

RESEARCH ARTICLE

Phenotypic variation in populations of the mosquito vector, *Aedes aegypti*, and implications for predicting the effects of temperature and climate change on dengue transmission

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Abstract

There is concern that increases in temperature due to climate change could lead to shifts in the transmission dynamics and distribution of mosquito vectors. Many current models assume there are ‘average’ thermal performance curves for a given vector species’ life-history traits. However, this ‘one-size-fits-all’ assumption ignores the potential for standing phenotypic variation in life-history traits to create population-specific differences in thermal performance. In this study, we explored thermal performance of five independent field populations of *Ae. aegypti* from Mexico, together with a standard laboratory strain. We reared these six populations at temperatures between 13°C– 37°C to generate thermal performance curves for a suite of life-history traits. Composite models integrating these traits revealed the effects of temperature on population growth rates and dengue virus transmission potential. The results provide strong evidence for the potential for local adaptation in *Ae. aegypti* populations, challenging the applicability of ‘one-size-fits-all’ thermal performance models to assess climate impact on mosquito-borne diseases.

Author summary

How climate affects the dynamics and distribution of mosquito-borne diseases is of considerable public health relevance, especially in a warming climate. Models often assume the relationship between temperature and transmission is fixed for

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mosquito species and can be extrapolated over time and space. We challenge this assumption with evidence for standing variation in populations of *Aedes* mosquitoes, the primary vectors of dengue, Zika, and chikungunya viruses. We show variation in thermal sensitivity of life-history traits for five field populations of mosquitoes and one laboratory-adapted population across 11 temperatures. We then use mechanistic models which integrate these life-history traits to understand the potential for differences in fitness and transmission for mosquito populations. Such effects will increase variation in the expected impact of climate and challenge the utility of 'one-size-fits-all' models to predict the effects of climate change on vector-borne disease transmission.

Introduction

Dengue is the most widespread vector-borne disease of humans, with more than 3.9 billion people estimated to be at risk in over 128 countries [1]. Dengue virus is transmitted by mosquitoes, with *Aedes aegypti* as the principal vector [2]. Transmission of dengue virus is strongly influenced by temperature, humidity, rainfall along with other climate factors [2–5] and as such, there is substantial interest in the extent to which transmission will be affected by climate change [6]. Numerous studies suggest a likely net increase in the overall size of the population at risk of dengue and other arboviruses in the coming decades [7–14].

The climate-sensitivity of mosquito-borne diseases derives from the fact that many mosquito and pathogen life-history traits are strongly affected by temperature. Traits of many ectotherms are temperature-dependent, often exhibiting nonlinear thermal performance curves [15–17]. For mosquitoes and their pathogens, these traits include both fitness traits, such as larval survival, development rate, adult survival, fecundity, vector competence, and pathogen development rate, as well as behavioral traits such as biting rate, mating and foraging behaviors [18–29]. Additionally, these traits show variation between individuals depending on nutritional status, body size, and genetics [30–33].

Thermal performance curves provide a framework to assess how environmental temperature affects biochemical and physiological processes. In order to understand how changes in vital rates impact transmission, it is necessary to integrate individual traits into temperature-dependent fitness metrics such as the Basic Reproduction Rate (R_0 , defined as the number of secondary cases resulting from an initial primary case introduced into a population of susceptible hosts), or vectorial capacity (a measure of the transmission potential of a mosquito population defined as the number of potentially infectious bites that would eventually arise from all the mosquitoes biting an infectious host on a single day). These temperature-dependent transmission metrics have been used extensively to investigate variation in the relative environmental suitability for transmission over time and space [7–11, 19, 27, 34–41].

Common to nearly all mechanistic models that follow the thermal performance- R_0 approach, is the assumption that thermal performance curves are fixed for a given

mosquito species and associated pathogen. However, this assumption ignores the potential for the environment to impact thermal performance curves at the local population level [42]. Local adaptation can occur when there is spatial variation in selection due to interactions with the environment leading to a relative increase in fitness at a local level [42]. The evidence for local thermal adaptation in insects is mixed. Some studies indicate the potential for populations to shift thermal performance curves through evolutionary or plastic responses [43–48], while others suggest limited adaptation in response to variation in climate [49–52]. Additionally, it is observed in insects that there is greater potential for local adaptation at cold temperatures, though observed non-lethal adaptation to warmer temperatures is possible [53–55]. In general, it is expected that short generation times and high intrinsic population growth rates, both of which are true for mosquito vectors, should increase the probability of adaptation to changing conditions [56,57]. Local adaptation in mosquitoes to other environmental drivers, such as insecticide exposure, humidity, or daylength, support this suggestion [57–63].

Common garden experiments, in which populations collected from distinct geographic locations are examined together under shared conditions, have been used to compare thermal performance of different insect populations collected across environmental gradients and isolate differences between populations due to genetic variation [31,64–68]. Common garden experiments are designed to study the adaptive genetic variation among populations when stripped of environmental influence [67,69,70]. The rationale behind the experimental design is to understand the difference in the genetic basis of complex traits by reducing effects of genotype-by-environment interactions along with phenotypic plasticity (*Text A in S1 Appendix*) and as such are often used to test for signals of local adaptation [71–73]. Recently, we followed this approach to demonstrate differences in thermal tolerance (measured as knockdown rate in response to exposure to stressful high temperature) between five field-derived populations of *Ae. aegypti* from different locations in Mexico, together with a longstanding lab colony [47]. These results were strongly suggestive of local adaptation, but knockdown rate does not describe overall fitness, nor enable us to explore possible implications for transmission. The aim of the current study, therefore, is to extend research in this system to characterize thermal performance of a suite of life-history traits and determine whether there are between-population differences in thermal dependence of mosquito fitness and dengue transmission potential. We find strong evidence for genetic differences and local adaptation, challenging the utility of ‘one-size-fits-all’ thermal performance models to capture the spatial or temporal influence of temperature and temperature change on transmission risk.

Materials and methods

Ethics statement

All experiments were conducted under Penn State IBC protocol # 48219. Mosquito populations were imported under CDC import permit # 2018-03-181.

Mosquito Collection

Aedes aegypti mosquitoes were collected from the field in five different locations in Mexico (Cabo San Lucas, Acapulco, Monterrey, Ciudad Juárez, and Jojutla) using ovitraps. Populations from Mexico were founded with at least 100 females and to decrease the influence of causal maternal effects [74,75], mosquitoes were reared in the lab for at least one generation in standard laboratory conditions (27°C, 80% humidity, 12:12hr photoperiod) prior to experimentation. Two populations, Jojutla and Ciudad Juárez, were reared for an additional generation to ensure a large enough population for subsequent experiments. The field locations were chosen to capture a gradient of the climate and landscape (see Table A in *S1 Appendix*). The field populations were compared to a laboratory population (Rockefeller strain) that were maintained at Penn State University under standard insectary conditions (as described above) over many years [76].

Experiments to generate temperature-dependent data

Mosquito life-history traits including egg-to-adult survival, mosquito development rate (or the inverse of time to adult stage), mean adult survival, fecundity, and biting rate were measured in mosquitoes reared at 13°C, 15°C, 19°C, 23°C, 25°C, 27°C, 29°C, 31°C, 33°C, 35°C, 37°C, each $\pm 0.2^\circ\text{C}$ and $80 \pm 10\%$ relative humidity in environmentally controlled incubators with conditions monitored by data loggers [77]. These life-history measurements were replicated three times at each temperature for each population. We began with eggs from the five field populations and one laboratory line that were hatched at 27°C for 24 hours. Then, 200 first instar larvae were put into 1.89 L containers with 1 L of deionized water and 0.20 mg of larvae bovine liver powder (MP Biomedicals) and each of the three replicates were placed in the incubator at their respective temperatures. We fed larvae 0.20 mg of liver powder per larvae every other day until pupation, but once pupation began we scaled their food to the remaining number of larvae. Pupae, both living and dead, were removed and counted on the day of pupation and placed in a small cup (30 mL) with water from their original environment to allow for eclosion. Pupae were then added to a small cage (17.5 cm³) with continuous access to 10% sugar solution (dextrose anhydrous and deionized water). We counted the number of adults that eclosed every day. We measured mosquito development rate and egg-to adult survival for 200 individuals for every replicate at each temperature for each population. After 95% of surviving females emerged, we blood-fed females after 3–5 days using an artificial feeder (Hemotek). We used blood from de-identified human donors (BioIVT, Corp.) and so Institutional Review Boards approval and human subjects' approval was not needed. We immediately counted the total number of blood-fed females and placed up to 10 individual females into separate containers (50 mL polypropylene centrifuge tubes) that were lined with filter paper and 7 mL deionized water to measure individual fecundity. We also placed up to 20 females into two small cages (10 in each) with a small filter paper for egg laying and to monitor adult survival (measuring fecundity for up to 30 females). We recorded the day that females in individual containers first laid eggs, which we used for fecundity measures and to approximate the biting rate (1/gonotrophic cycle length), after which we removed them from their containers and placed them into the group cages (Fig A in S1 Appendix). We extracted the water from the containers to let the filter paper dry in their respective incubators and then we counted the number of eggs from individual mosquitoes. For the course of the experiment, we offered each cage a blood meal every 4 days and counted the number of adults (both male and female) that died every day (up to 200 individuals per replicate per treatment). All treatment groups were provided equal access to blood meals and mating opportunities, ensuring that any behavioral differences influencing longevity were inherently accounted for. We censored this experiment 4 weeks after the first egg lay at each temperature. Methods used in the current study closely follow those outlined in Dennington et al. 2024 [47].

Models of thermal performance curves

To analyze the thermal performance curve data we used a Bayesian approach following methods described in Johnson et al. (2015). In some cases, we fit multiple thermal response functions to each trait including quadratic, Brière, Poisson and binomial distributions, depending on what was appropriate given the data [36]. We fit a symmetric thermal response function to our data for fecundity (number of eggs per female for the first gonotrophic cycle) and egg-to-adult survival using a quadratic equation:

$$f(T) = \begin{cases} -c (T - T_0) (T - T_m) & \text{if } T_0 \leq T \leq T_m \\ 0 & \text{otherwise} \end{cases}$$

Mosquito development rate and biting rate were described by a Brière function:

$$f(T) = \begin{cases} -cT (T - T_0) (\sqrt{T_m - T}) & \text{if } T_0 \leq T \leq T_m \\ 0 & \text{otherwise} \end{cases}$$

where T_0 is the thermal minimum (below which the function is zero), T_m is the thermal maximum, and c is a positive constant that controls the curvature of the function (and thus the height of the curve for a given value of T_0 and T_m). Blood feeding rate was approximated as the reciprocal of the duration of the first gonotrophic cycle, a standard assumption used in many studies [10,78–80].

We assume that observed values for fecundity, mosquito development rate, and biting rate must be non-negative, and are thus modeled with a truncated normal likelihood:

$$F \sim TN(\mu = f(T), \sigma^2, 0, \infty)$$

We chose priors for T_0 and T_m to restrict each trait to its biologically realistic range, assuming temperatures below 0°C and above 45°C were fatal as previously measured [10,11,36,37]. For other parameters we chose relatively uninformative priors (Text B in S1 Appendix).

In contrast to fecundity, biting rate, and development rate, egg-to-adult survival is a probability and must be constrained to lie between 0 and 1. Thus, we modeled these data as being binomially distributed:

$$Y_i \sim \text{Bin}(p = f(T_i), n_i)$$

where n is the number of total observations of which Y were successes (i.e., survival to become adults) and the probability of a success at a particular temp, p , depends on temperature ($f(T)$), specifically being a piecewise quadratic, as above, but being constrained to be less than or equal than 1.

We also measured survival times (life spans) for adult mosquitos by counting the number of mosquitoes that died each day. Time to death for adult mosquitoes in each treatment were observed until a censoring time T_{cut} ; i.e., for each temperature, survival observations were censored 28 days after the first egg lay. Thus, at each temperature for each population most mosquitoes were observed until they died, but a portion of them were still alive at the end of the 28 days, and so the survival times were right-censored. We used a variation of a Bayesian Weibull survival model. We assume that the observed lifetimes, y_i , at some particular temperature are drawn from a Weibull distribution with rate parameter β and shape parameter k , with pdf,

$$f(y; \beta, k) = \beta k (\beta y)^{k-1} e^{-(\beta y)^k},$$

and corresponding CDF notated as $F(y; \beta, k)$. The median, m , of the Weibull is defined as

$$m = \frac{(\ln 2)^{1/k}}{\beta}$$

which, can be rearranged to solve for β . For interpretability, we assume that the median lifetime decays exponentially with temperature across the experimental temperature range studied, that is,

$$\ln(m) = a - bT$$

so that the median thermal performance curve, $g(T)$, is

$$m = g(T) = \exp(a - bT)$$

where T is the temperature, and a and b are parameters to be estimated.

The likelihood for the survival data is comprised of two components, one describing the individuals that were observed to die within the study period ($\delta_i = 1$), and those who are censored (i.e., that survive the study period, $\delta_i = 0$). Thus, the likelihood is given by

$$\mathcal{L} = \prod_i^n [f(y_i; \beta, k)]^{\delta_i} [F(y_i = T_{cut}; \beta, k)]^{1-\delta_i},$$

where the rate parameter is defined in terms of the median thermal performance curve, $\beta = \frac{(\ln 2)^{1/k}}{g(T)}$.

We fit all models described above using Markov Chain Monte Carlo (MCMC) sampling that is implemented in JAGS, using the R package *R2jags* [81–83]. For each life-history trait or thermal response, we ran five MCMC chains with a 5,000-step burn-in and saved the subsequent 10,000 steps. We thinned the posterior samples by saving every eighth sample, for a total of 3125 posterior samples of parameters. We used these posterior samples to produce samples from the posterior distribution of each trait across temperature. We then summarize the relationship between temperature and each trait by calculating the mean and 95% highest posterior density interval (HPD interval) for the function across temperature. The HPD interval is a type of credible interval that includes the smallest continuous range containing 95% of the probability, which is implemented in the coda package [84].

Mosquito Fitness and Transmission Calculations

To characterize overall fitness, we used a temperature-dependent model for population growth $r(T_i)$ as previously described in Amaraesekare and Savage [85]:

$$r(T_i) = -\mu(T_i) + MDR(T_i)W\left(\frac{E(T_i)e^{\mu(T_i) - \frac{\mu_j(T_i)}{MDR(T_i)}}}{MDR(T_i)}\right) \quad (1)$$

Here MDR is mosquito development rate, E is eggs per female measured at the first gonotrophic cycle, μ is adult mortality rate and μ_j is juvenile mortality rate (Fig B and Table G in S1 Appendix). $W(x)$ is the upper branch of the Lambert function. We combined the thermal performance curves for each trait to calculate temperature-dependent fitness, $r(T_i)$, creating a unimodal curve. We followed Amaraesekare and Savage [85] and truncated the results at $r(T_i) = 0$ rather than allowing them to go to negative values.

We estimated the posterior distribution of $r(T_i)$ and used it to calculate the key temperature values for relative temperature dependent population fitness. We used the mean and 95% credible intervals (95% CI) for the critical thermal minimum, maximum and optimum temperatures for population fitness.

We used temperature-dependent models of transmission to investigate the potential implications for transmission of dengue virus, utilizing a previously published framework [10,11,36,37]. This approach models transmission rate as the basic reproduction rate R_0 , which is defined as the number of secondary infections originating from an initial infection when introduced to a completely susceptible population. The temperature dependent R_0 is given by:

$$R_0(T) = \left(\frac{a(T)^2 b(T) c(T) e^{-\frac{\mu(T)}{PDR(T)}} EFD(T) \rho_{EA}(T) MDR(T)}{N r \mu(T)^3} \right)^{1/2} \quad (2)$$

In this equation, (T) indicates that the trait is a function of temperature, a is the biting rate per mosquito, b is the proportion of infectious bites that infect susceptible humans, c is the proportion of bites on infected humans that infect uninfected mosquitoes ($b \times c$ = vector competence), μ is the adult mosquito mortality rate, PDR is the pathogen development rate (the

inverse of the extrinsic incubation period), EFD is the number of eggs a female produces each day, ρ_{EA} is the survival probability of mosquitoes from egg to adult, MDR is the mosquito development rate (the inverse of the egg-to-adult development time), N is the density of humans, and r is the human recovery rate.

To use this metric in this study, we have to make two approximations to connect the data and fits obtained from our empirical study to this expression. The first is in the adult mosquito mortality rate. In the original derivation of R_0 , it is assumed that mosquito lifetimes are exponentially distributed with rate parameter μ . Thus, under this assumption, the mean lifetime, λ , is $1/\mu$, and the median lifetime, (denoted at m above), would be equal to $\frac{\ln(2)}{\mu}$. Thus, everywhere in the R_0 equation we let $\mu = \frac{\ln(2)}{m}$. Similarly, we must approximate the mosquito development rate by taking the 1/ mosquito development time to get the rate of development.

In the current study we did not examine infected mosquitoes and so we used previously published thermal performance curves from Mordecai et al. (2017) for vector competence and pathogen development rate for dengue virus in *Ae. aegypti* [10]. Also, because we have no measures of human density or recovery rate we follow the approach of Mordecai et al. (2017) and normalize the R_0 curves to a scale of 0–1. This measure of Relative R_0 enables comparison of key features of thermal dependency including the critical minimum temperature (CTmin), the critical maximum temperature (CTmax), the optimum temperature (Topt) and the thermal breadth (Tbreadth), defined as the range where performance is above 80% optimal [55,86] but does not provide estimates of maximum performance (Pmax).

Testing for differences between populations

We used DIC (Deviance information criterion) to test for statistically significant differences between the thermal performance curves of different populations as previously described [87–89]. Specifically, for each trait, we compared the DIC of a global model fit to the data from all populations to the sum of DIC scores from the models fit separately to data from each population (equivalent to fitting a single model assuming all parameters may vary between populations). Populations were considered significantly different for a given trait if the sum of DIC scores from the separate models was ≥ 2 DIC units lower than the DIC score from the global model.

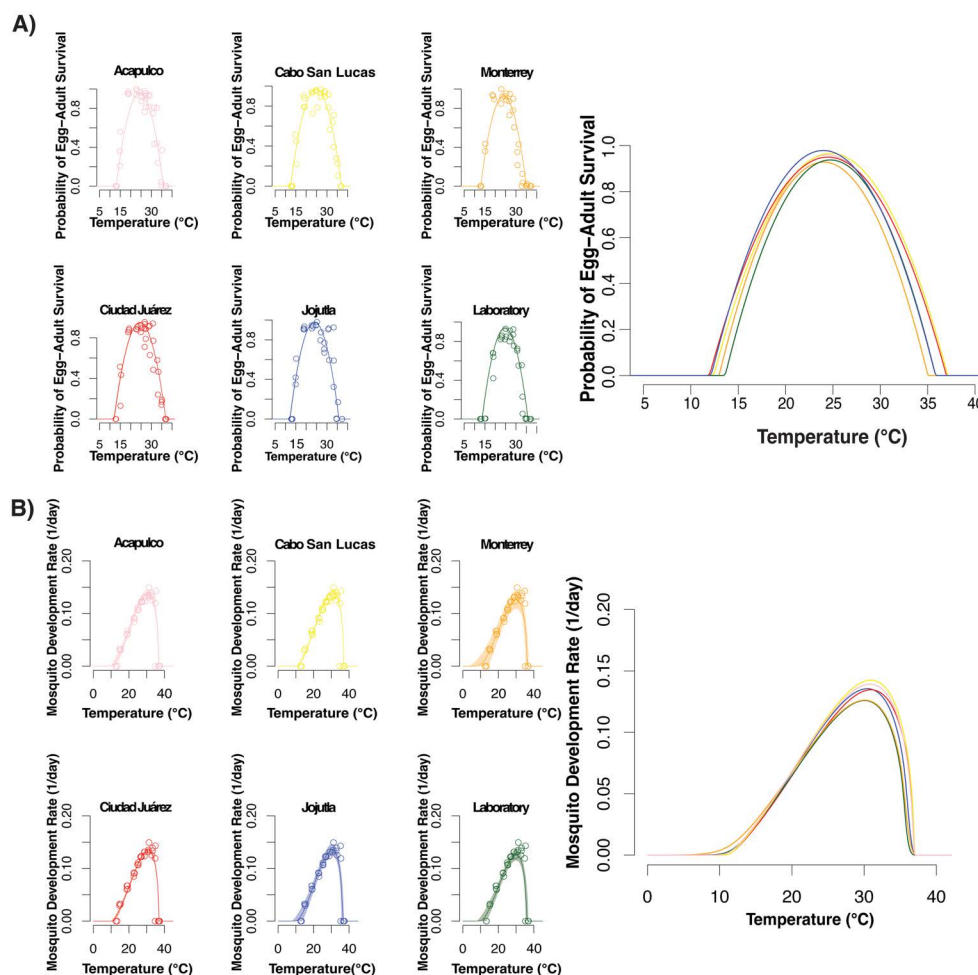
Results

The estimated thermal performance curves for egg-to-adult survival probability, mosquito development rate, fecundity, biting rate, and mean adult survival indicated by both the empirical data and the Bayesian model fits are presented in Fig 1A–E, with the key features of these curves (i.e., the thermal optimal temperature (Topt), the maximal performance (Pmax), the critical thermal minimum (CTmin), critical thermal maximum (CTmax) and thermal breadth (Tbreadth) summarized in Tables B–F in S1 Appendix.

The between-population differences in the thermal performance curves for the juvenile traits of egg-to-adult survival and development rate were relatively small, with 1°C or less for the differences between the respective CTmin, CTmax, Tbreadth values of the different populations, although still significant according to the Deviance Information Criterion (DIC) (Fig 1A and 1B and S2–S6 Tables in S1 Appendix). For the adult traits of fecundity, survival and biting rate, the differences were more marked. Specifically, for eggs per female, there was an approximate 2°C difference between the lowest (Monterrey population) and highest (Acapulco population) values for CTmin, and 3°C difference between lowest (Jojutla population) and highest (Monterrey population) values for CTmax and clear variance between populations (Fig 1C). For the biting rate approximation, there was an approximate 6.6°C difference between the lowest (Jojutla population) and highest (Monterrey population) values for CTmin, and 4.5°C difference between lowest (Monterrey population) and highest (Jojutla population) values for CTmax (Fig 1D). For adult survival, the data did not exhibit a clear unimodal pattern across the temperature range studied so it is not possible to define values for CTmin and CTmax (Fig 1E). Nonetheless, the thermal performance models indicate significant differences between populations according to the DIC criteria. For the field strains, the population from Ciudad Juárez survived the worst at lowest temperatures while the population from Cabo

San Lucas survived the best (highest median survival). Alternatively, the population from Cabo San Lucas survived the worst with the lowest median survival at high temperatures while the population from Monterrey survived the best with the highest median survival. Notably, the longstanding lab strain exhibited the most pronounced thermal response, with the highest survival at cool temperatures and the lowest survival at warm temperatures.

The combined effects of variation in individual traits are shown in the thermal performance curves for overall mosquito fitness, r_m (Fig 2). Significant differences in the DIC of the individual thermal performance curves translate to significant differences in overall fitness curves between populations. The key summary statistics for these models are given in Table H in S1 Appendix. The lowest CTmin was 17.8°C for the Monterrey population while the highest CTmin was 19.7°C for the Acapulco population. The lowest CTmax was 31.1°C for the Jojutla population while the highest CTmax was 34.2°C for Monterrey. The lowest Topt was 26.1°C for Monterrey and the highest Topt was 28.3°C for Juárez. The population from Monterrey had both the lowest CTmin and the highest CTmax, giving it the greatest thermal breadth of 8.4°C, while the smallest Tbreadth of 6.2°C was observed for Acapulco and Jojutla populations. There were also varying Pmax values (the fitness value at the optimum temperature) with the highest Pmax being 0.504 for Cabo and the lowest Pmax being 0.358 for Jojutla. Pearson's correlations revealed a positive correlation between fitness Pmax and Topt ($r=0.882$), as well



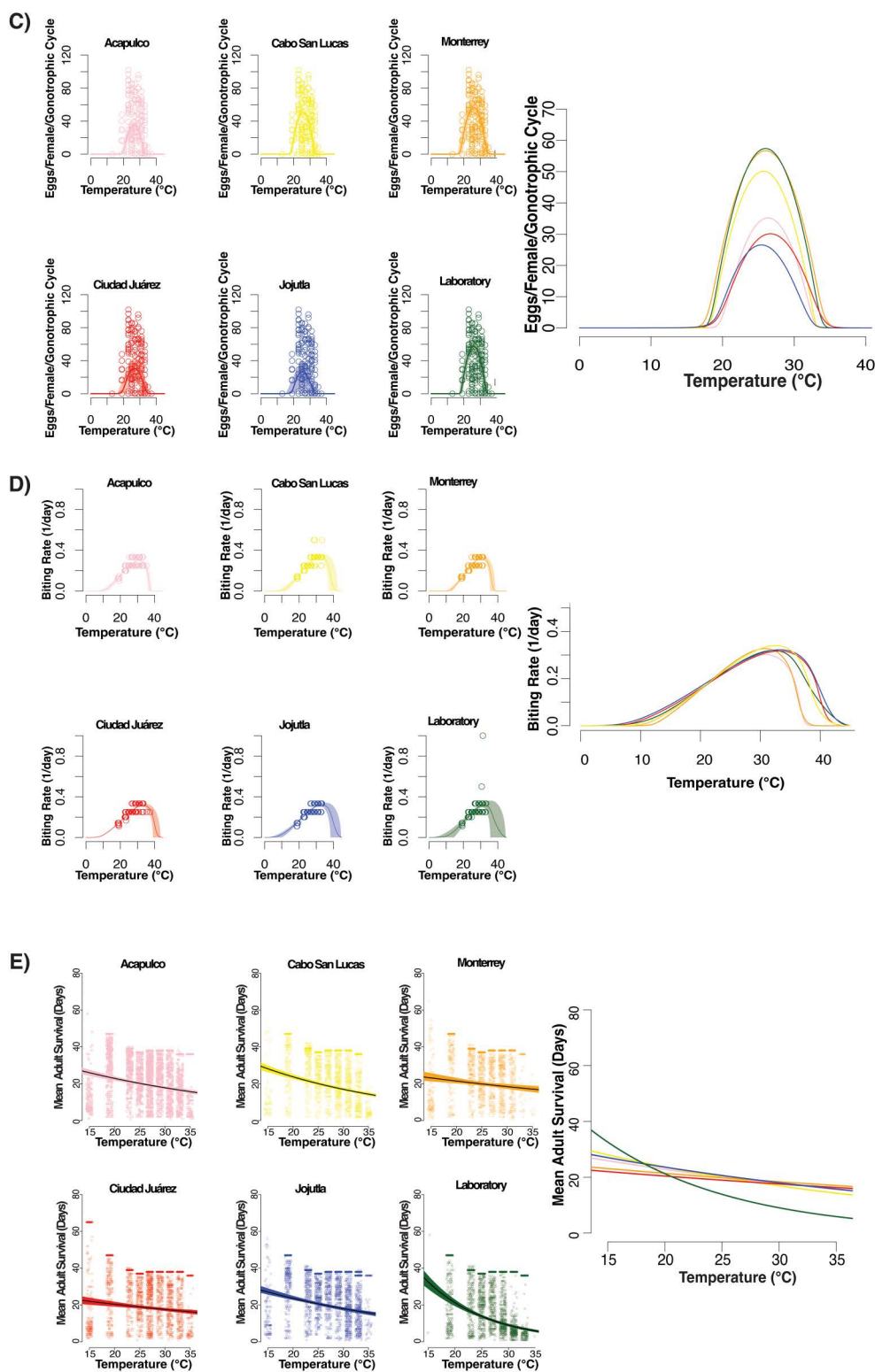


Fig 1. Life history traits measured for *Ae. aegypti* mosquitoes reared at 13°C, 15°C, 19°C, 23°C, 25°C, 27°C, 29°C, 31°C, 33°C, 35°C, 37°C. We measured life history traits for five populations from Mexico (Cabo San Lucas (yellow), Acapulco (pink), Monterrey (orange), Ciudad Juárez (red), and Jojutla (blue)) compared to a laboratory adapted line (shown in green). The data points for figures are the values from three replicates for each

corresponding population at each temperature with individual values for adult survival and fecundity along with mean values for each replicate for biting rate, mosquito development rate and egg-to-adult survival probability. Thermal performance curves for life-history traits for the six populations were fit using Bayesian inference with weakly informative priors are shown (Model values can be found in Tables B-F in [S1 Appendix](#)). Each mosquito line was tested between 13°C–37°C, but individuals did not survive and reproduce at 13°C and 37°C. **A)** Egg-to-adult survival measured as the probability of individuals surviving to the adult stage. **B)** Mosquito development rate is the inverse of the amount of time that it takes to reach the adult stage. **C)** Fecundity is measured as individual egg production for the first gonotrophic cycle. **D)** Model fits for approximated biting rate (1/gonotrophic cycle length). **E)** Model fits for estimated mean adult survival (in days) derived from measures of daily survival of adults over 28 days post initial blood meal, censored individuals are clustered at the last day tested.

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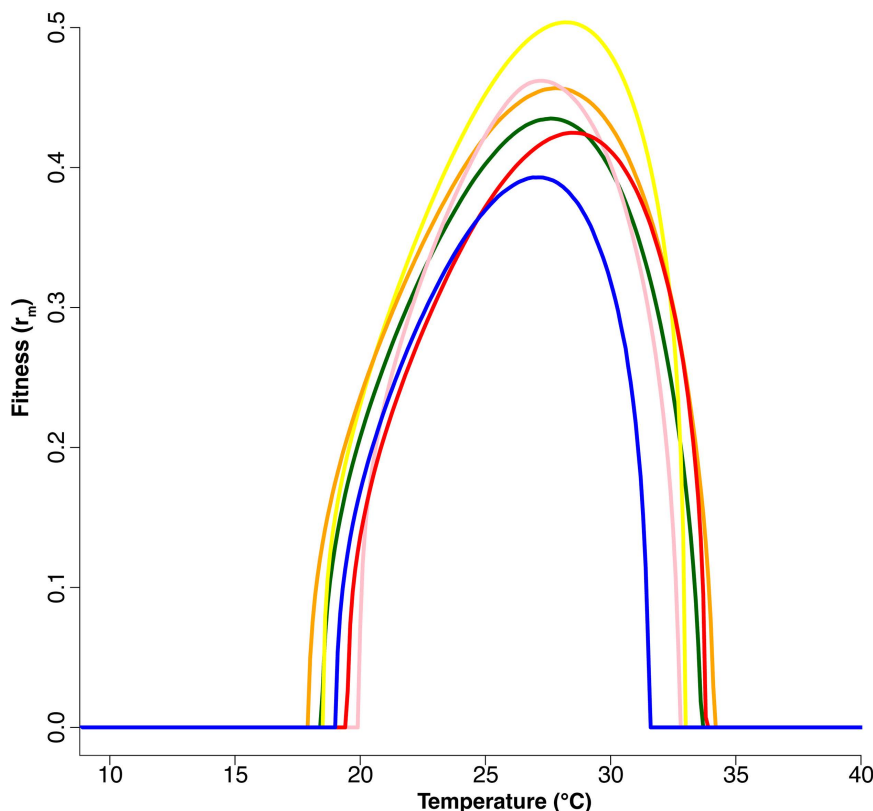


Fig 2. Temperature-dependent fitness (intrinsic rate of increase, r_m) derived from individual life-history traits measured for *Ae. aegypti* mosquitoes reared at 13°C, 15°C, 19°C, 23°C, 25°C, 27°C, 29°C, 31°C, 33°C, 35°C, 37°C. We measured life history traits for five populations from Mexico (Cabo San Lucas (yellow), Acapulco (pink), Monterrey (orange), Ciudad Juárez (red), and Jojutla (blue)) compared to a laboratory-adapted line (shown in green). The lines indicate mean model fits. Fits for individual populations that include the credible intervals and values are presented in Fig C and Table H in [S1 Appendix](#).

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as fitness P_{max} and $T_{breadth}$ ($r=0.861$) ([Fig 3](#)). Lastly, we used Pearson's correlation which indicated a strong positive correlation between fitness T_{opt} and the latitude of the home environment ($r=0.863$) ([Fig E](#) in [S1 Appendix](#)).

Finally, possible implications for transmission are presented in [Fig 4](#), which shows the thermal performance curves for dengue virus transmission potential for each population using relative R_0 as a comparative metric. The key summary statistics for these models are given in Table I in [S1 Appendix](#). We observe clear differences in the temperature sensitivity of transmission between individual populations. The lowest CT_{min} was 17.4°C for the Jojutla population and the highest CT_{min} was 20.2°C for the Acapulco population. The lowest CT_{max} was 32.8°C for Acapulco and the highest CT_{max} was

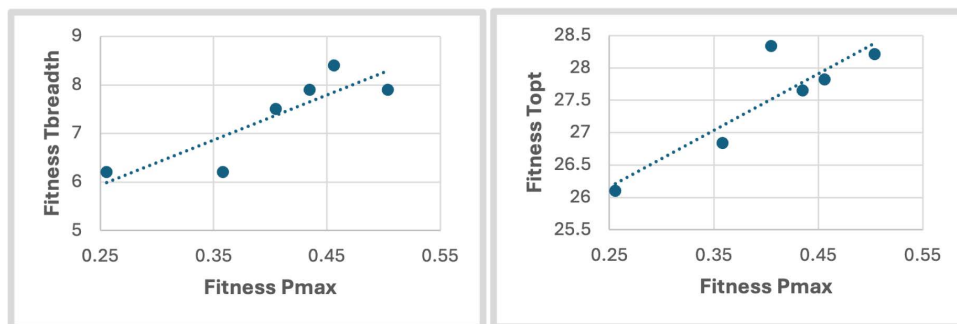


Fig 3. Summarized values for thermal performance curves for each population showing the relationship between (a) breadth of the curve (Tbreadth) and maximum performance (Pmax). Pearson's correlation indicates significant strong positive relationship between Pmax and Tbreadth ($r = 0.882$) and Pmax and Topt ($r = 0.861$).

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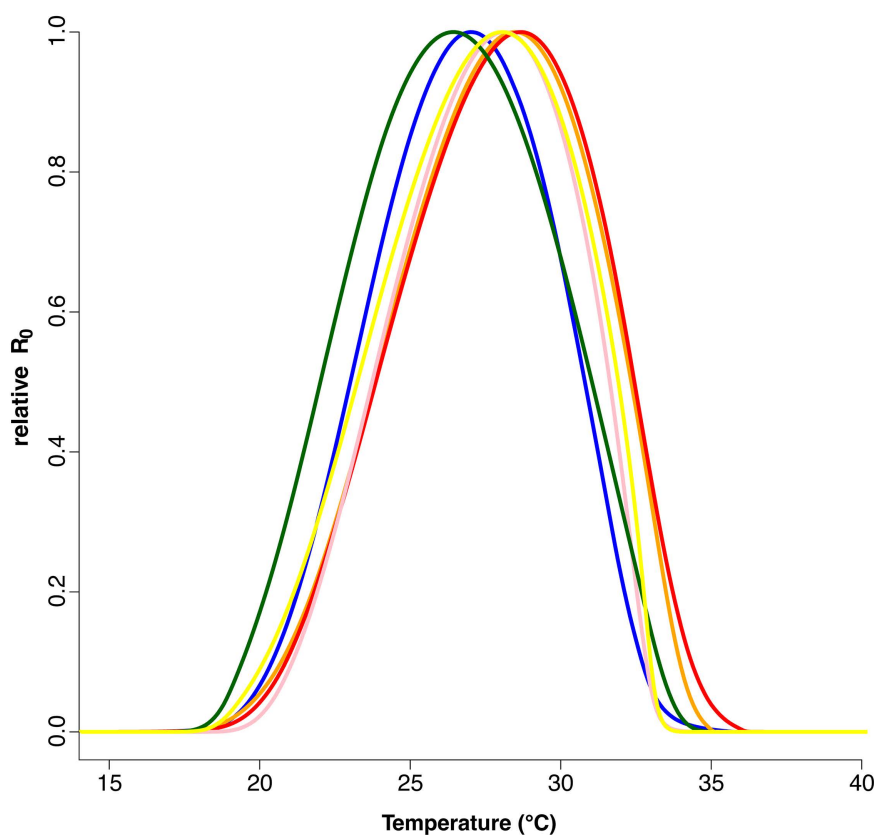


Fig 4. Temperature-dependent relative R_0 (transmission rate as the basic reproduction rate R_0) derived from individual life history traits measured for *Ae. aegypti* mosquitoes reared at 13°C, 15°C, 19°C, 23°C, 25°C, 27°C, 29°C, 31°C, 33°C, 35°C, 37°C. We measured mosquito life-history traits for five populations from Mexico (Cabo San Lucas (yellow), Acapulco (pink), Monterrey (orange), Ciudad Juárez (red), and Jojutla (blue)) compared to a laboratory-adapted line (shown in green). The lines indicate mean model fits. Fits for individual populations that include the credible intervals and model summary values are presented in Fig D and Table I in [S1 Appendix](#).

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33.7°C for Monterrey. The lowest T_{opt} was 26.1°C for the laboratory adapted population and the highest T_{opt} was 28.6°C for the population from Juárez.

Discussion

In this study, we used a common-garden laboratory experiment to examine the thermal performance of five field-derived populations of *Ae. aegypti*, together with a longstanding lab strain. This approach, that minimizes the impact of environmental variation, is designed to reveal phenotypic differences across populations due to genetic variation [67,69,70]. Specifically, we measured individual life-history traits and created composite metrics for both population fitness and dengue transmission potential. The results reveal significant between-population differences in several life-history traits leading to distinct thermal performance curves for fitness and transmission potential. These results have important implications for understanding the effects of temperature and climate change on the transmission of vector-borne disease.

Examination of individual life-history traits reveals a slightly mixed picture, with large between-population differences in thermal performance of certain traits (e.g., fecundity) but more conserved performance curves for others (e.g., mosquito development rate). Previous studies in a range of other taxa reveal differences in thermal performance curves among traits and life stages [90–94], indicating that thermal responses are not necessarily adapted predictably or uniformly across all traits [95,96]. These studies predicted that the rate of thermal adaptation in an arthropod population is constrained by changes in peak performance temperatures for key life-history traits [96].

Changes in the growth rate of populations are directed by shifts in thermal performance curves of individual traits, which are expected to shift more rapidly than overall fitness with selection because of more thermodynamic constraints [97–99]. To determine overall differences in thermal performance between populations, we therefore combine individual life-history traits into measures of population fitness. This is an important step as most studies do not characterize all traits necessary to estimate fitness [94]. In this study, these fitness models further reveal differences in thermal performance curves between populations (Figs 2 and C and Table H in S1 Appendix).

The physiological and evolutionary factors that shape variation in thermal performance curves have been the subject of much research and center around two main hypotheses. The ‘hotter-is-better’ hypothesis argues that because of thermodynamic constraints, the maximal performance of organisms with high optimal temperatures should be greater than that of organisms with low optimal temperatures and will tend to have greater thermal breadth [48,100–103]. The ‘jack-of-all-temperatures’ hypothesis argues that a trade-off should exist between maximal performance and breadth of performance because different factors of a thermal performance curve can evolve independently and the association between these factors would be shown through evolutionary trade-offs [104–108]. In our fitness curves, the positive correlation between maximum fitness (P_{max}) and optimum temperature (T_{opt}), as well as maximum fitness (P_{max}) and thermal performance breadth ($T_{breadth}$) (Fig 3) provide no signal of a generalist-specialist trade-off and are more consistent with the ‘hotter-is-better’ hypothesis.

The differences in thermal performance of the individual mosquito populations further lead to differences in temperature-dependent transmission potential of dengue virus (Fig 4). Interpreting these results in terms of absolute transmission risk is not possible as we did not measure infection traits empirically. Instead, we used previously published data for the thermal performance curves of vector competence and pathogen development rate that are not specific to our populations [10]. However, as with other traits, vector competence and pathogen development rate might differ between populations [109,110]. Further, estimating absolute R_0 requires estimates of the vector-host ratio and we do not have measures of human density in the different locations, nor can we predict absolute vector densities since these could vary due to a range of factors independent of temperature. Nonetheless, the estimates of relative R_0 enable us to draw several important insights concerning the possible effects of temperature and temperature change on dengue transmission potential with local adaptation of the mosquito vector.

First, transmission potential is expected to differ between populations at particular temperatures. For example, at 29°C the population from Ciudad Juárez is at its maximum transmission potential whereas the population from Jojutla is only at 60%. Conversely, at 25°C the lab and Jojutla populations are at their maximum, whereas Ciudad Juárez is only 60%. Further towards the thermal limits, at 20°C the transmission potential for Acapulco is close to zero yet relative R_0 for the lab population is 15%, while at 33°C both Cabo San Lucas and Acapulco are close to zero, yet Monterrey and Ciudad Juárez have relative R_0 values above 40%. While we did not directly measure vector competence traits, we indicate substantial effect sizes and clearly demonstrate that thermal dependence of transmission potential differs between populations and is not well represented by any of the single models. To illustrate this point further, the generic thermal performance curve for relative R_0 developed by Mordecai et al. (2017) using data from multiple published studies has a T_{opt} of 29.1°C (95% CI: 28.4–29.8°C), a CT_{min} of 17.8°C (95% CI: 14.6–21.2°C) and CT_{max} of 34.6°C (95% CI: 34.1–35.6°C) [10]. In our relative R_0 models we see the T_{opt} of the individual populations ranging from 26.1 (95% CI: 27.1–25.9°C) to 28.4°C (95% CI: 28.3–28.5°C), CT_{min} from 17.4 (95% CI: 16.6–23.0°C) to 20.2°C (95% CI: 23.1–18.7°C), and CT_{max} from 32.7 (95% CI: 31.3–33.7°C) – 36.1°C (95% CI: 28.6–36.9°C). As an additional observation, while our field populations differ from one another, the largest outlier is the long-standing lab strain. Accordingly, our results provide a possible cautionary note to the many studies that explore aspects of transmission of vector-borne diseases using data from lab strains alone. This result might be expected among long-standing lab strains as they are often maintained in constant conditions over many years.

Second, a common approach to explore the possible implications of climate warming is to track changes in transmission across the R_0 thermal performance curve [7,9–11,27,35–38]. With a single curve, a particular shift in temperature yields a predictable response. However, if thermal response curves differ between individual populations the responses to shifts in temperature will be more idiosyncratic. For example, a warming of 3°C from 26 to 29°C would suggest an increase in relative R_0 of around 10% for Monterrey but a decline of 30% for Jojutla. A shift from 29 to 32°C would cause a decline in transmission potential in all populations but for Ciudad Juárez the relative R_0 would still be at 25%, whereas transmission potential for Acapulco would be almost zero.

Third, the standard approach of applying thermal performance curves to predict future changes in transmission due to warming assumes that the thermal performance curves themselves remain static. However, the fact that we see variation in thermal performance between individual populations indicates thermal performance curves are not fixed. So, while short-term changes in temperature might shift transmission along existing thermal performance curves [42], adaptation could modify the thermal responses in the medium- to longer-term [47]. While absolute limits to adaptation will exist [49,111,112] ongoing adaptation to a changing environment could make responses to climate change more dynamic.

Previous research suggests genetic differentiation between discrete populations of *Ae. aegypti* in Mexico sampled across similar spatial scales to ours [113,114]. Despite using a common garden design, we cannot fully rule out the effects of environment on our phenotypic variation in thermal performance. Furthermore, because we examined a relatively small number of mosquito populations, we have limited power to correlate observed differences in thermal performance curves with specific features of the respective home environments. Hence, it is difficult to conclude that the patterns we observe are a result of adaptation to temperature alone. Research on populations of *Drosophila* species and the mosquito *Culex tarsalis* have demonstrated correlations between thermal performance and proxies of environmental temperature such as gradients in latitude or altitude [64,65]. Other research on the mosquito *Nyssorhynchus darlingi* indicates that variation in life history traits between populations results from both genetic differences among localities as well as plastic responses to differences in temperature [68].

Our results expose the difference in reaction norms, or the range of genetic expression in each trait, across experimental temperatures to understand phenotypic plasticity and adaptation [115]. It is likely, therefore, that the phenotypic differences we observe between populations are a consequence, at least in part, of adaptive responses to temperature. Further analysis indicate that fitness thermal optima are strongly correlated to the latitude of the home environment (Fig E in S1 Appendix). These results show that differences in thermal performance between populations are directionally linked to the

home environment, not due to random genetic drift or other external forces, but likely evidence of adaptation. Indeed, in previous research we used experimental passage to demonstrate that differences in thermal performance curves could be generated within 10 generations in response to differences in background temperature alone [47]. Whether the differences in this study are due to genetic adaptation, genetic variation in phenotypic plasticity, or a combination of both, does not alter the functional significance of our results. Future studies should integrate new age genomic techniques such as next-generation sequencing technology to understand the genetic differences between populations [67].

Overall, our study demonstrates between-population differences in thermal performance *Ae. aegypti* mosquitoes that influence the predicted effects of temperature on mosquito fitness and dengue transmission potential at the local level. These results add complexities for extrapolating single thermal performance models over space and time, since existing adaptation could result in idiosyncratic responses of individual populations, and future local adaptation could further shift thermal performance curves. Given the public health significance of the multitude of pathogens transmitted by *Aedes* and other mosquitoes (e.g., dengue, Zika, Chikungunya, Yellow Fever, malaria, West Nile, filariasis, Ross River virus) and interests in the influence of climate change, this research highlights the importance of better characterizing the thermal dependence of mosquitoes and their pathogens. More generally, the interacting effects of local adaption and climate change could extend to many systems, including other vector-borne diseases of humans (e.g., Chagas disease transmitted by triatomine bugs [116–118]), animals (e.g., Bluetongue virus transmitted by culicoid midges [119–122]) and plants (e.g., numerous viruses transmitted by Hemiptera [123,124]).

Supporting information

S1 Appendix. Text A. Quantitative genetics variance decomposition model. **Text B.** Expanded mathematical models supporting the methods. **Fig A. Lifespan fecundity.** Thermal responses for *Aedes aegypti* eggs per female per day for mosquitoes from Mexico compared to a laboratory line. Uninformative priors were used, and the models were fit to average fecundity for each replicate. We measured life history traits for five populations from Mexico (Cabo San Lucas (yellow), Acapulco (pink), Monterrey (orange), Ciudad Juárez (red), and Jojutla (blue)) compared to a laboratory adapted line (shown in green). Each line was tested between 13°C–37°C, but individuals could not survive and reproduce at 13°C and 37°C. **Fig B. Juvenile mortality rate thermal performance curve.** Thermal responses for *Aedes aegypti* juvenile mortality rate for mosquitoes from Mexico compared to a laboratory line. Uninformative priors were used, and the models were fit to raw data. We measured life history traits for five populations from Mexico (Cabo San Lucas (yellow), Acapulco (pink), Monterrey (orange), Ciudad Juárez (red), and Jojutla (blue)) compared to a laboratory adapted line (shown in green). Each line was tested between 13°C–37°C, but individuals could not survive and reproduce at 13°C and 37°C. **Fig C. Temperature-dependent fitness models.** Temperature-dependent fitness (intrinsic rate of increase, r_m) derived from individual life history traits measured for *Ae. aegypti* mosquitoes reared at 13°C, 15°C, 19°C, 23°C, 25°C, 27°C, 29°C, 31°C, 33°C, 35°C, 37°C. We measured life history traits for five populations from Mexico (Cabo San Lucas (yellow), Acapulco (pink), Monterrey (orange), Ciudad Juárez (red), and Jojutla (blue)) compared to a laboratory-adapted line (shown in green). The lines indicate mean model fits while the shaded area indicates the 95% credible intervals. **Fig D. Temperature-dependent relative R_0 models.** Temperature-dependent relative R_0 (transmission rate as the basic reproduction rate R_0) derived from individual life history traits measured for *Ae. aegypti* mosquitoes reared at 13°C, 15°C, 19°C, 23°C, 25°C, 27°C, 29°C, 31°C, 33°C, 35°C, 37°C. We measured mosquito life history traits for five populations from Mexico (Cabo San Lucas (yellow), Acapulco (pink), Monterrey (orange), Ciudad Juárez (red), and Jojutla (blue)) compared to a laboratory-adapted line (shown in green). The lines indicate mean model fits while the shaded area indicates 95% credible intervals. Table A. Information on locations for *Aedes aegypti* mosquito collection in Mexico. Data collected over multiple years in each city. Each mean represents the grand mean across multiple years. These populations were compared to a standard laboratory adapted line (Rockefeller strain) maintained at Penn State at standard insectary conditions. **Table B. Briere model output for mosquito development rate for *Aedes aegypti* from**

Mexico compared to a laboratory adapted line. Data for mosquito development rate for five populations of *Ae. aegypti* mosquitoes from Mexico compared to one laboratory adapted line were used to generate briere model. Mean and 95% credible interval (95% HPD interval) for the critical thermal minimum (T_o), maximum, (T_m), and a rate constant (c) are given for mosquito development rate. The Deviance Criterion Information (DIC) is given to compare model fits. We are comparing this model to one that fits all of the points together giving a DIC of -1069.219. **Table C. Quadratic model output for egg to adult survival for *Aedes aegypti* from Mexico compared to a laboratory adapted line.** Data for egg to adult survival on *Ae. aegypti* from 5 population from Mexico compared to one laboratory adapted line were used to generate quadratic model. Mean and 95% credible interval (95% HPD interval) for the critical thermal minimum (T_o), maximum, (T_m), and a rate constant (c) are given for egg-to-adult survival. The Deviance Information Criterion (DIC) is given to compare model fits. We are comparing this model to one that fits all of the points together giving a DIC of 6133. **Table D. Quadratic model output for eggs per female per gonotrophic cycle for *Aedes aegypti* from Mexico compared to a laboratory adapted line.** Data for eggs per female per day on *Ae. aegypti* mosquitoes selected over ten generations were used to generate quadratic model. Mean and 95% credible interval (95% HPD interval) for the critical thermal minimum (T_o), maximum, (T_m), and a rate constant (c) are given for fecundity. The Deviance Criterion Information (DIC) is given to compare model fits. We are comparing this model to one that fits all of the points together giving a DIC of 9027.19. **Table E. Weibull survival model output for adult survival.** Data for adult survival on *Ae. aegypti* mosquitoes from Mexico along with one laboratory population were used to generate a Bayesian Weibull survival model. Mean and 95% credible interval (95% HPD interval) for the observed lifetimes (y_i) at some particular temperature are drawn from a Weibull distribution with rate parameter (β) and shape parameter (k). The Deviance Information Criterion (DIC) is given to compare model fits. We are comparing this model to one that fits all of the points together giving a DIC of 104,189. **Table F. Briere model output for biting rate for *Aedes aegypti* from Mexico compared to a laboratory adapted line.** Data for eggs per female per day taken from groups of mosquitoes across their lifetime for five populations of *Ae. aegypti* mosquitoes from Mexico compared to one laboratory adapted line were used to generate quadratic model. Mean and 95% credible interval (95% HPD interval) for the critical thermal minimum (T_o), maximum, (T_m), and a rate constant (c) are given for eggs per female per day. The Deviance Criterion Information (DIC) is given to compare model fits. We are comparing this model to one that fits all of the points together giving a DIC of -3382.774. **Table G. Quadratic model output for juvenile development rate for *Aedes aegypti* from Mexico compared to a laboratory adapted line.** Data for juvenile mortality rate on *Ae. aegypti* mosquitoes from Mexico compared to a laboratory adapted line were used to generate quadratic model that is used in the fitness model. These data are from an approximation using larval survival rate and the amount of time to the adult stage. Mean and 95% credible interval (95% HPD interval) for the critical thermal minimum (T_o), maximum, (T_m), and a rate constant (c) are given for mosquito development rate. The Deviance Criterion Information (DIC) is given to compare model fits. We are comparing this model to one that fits all of the points together giving a DIC of -320.1. **Table H. Model output for temperature dependent fitness (r).** Data for mosquito temperature dependent population fitness on *Ae. aegypti* mosquitoes from Mexico along with one laboratory population were used to generate a composite model from mosquito development rate, eggs per female per gonotrophic cycle, adult survival, and juvenile mortality rate. Mean and 95% credible interval (95% HPD interval) for the critical thermal minimum (CTmin), maximum, (CTmax), optimum (Topt), thermal breadth (Tbreadth) and maximum thermal potential (Pmax) are given for fitness (r). We use the best fit model from each individual life history trait, making this the best fit model. **Table I. Temperature-dependent relative R_0 (transmission rate as the basic reproduction rate, R_0).** Temperature-dependent relative R_0 (transmission rate as the basic reproduction rate R_0) derived from individual life history traits measured for *Ae. aegypti* mosquitoes reared at 13°C, 15°C, 19°C, 23°C, 25°C, 27°C, 29°C, 31°C, 33°C, 35°C, 37°C. We measured mosquito life history traits for five populations from Mexico (Cabo San Lucas, Acapulco, Monterrey, Ciudad Juárez, and Jojutla) compared to a laboratory-adapted line. Mean and 95% credible interval (95% HPD interval) for the critical thermal minimum (CTmin), maximum, (CTmax), optimum (Topt), thermal breadth (Tbreadth)

and maximum thermal potential (P_{max}) are given for fitness (r). We use the best fit model from each individual life history trait, making this the best fit model.

(DOCX)

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