 1.2; *Mansonia*, 1.1; and *Aedes* 0.8 (Fig. 4; Table S2) and the diﬀerences between the genera were significant (ANOVA: F3,127 =3.4, *p* =0.02; the non-parametric Kruskal Wallace: , *p*<0.01).

**Comparison of longevity estimates from two methods**

Using the data collected from a literature search, we estimated that the first gonotrophic cycle duration had a mean of 4.3 days (std. error: 0.4 days) and, for subsequent cycles, the mean was 3.9 days (std. error: 0.4 days; see SOM). To compare the two methods, we converted numbers of gonotrophic cycles (physiological age) into lifespan (chronological age) as described in the SOM using these estimates of gonotrophic cycle duration. Table S3 provides posterior summaries of chronological for the species and genera in the dissection dataset (see also Fig. S10). For ten species, we had enough data from both species to make a comparison, and there was a positive correlation (not statistically significant; Pearson correlation *ρ* = 0*.*42, *n* = 10, *p* = 0*.*23) between the two measures (Fig. 5), and in only one case – for *A. darlingi* - there was a significant diﬀerence in the time-series level LBLs (Table S4).

**Evidence for age-dependent mortality**

The survival model upon which the above analyses are based is the single-parameter exponential model which assumes an age-invariant mortality hazard. We also fitted five multi-parameter models that allow, in diﬀerent ways, mortality to vary with age. We did this to maximise our chance of detecting age-varying mortality (though aware of the risks of false positives with multiple estimations).

In Fig. 6, we compare the performance of the six models for describing lifespan in MRR studies of 33 species using K-fold cross-validation. We categorised the evidence for age-dependent mortality in each species according to the performance of the five age-dependent models versus the exponential: ‘+’ indicated that all age-dependent models outperformed the exponential; ‘?’ indicated that the exponential outperformed one or more age-dependent models; and ‘-’ indicated that the exponential performed at least as well as all other models. Overall, we estimated that there were 8 ‘+’ species, where age-dependent mortality fit the data better; 11 ‘?’ species where the evidence was mixed; and 14 species where constant mortality models performed at least as well. The species where age-dependent mortality best fit the data included *Ae. Aegypti*, the main vector of dengue fever, Zika and chikungunya. These studies also tended to include multiple release MRR studies which, on average, were conducted over a longer period of time than the others, which may be why we failed to detect age-dependence in the latter (Fig S11).

In Fig. 7, we compare the performance of the six models for describing lifespan in dissection studies of 25 species using K-fold cross-validation, and categorise the evidence in the same way as for the MRR analysis. By our metric, we determined that there were only two species with evidence for age-dependent mortality (*A. gambiae s.l.* and *A. minimus*).

Overall, we conclude that there is mixed evidence for age-dependent mortality from studies of mosquitoes in the field. It is possible that some of the mosquito species do not live long enough in the wild to experience physiological decline. A Spearman’s rank correlation test indicated that there was a correlation between the ranked estimated LBLs of the species and the ranked mean predictive accuracy of age-dependent models for the MRR analysis (*ρ*=0.19, p=0.01), however was not significant for the dissection analysis (*ρ*=0.07, p=0.43). Similarly, a recent study determined that the degree of senescence varies according to season for semi-wild populations of *Ae. aegypti* (Hugo et al., 2014), and it is possible that by pooling data from diﬀerent geographies and seasons that we failed to detect age-dependent mortality in some cases.

**Estimates of the fraction mosquitoes capable of transmitting disease**

We can use the posterior parameter estimates from our Bayesian analysis to estimate the fraction of mosquitoes that live beyond a certain age. In order to transmit a disease, a mosquito must live longer than the length of the intrinsic incubation period (the time taken for a pathogen ingested in one blood meal to be ready to be transmitted during a future feeding event). This is a lower bound as it does not include the waiting time to find a host after feeding or egg maturation. In Fig. 8, we plot the fraction of the mosquito population that pass this threshold using estimates from both MRR and dissection studies for vector species (see SOM for references used to identify species as vectors) and their most significant diseases.

For malaria, estimates of the minimum fraction of the population that can transmit the disease vary from <0.1% for *A. subpictus* (posterior median; from the MRR analysis, as noted above likely to be due to the LBL substantially underestimating lifespan) to 52% (posterior median) for the drought-adapted and long-lived *A sergentii.* The proportions surviving long enough to become infectious for *A. gambiae s.l.*: 10% (MRR) and 27% (dissection); and for *A.* *funestus s.l.*: 9% (MRR). Using the individual time series estimates, thereevidence for a diﬀerence in EIP between the species (Kruskal-Wallis used due to non-normality of data; MRR: , *p* <0.01; dissection: = 38*.*9, p<0.01).

*Ae. aegypti* and *Ae. albopictus* are the main vectors of dengue, chikungunyaand Zika viruses. Because of their short intrinsic incubation periods a greater fraction of mosquito potentially live long enough to transmit diseases (Fig. 8), rising to a maximum of 84% for *Ae. albopictus* transmitting chikungunya.