

The dynamics, transmission, and population impacts of avian malaria in native Hawaiian birds: a modeling approach

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Abstract. We developed an epidemiological model of avian malaria (*Plasmodium relictum*) across an altitudinal gradient on the island of Hawaii that includes the dynamics of the host, vector, and parasite. This introduced mosquito-borne disease is hypothesized to have contributed to extinctions and major shifts in the altitudinal distribution of highly susceptible native forest birds. Our goal was to better understand how biotic and abiotic factors influence the intensity of malaria transmission and impact on susceptible populations of native Hawaiian forest birds. Our model illustrates key patterns in the malaria–forest bird system: high malaria transmission in low-elevation forests with minor seasonal or annual variation in infection; episodic transmission in mid-elevation forests with site-to-site, seasonal, and annual variation depending on mosquito dynamics; and disease refugia in high-elevation forests with only slight risk of infection during summer. These infection patterns are driven by temperature and rainfall effects on parasite incubation period and mosquito dynamics across an elevational gradient and the availability of larval habitat, especially in mid-elevation forests. The results from our model suggest that disease is likely a key factor in causing population decline or restricting the distribution of many susceptible Hawaiian species and preventing the recovery of other vulnerable species. The model also provides a framework for the evaluation of factors influencing disease transmission and alternative disease control programs, and to evaluate the impact of climate change on disease cycles and bird populations.

Key words: *climate*; *Culex quinquefasciatus*; *Hemignathus virens*; *Himatione sanguinea*; *mosquitoes*; *Plasmodium relictum*; *rainfall*; *SIR model*; *temperature*; *Vestiaria coccinea*; *wildlife disease*; *Zosterops japonicus*.

INTRODUCTION

The introduction of vector-borne avian malaria (*Plasmodium relictum*) to the Hawaiian Islands in the early 20th century (Scott et al. 1986) is a leading example of the potentially devastating effect of invasive disease on naive populations (Daszak et al. 2000, Dobson and Foufopoulos 2001, Harvell et al. 2002). An effective disease vector, the southern house mosquito (*Culex quinquefasciatus*), was introduced as early as 1826. This disease posed a major new threat to immunologically naive Hawaiian birds, especially honeycreepers (Drepanidinae), which have suffered numerous species extinctions and have limited altitudinal distribution and diversity on the Hawaiian Islands. Although habitat loss and degradation, introduced

predators, stochastic events associated with hurricanes and volcanic eruptions, and competitors have all contributed to these declines, since the 1920s avian malaria has been suggested as one of the most widespread and devastating factors (Scott et al. 1986).

Van Riper et al. (1986) concluded that avian malaria was responsible for a wave of extinctions of native bird species that began after the 1920s, and subsequently native birds below 1500 m elevation, where mosquitoes were common, were at continual risk from malaria. Above that elevation mosquitoes were rare, so disease risk was greatly reduced, allowing native forest bird populations to survive. Later studies reported high prevalence of malaria infection, differences in susceptibility among native species and between native and nonnative species, and chronic infections in native species, which made them effective reservoirs for avian malaria (Atkinson et al. 1995, 2000, 2001a, b, 2005, Woodworth et al. 2005). Thus, many endemic Hawaiian species are highly susceptible to avian malaria, effective disease transmitters, and long-term reservoirs of disease

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(Atkinson and LaPointe 2009*b*, Atkinson and Samuel 2010). In contrast, malaria has minimal impact on the survival of nonnative birds, and these nonnative species have low prevalence (Atkinson et al. 2005, Atkinson and Samuel 2010) and a limited period of disease transmission (Appendix B: Table B5).

The dynamics of avian malaria in Hawaiian bird communities are influenced by interrelated factors that are likely to be complex, nonlinear, and include feedback mechanisms that produce unexpected patterns. These factors include endogenous components of the disease system (vector and host abundance) and exogenous components that drive the system (weather), as well as landscape components (elevation and habitat) that influence biological processes (Ahumada et al. 2009). Due to the steep slopes of many Hawaiian Islands, climate, especially temperature, changes quickly from one location to another, creating strong spatial differences in the system dynamics. Because of the ecological dynamics and landscape scale of avian malaria, we consider modeling to be a crucial tool for understanding the spatial and temporal complexity of the system, evaluating the impacts of disease on native Hawaiian avifauna, assessing alternative conservation strategies, and predicting how climate change or other risk factors may affect disease dynamics.

The goal of our study was to develop a model of the dynamics of avian malaria in the Hawaiian forest ecosystem to better understand the impacts of biotic and abiotic factors on intensity of transmission and impacts on native birds. The model was implemented using ordinary differential equations (ODEs) for susceptible, acutely infected, and recovered (SIR) birds and susceptible, exposed (latent), and infectious (SEI) mosquitoes. The model incorporates dynamics of the host, vector, and parasite. We modeled three native species that represent the spectrum of disease susceptibility/tolerance and one abundant nonnative species. Model parameters were estimated from the published literature, experimental studies conducted by the authors, and scientific expertise of the authors and other researchers. The model, too complex to solve analytically, is solved numerically. We compared model predictions against independent data collected during a four-year study at nine sites in low-, mid-, and high-elevation forests on the eastern slope of Mauna Loa, Hawaii. In this paper we used the model to evaluate the potential impact of avian malaria on Hawaiian birds, evaluate how elevation and mosquito habitat influence malaria dynamics, determine which model variables have the strongest influence on our results and therefore might form the basis of conservation actions, and compare model predictions to observed field data.

METHODS

Simulation model

Our model describes the population dynamics of female southern house mosquitoes (*Culex quinquefascia-*

tus), three endemic Hawaiian honeycreepers, the Hawaii Amakihi (*Hemignathus virens*; see Plate 1), Apapane (*Himatione sanguinea sanguinea*), and Iiwi (*Vestiaria coccinea*), and the most common introduced bird in Hawaiian forests, the Japanese White-eye (*Zosterops japonicus*). Other native and introduced bird species were not considered in our model due to low abundance, limited distribution among elevations, or inapparent susceptibility to avian malaria. Mosquitoes and all bird species were divided into immature and adult stages. Immature mosquitoes contain eggs, larvae, and pupae, which have the same mortality and development rates (Ahumada et al. 2004). Adult mosquitoes were divided into susceptible, latent, and infectious disease stages. Juvenile (susceptible when hatched) and adult birds are tracked by susceptible, acutely infected, and recovered stages. Acutely infected birds suffer from disease-induced mortality and have a high parasitemia (Yorinks and Atkinson 2000). Recovered (chronically infected) native birds are immune to subsequent infection (Atkinson and Samuel 2010); however, they are likely to remain infectious and able to transmit malaria parasites to mosquitoes with only slightly lower probability than the acutely infectious stage based on experiments with chronically infected Amakihi (C. Atkinson, *unpublished data*). The Japanese White-eye, which is characteristic of most introduced birds, does not suffer from disease-induced mortality following inoculation with infected blood (van Riper et al. 1986) or infective mosquitoes bites, and four mosquito infected birds were only infectious for 34 days (C. Atkinson, *unpublished data*). By convention, juvenile birds become adults on 1 January of the year after they fledged.

In many ODE models, the transition rates are constant with exponentially distributed transition times. However, the transition times for development of immature mosquitoes, latency of infected adult mosquitoes, transition of juvenile birds to adult, and recovery of acutely infected birds typically follow a unimodal distribution that peaks after a fixed time lag. To improve model predictions, especially during relatively short transition periods found for mosquito dynamics (<7–14 days), we incorporated a gamma distribution into our ODE models (Anderson 1980, Lloyd 2001, Feng et al. 2007) by subdividing a stage into $k = 5$ substages and requiring transition through all substages before the next developmental or disease stage is reached. The gamma distribution with shape parameter $k = 1$ is an exponential distribution, but if $k \geq 2$, the shape becomes a normal distribution, and higher values of k narrow the time interval for transition to the next stage, creating a time lag or cohort effect. We used five substages as a compromise between model complexity and an improved biological model with time lags. The SEI mosquito and SIR bird models are illustrated in Fig. 1 and described in the next sections, while equations describing the models, parameter definitions, and parameter values are provided in Appendices A and B.

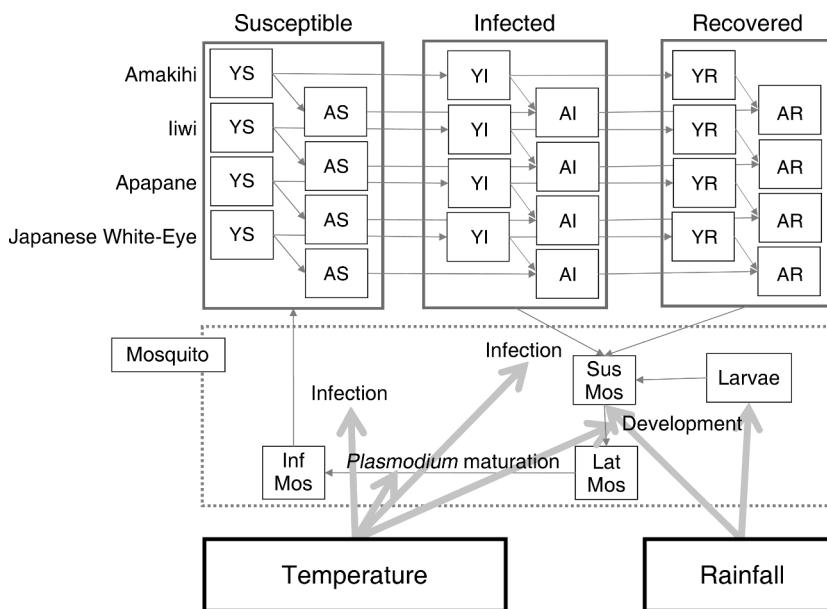


FIG. 1. Malaria-forest bird epidemiological model in three endemic Hawaiian honeycreepers, the Hawaii Amakihi (*Hemignathus virens*), Apapane (*Himatione sanguinea sanguinea*), and Iiwi (*Vestiaria coccinea*), and the most common introduced bird in Hawaiian forests, the Japanese White-eye (*Zosterops japonicus*). Mosquitoes develop from larvae to susceptible adults (Sus Mos). They become infected, but not infectious (Lat Mos) after feeding on acutely infected (YI/AI) or chronically infected (YR/AR) birds. Once malaria parasites mature in a latent mosquito, it becomes infectious (Inf Mos) to susceptible (YS/AS) birds. Temperature and rainfall affect the rates of mosquito development (Larvae→Sus Mos), malaria (*Plasmodium*) maturation (Lat Mos→Inf Mos), and infection.

Mosquito model

Culex quinquefasciatus is the most common bird-feeding mosquito in Hawaii, and is presently the only common mosquito above 900 m elevation. Mosquitoes are poikilotherms, and therefore climate directly influences their biology via temperature effects on larval maturation rate, gonotrophic cycle, and parasite development rate within an infected mosquito. Furthermore, droughts or strong rains decrease the survival of larvae and adults, respectively. Due to the steep slopes of many Hawaiian Islands, climate, especially temperature, changes quickly from one location to another, creating strong spatial differences in the system dynamics. Immature *C. quinquefasciatus* exhibit a linear rate of development as a function of temperatures above the lower threshold temperature for development (Ahumada et al. 2004, 2009). Because *C. quinquefasciatus* is predominantly a cavity breeder in Hawaii, rainfall dynamics and cavity availability also influence population growth (Ahumada et al. 2004: Eqs. 3–4 and Fig. 8). The mortality of immature mosquitoes increased as a function of drought (≤ 5 mm rainfall; Ahumada et al. 2004). Under favorable conditions (no dry days) in low-elevation forests, $\sim 65\%$ of immature mosquitoes survived to the adult stage, with an average maturation time of 14.4 days (Hayes and Hsi 1975; D. LaPointe, unpublished data) resulting in a daily survival of 97% for immature mosquitoes.

We assumed a constant number of female eggs (100) were laid per adult female after each gonotrophic cycle (Ahumada et al. 2004). We limited the immature mosquito population to larval carrying capacity (K_L) measured for each study site (Appendix B: Table B1), by reducing larval recruitment. Carrying capacity was the product of the cavity (tree and rock holes, as well as cavities created by feral pigs) density for each study site (D. LaPointe, unpublished data) times 100 immature female mosquitoes per cavity times the fraction of occupied cavities (0.59; D. LaPointe, unpublished data). At low-elevation sites, most cavities were lava rock holes containing 20 times more water than cavities at higher elevations (fallen trunks of tree ferns, *Cibotium* spp.) and were occupied by several mosquito species with $\sim 25\%$ *C. quinquefasciatus* (D. LaPointe, unpublished data). Therefore, at low-elevation sites, the cavity density was also multiplied by 0.25 and 20.

The daily survival rate of adult mosquitoes was estimated at 93% (D. LaPointe, unpublished data). In the case of a heavy rainfall event (rainfall > 255 mm in three days), the daily survival of adult mosquitoes was reduced to 5% (Ahumada et al. 2004). Warmer temperatures reduce the length of the gonotrophic cycle and increase the adult biting rate (Appendix B: Table B4); the inverse of the gonotrophic cycle length. We assumed malaria transmission from mosquitoes to birds was frequency dependent (Antonovics et al. 1995), with bird density sufficient for maximum mosquito biting

rate. For temperatures found in Hawaii, the development rate of *Plasmodium* increases (development time decreases) with higher temperatures (Appendix B: Table B4) when average daily temperature exceeded the minimum threshold of 12.6°C required for development (LaPointe 2000). The probability of disease transmission from an infectious mosquito to a susceptible bird was estimated at 0.98 per mosquito bite, based on experimental laboratory infections in native bird species (Appendix B: Table B6).

To model daily mosquito dynamics as a function of temperature and rainfall, we used ANUSPLIN (version 4.2; M. F. Hutchinson, *available online*)⁹ to fit thin plate smoothing splines to weekly temperature (linear function of elevation) and rainfall (quadratic function of elevation) data (1980–2004) for weather stations on Hawaii (National Climatic Data Center; *available online*).¹⁰ From these spline surfaces, we predicted weekly temperatures and rainfall for our study sites. Average daily temperatures were estimated using a Piecewise Cubic Hermite Interpolating Polynomial (PCHIP) procedure in MATLAB version 7.2 (MathWorks 2008). A random amount of the total weekly rainfall was assigned among days in a week to obtain daily rainfall.

Bird model

We modeled three Hawaiian honeycreepers representing the largest group of extant native forest birds with some of the highest survival rates of previously studied Hawaiian avifauna and a range of behavior, biology, and disease susceptibility. They also represent varying levels of landscape mobility from the relatively sedentary Amakihi to Apapane and Iiwi, which can make large-scale foraging flights across elevations during the nonbreeding season; likely exposing birds from high-elevation disease-free refugia to areas where disease transmission is high. Japanese White-eye, the most common introduced bird in Hawaiian forests, was included to investigate the potential effects of introduced bird species, which are typically poor disease amplifiers, in buffering transmission to native species.

Bird dynamics differ between elevations because biotic factors like food abundance, general weather patterns, and habitat differentially affect seasonal breeding cycles for low-, mid- and high-elevation sites. The daily reproductive rate was calculated as half (assuming a 1:1 sex ratio for breeding birds) of the number of fledglings produced within one breeding season divided by the length of the breeding season. The daily reproduction rate was multiplied by the fraction of breeding birds, which differed by species and elevation (Appendix C: Fig. C1). Reproduction was not affected by chronic malarial infection (Kilpatrick et al. 2006). We estimated the juvenile maturation rate required for

birds born in the middle of the breeding season becoming adults by 31 December. The middle of the breeding season for Amakihi, Apapane, Iiwi, and Japanese White-eye were estimated (Appendix C: Fig. C1) as 8 May, 29 April, 5 April, and 8 May, respectively.

The carrying capacities for each bird species were estimated at 1.5 times their highest observed abundance (Appendix B: Tables B2 and B5). The daily juvenile natural mortality rates were estimated from previous studies (Appendix B: Table B5) as 37.5%, 40%, 40%, and 22% during the first year for Amakihi, Apapane, Iiwi, and Japanese White-eye, respectively. Mortality rates reported in previously published studies (Appendix B: Table B5) resulted in population declines; therefore, rates were increased slightly to achieve stable bird densities observed at high-elevation sites (Appendix B: Table B2), where there is little disease.

The daily disease recovery rates (γ) of acutely infected birds were estimated by the inverse of the length of the acute infection periods (Appendix B: Table B5) and the proportion of acutely infected birds that survive avian malaria. Disease survival rates were 38% for Apapane (Yorinks and Atkinson 2000) and 10% for Iiwi (Atkinson et al. 1995), 83% for low-elevation Amakihi, and 40% for high-elevation Amakihi (Atkinson et al. 2000; C. Atkinson, *unpublished data*). Disease survival rates were similar for juvenile and adult birds. Japanese White-eyes experience low-level parasitemia from avian malaria that does not cause mortality (van Riper et al. 1986). The acute infection period of the Japanese White-eye was based on challenge of four Japanese White-eye by infective mosquito bites. The estimated probability of disease transmission to a susceptible mosquito was higher from acutely infected birds with higher parasitemias (Atkinson et al. 2000) than from recovered honeycreepers and increased with temperature, which increases oocyst development rate (Appendix B: Table B6; LaPointe et al. 2010). Transmission probability from acutely infected Japanese White-eyes to a susceptible mosquito was much lower (0.1) based on experimentally infected birds and transmission was negligible for recovered Japanese White-eyes (C. Atkinson, *unpublished data*).

Simulations

For each of our nine study sites, we performed simulations in the absence of disease to obtain reference points for the impact of avian malaria. Subsequently, we simulated the impact of introducing avian malaria to a disease-free bird community. Simulations were performed for a 24-year time period using climate data for 1980 to 2003. Independent of initial values and elevation, mosquito dynamics stabilized within a few years, thus, we used 100 susceptible or infectious adult mosquitoes per km² and no larvae as initial mosquito densities for simulations in the absence or presence of disease, respectively. In the absence of disease, initial adult bird densities were set to the average field densities

⁹ (<http://cres.anu.edu.au/outputs/anusplin.php>)

¹⁰ (<http://www.ncdc.noaa.gov/oa/ncdc.html>)

at high-elevation sites. For simplicity, we set all initial juvenile bird densities to zero. Using these initial values, bird densities were generally stable at the end of the simulation period in the absence of disease. We used these stable densities of juvenile and adult birds in the absence of disease as initial values for 24-year simulations (1980–2003) with avian malaria. We evaluated annual mosquito densities for the last three simulated years, because mosquitoes varied annually depending on weather conditions. We used the last simulated year for bird densities, which were still slowly declining at the end of the simulation. Seasonal patterns in juvenile and adult bird abundance and disease status were based on the last three years of the simulation. Simulations were performed in MATLAB version 7.5.0 using solver ode45 for ODEs (MathWorks 2008).

Sensitivity and uncertainty analyses

We analyzed the sensitivity of model outputs to 46 parameters and 5 initial state variables using Latin hypercube sampling (Blower and Dowlatbadi 1994). In the absence of a priori knowledge of the parameter probability distributions, we assumed a uniform distribution from 0.75 to 1.25 times the estimated value. Parameters based on probability were not allowed to vary outside the range of 0–1. We simulated 200 different sets of parameter values selected by Latin hypercube sampling without replacement from within these intervals. Adult mosquito mortality rates under normal and heavy rainfall were analyzed separately. We assumed that bird species do not compete for resources and only considered demographic parameters and initial values for each species. Malaria mortality and transmission rates from recovered Japanese White-eye to susceptible mosquitoes were not part of the sensitivity analysis because these are negligible (C. Atkinson, unpublished data).

We calculated semi-partial rank correlation coefficients (SPRCCs) between the parameters or initial values and the model outputs for the density of birds and adult mosquitoes. SPRCCs measure the proportion of response variance accounted for by each predictor variable. We used bird densities from the last year, and we averaged mosquito densities for the last three years of each 24-year simulation. To study the effect of elevation, we created one climate scenario for low, mid, and high elevations by averaging daily temperature and rainfall for all study sites within each elevation category. Similarly, we estimated the average carrying capacity of mosquito larvae for each elevation category. We performed a sensitivity analyses in the absence of disease and for the disease impact on native bird populations (bird density without disease minus bird density with disease).

We also used Latin hypercube sampling to assess the uncertainty of our model predictions (Helton and Davis 2003). The goal of this analysis was to determine the uncertainty of model predictions as a function of

uncertainty in the model parameters. Uncertainty of the model parameters was calculated (or in a few cases estimated) based on published and experimental studies used to generate model parameters (see Appendix B: Tables B4–B6 for parameter uncertainty). The Latin hypercube methods provide a Monte Carlo procedure for the propagation of uncertainty in complex models (see Helton and Davis 2003 for details). As with the sensitivity analysis, we simulated 200 different sets of parameter values and estimated mean, 10th, 25th, 50th, and 90th percentiles to compare model outputs with field data.

Comparison of model predictions with field data

We collected data on bird density, mosquito abundance, mosquito larval cavities, and malaria infection rates in both mosquitoes and birds at three low-elevation (25–314 m), four mid-elevation (885–1247 m), and two high-elevation (1678 and 1686 m) 1-km² study sites along the eastern slope of Mauna Loa and Kilauea Volcanoes (Appendix C: Fig. C2) on the Island of Hawaii during 2002–2004 (Appendix B: Tables B1 and B2). Annual bird densities (Appendix B: Table B2) were estimated using variable circular plot methods. Malarial diagnostics were performed using a combination of microscopy and serology to identify birds with acute (smear positive, antibody negative) or chronic infections (smear positive or negative, antibody positive) and species-specific prevalence included both categories of infection (Atkinson and Samuel 2010); we only used sites where >5 birds were captured and tested. Mosquito abundance at each study site was measured by the number of mosquitoes per trap night and cannot be converted into density. Instead, we calculated the relative abundance (0–1) of adult mosquitoes at each site compared to the site with the highest abundance. The relative abundance for each field site was compared to model predictions of mosquito density (Appendix B: Table B1) that were rescaled to a similar relative index. Prevalence of latent or infectious mosquitoes (determined using methods in LaPointe et al. 2010) was available during 2001–2005 for all low- and mid-elevation sites. From the field data, we used only site-specific mosquito larval cavity data, species-specific temporal breeding patterns, and species-specific population density (both maximum for all sites and specifically at high-elevation sites) to calculate larval carrying capacity (K_L), proportion of breeding adults ($P(t)$), bird carrying capacity (K_b), and help adjust adult survival rates (d_a) to achieve stable populations, respectively, in our simulation model (Appendix B: Tables B4 and B5). All other model parameters were based on previous studies or experimental data (Appendix B: Tables B4–B6). We compared independent model predictions to the density and malaria prevalence of birds, relative abundance of adult mosquitoes, and prevalence of latent and infectious mosquitoes at each forest study site. We conducted rank correlation analysis

and other qualitative comparisons of model predictions vs. field observations to assess model fit. We also compared elevational trends and seasonal dynamics of the model predictions to previous studies and field observations.

RESULTS

Climate data

The estimated annual temperature during 1980–2003 at each study site ranged from 21.7–22.8°C, 16.1–17.4°C, and 14.0–14.5°C for low, mid, and high elevations, respectively (Appendix B: Table B1). Mean yearly rainfall during the same period ranged from 2403–3161 mm, 2095–4081 mm, and 2094–2102 mm. Temperatures were 5.2–5.6°C higher in July or August than in January, and rainfall was 202–384 mm higher during fall than in the spring, depending on the site. The percentage of dry days per year (<5 mm rainfall) ranged from 71–72%, 72–86%, and 84–89%, while there was an average of 1.6–2.0, 1.5–4, and 0.7–1.8 heavy rainfall events (>255 mm in three days) for low-, mid-, and high-elevation study sites, respectively.

Mosquito abundance

Our model predicted that mosquito dynamics varied seasonally, annually, across the elevational gradient, and among study sites within the same elevation. Maximum density of mosquitoes was limited by the larval carrying capacity at each site (Appendix B: Table B1), but carrying capacity was seldom reached except at low-elevation sites. Mosquito larvae were predicted at 91–94% and 43–75% of their estimated carrying capacity at low- and mid-elevation sites, respectively. Densities of immature and adult mosquitoes were higher at some low- and mid-elevation sites than other sites at the same elevation (Appendix B: Table B1). In contrast, mosquitoes were rare at high elevation. The seasonal density of mosquito larvae was relatively constant at low elevation, but followed strong seasonal temperature patterns with late-summer peaks and winter lows at mid elevation (Appendix C: Fig. C3). The densities of larval and adult mosquitoes fluctuated strongly over the timescale of a few days due to the effect of high rainfall events on adult mortality, drought on mosquito larvae, or temperature on population processes. This seems to be the primary factor causing temporary population declines in low-elevation forests (Appendix C: Fig. C3). The temporal patterns of latent (L_m) and infectious (I_m) adult mosquitoes were similar to those of total adult mosquitoes. At low elevation, the percentage of latent (L_m) mosquitoes (8.2–11.5%) was typically smaller than infectious (I_m) mosquitoes (11.5%). At mid-elevation sites, the percentage of L_m (0.5–4.6%) and I_m (7.1–8.7%) mosquitoes were typically less than low-elevation sites.

Bird abundance

In the absence of avian malaria, predicted bird density was limited by carrying capacity (see *Methods*), mortal-



PLATE 1. Hawaii amakihi, *Hemignathus virens*, one of a few Hawaiian honeycreeper species still common in native forests despite the high incidence of introduced avian malaria, *Plasmodium relictum*. Photo credit: D. A. LaPointe.

ity, and reproduction (Appendix C: Fig. C1); therefore, predicted density was similar among study sites at the same elevation (Fig. 2). Abundance of all four species was reduced at high-elevation sites, compared with low- and mid-elevation sites, primarily because shorter breeding seasons reduced annual recruitment. Apapane were the most abundant, followed by Japanese White-eye, Amakihi, and Iwi, except at high-elevation sites, where Iwi were more abundant than Amakihi. The abundance of juvenile birds was below 6.8–14% of species abundance for all sites and was highest in spring and lowest in winter.

Native bird density declined sharply following the introduction of avian malaria in our model simulations, followed by a continued slow decline during our 24-year simulation period. During the last three years of the simulation, Apapane densities were stable at all sites, and Amakihi and Iwi abundance decreased by < 3% for all sites. Japanese White-Eye populations were not affected by avian malaria. Avian malaria decreased the abundance of Amakihi, Apapane, and Iwi by 26%, 61%, and 97%, respectively, at low-elevation sites (Fig.

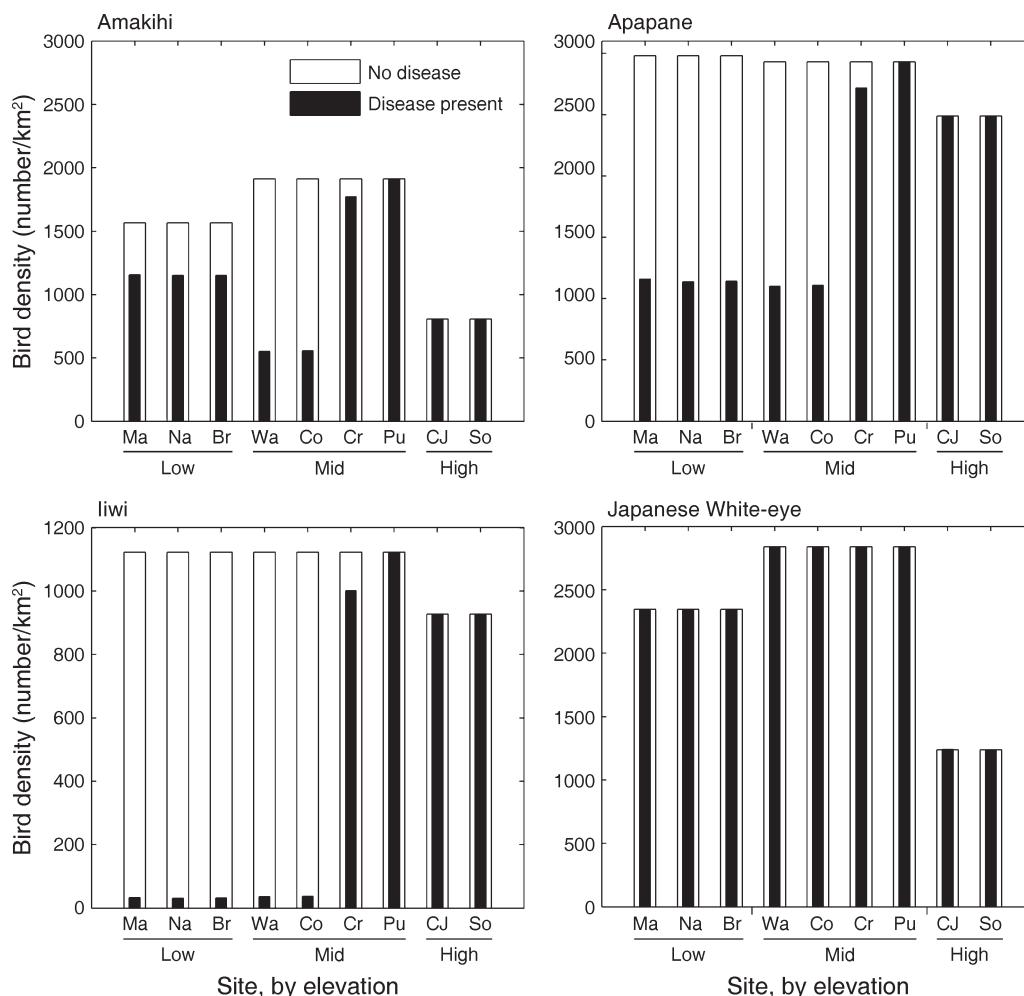


FIG. 2. Predicted mean annual densities of three Hawaiian honeycreepers (Amakihi, Apapane, and Iiwi) and the nonnative Japanese White-eye in the presence and absence of avian malaria at nine study sites in low-, mid-, and high-elevation forests. Bird density for Iiwi is lower than the other three species. Model predictions are based on parameters in Appendix B (Tables B3–B6). Site abbreviations are: Ma, Malama Ki; Na, Nanawale; Br, Bryson's; Wa, Waiakea; Co, Cooper; Cr, Crater; Pu, Pu'u, CJ, CJR; and So, Solomon's.

2). At mid-elevation sites, predicted reductions in bird densities varied among sites ranging from negligible or minor reductions (7–11%) to substantial declines (62–97%), depending on the site and native bird species. Avian malaria had no impact on high-elevation bird populations because mosquito abundance and malaria transmission were negligible.

Malaria infection

The intensity and seasonal patterns in avian malaria transmission varied dramatically among low, mid, and high elevations (Fig. 3). Acutely infected birds were <3% of the native bird populations for all sites; however, recovered birds constituted 90–97% of populations at low-elevation and some mid-elevation study sites. Many native juvenile birds, 75–99% at low-elevation sites and 66–85% at some mid-elevation sites, were infected with malaria. At low elevation,

infection occurs rapidly throughout the annual cycle, and there are relatively few susceptible juvenile birds remaining shortly following hatch. Adult birds at low-elevation sites are the juveniles from the previous year's cohorts of malaria survivors. At mid-elevation sites, susceptible juveniles are common until malaria transmission begins during late summer and early fall. In years or at study sites with lower transmission, some susceptible juveniles mature to become susceptible adults. The annual dynamics of malaria infection also varies in intensity among years depending on weather patterns and mosquito population dynamics (Fig. 3). Seasonal patterns in malaria transmission are especially evident at mid-elevation sites, with weaker seasonal patterns at low elevation. At high elevation, the lack of avian malaria transmission provides a disease-free refuge.

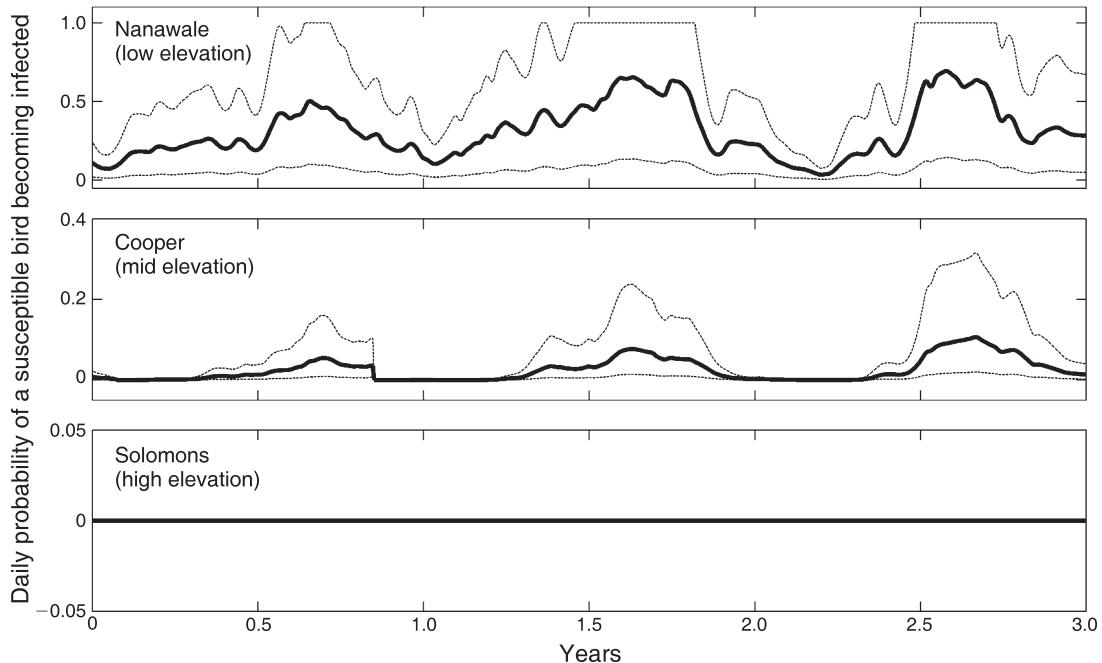


Fig. 3. Daily probability of malarial transmission (dark lines, with 10th and 90th percentile prediction intervals) to susceptible native birds (daily incidence rate) for three years at the low-elevation site Nanawale, the mid-elevation site Cooper, and the high-elevation site Solomon's. Results are from model simulations using parameters in Appendix B (Tables B3–B6) and uncertainty analysis described in the *Methods*.

Comparison with field data

Overall model predictions of mosquitoes followed the same trends observed at our study sites; low abundance and absence of latent and infectious mosquitoes at high elevation, intermediate levels of latent and infectious mosquitoes at mid-elevation sites, and higher levels of infectious mosquitoes at low-elevation sites (Appendix C: Fig. C4). Observed and predicted prevalence of infectious mosquitoes followed the same elevational trend; however, predicted prevalence of infectious and latent mosquitoes was similar among low-elevation sites, while observed variation was higher among these sites. Model predictions generally underestimated these variables in mid-elevation forests, especially at Pu'u. However, our model correctly predicted the seasonal patterns of avian malaria transmission (Fig. 3) reported in mid-elevation forests (Atkinson and Samuel 2010). At low elevation, the model predicted higher mosquito densities at one site (Nanawale), primarily as a function of higher larval carrying capacity.

Our model correctly predicted that Apapane and Iwi abundance would follow an elevational gradient with high densities in high-elevation disease-free forests to low densities at low elevation (Fig. 4). Predicted bird densities strongly reflected the influence of mosquito abundance and transmission of avian malaria on native bird survival (Fig. 2). Observed and predicted Iwi abundance in mid-elevation forests was similar, except at Crater and Pu'u, which had lower observed abundance. Predicted and observed Apapane abundance also

varied among mid-elevation sites, with higher predicted density at Pu'u and Coopers. Predicted Amakihi abundance was slightly lower at high elevation than at low elevation, as a result of malaria tolerance in low-elevation Amakihi populations (Woodworth et al. 2005). Predicted and observed Amakihi abundance was similar at most low- and high-elevation sites. However, Amakihi were generally less abundant at mid-elevation sites than predicted by our model. Like other native honeycreepers, predicted Amakihi abundance was higher than observed at Craters and Pu'u. Observed Japanese White-eye abundance was higher in low-elevation forests and lowest in high-elevation forests. Our model predicted highest Japanese White-eye densities at mid-elevation sites, with lowest abundance at low elevation.

Predicted and observed malaria prevalence (acutely infected and recovered) for native birds was high at low-elevation, low at high-elevation, and varied among mid-elevation study sites (Fig. 5). At low elevation, observed malaria prevalence was >70% in native Hawaiian honeycreepers, and it was uncommon to capture susceptible birds at any time of year, indicating intense transmission throughout the year. Predicted patterns were similar to observed prevalence at both low and high elevations. At mid-elevations, model predictions and observed prevalence of malaria varied by sites. We found higher observed malaria prevalence for Apapane and Iwi at Pu'u than predicted by our model, likely corresponding to the higher observed mosquito density

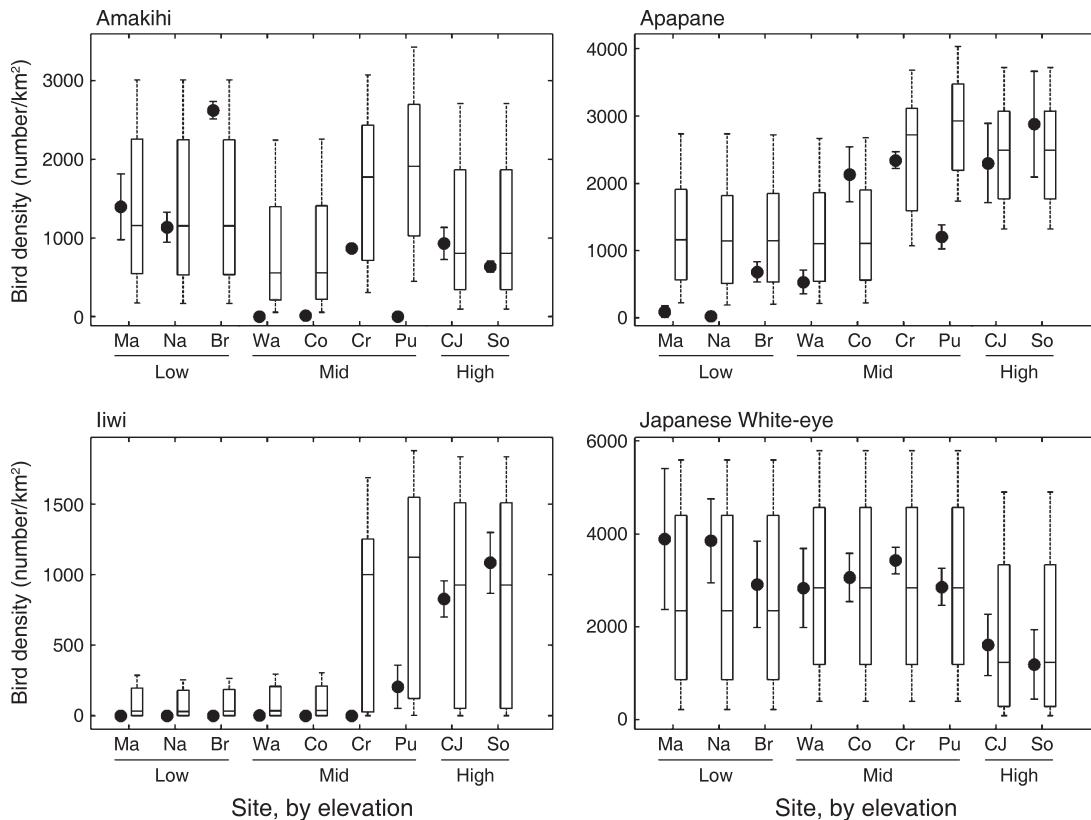


FIG. 4. Mean annual observed and predicted densities of three Hawaiian honeycreepers and the nonnative Japanese White-eye at nine study sites in low-, mid-, and high-elevation forests as predicted by the model (boxplots) and observed in the field (solid dots, with 10th and 90th percentile whiskers). Model prediction boxplots include mean, 10th, 25th, 75th, and 90th percentiles based on the last year of the simulation period. See Fig. 2 for site abbreviations.

and infection rate contributing to the lower observed abundance of native birds at this site. Predicted prevalence of malaria at Coopers was higher than observed, perhaps also contributing to the lower observed than predicted abundance of native birds.

Many of the trends in observed data at field sites were correlated with trends in model predictions. Correlations were also conducted excluding Pu'u because large differences between predicted and observed mosquito density at this site affected model predictions for other variables. These differences are likely related to our discovery that an investigator at Hawaii Volcanoes National Park had placed large pans filled with water on transects adjoining Pu'u as part of another study, significantly increasing available larval habitat for mosquitoes at this study site. Most of the rank correlation coefficients between predicted and observed data were >0.50 and many exceeded 0.70 (Table 1), despite the small sample size ($n < 9$) and the complexity of our model.

Sensitivity analysis

In the absence of avian malaria, demographic parameters were the most important semi-partial rank

correlation coefficients (SPRCCs) influencing bird abundance (Appendix B: Table B7). For Apapane and Iiwi, carrying capacity (K_b), fecundity (F), and proportion of breeding adults ($P(t)$) were the primary variables increasing abundance. In contrast, adult and juvenile mortality (d_a and d_h , respectively) was the primary factor reducing abundance. The same factors were important for Amakihi, but their relative importance depended on elevation. Japanese White-eye abundance was influenced by mortality, maturation of juvenile birds (m), and proportion of breeding adults more than native birds.

Hawaiian honeycreepers were substantially reduced by avian malaria at most low- and mid-elevation forest sites, and malaria impact was most sensitive to disease mortality and recovery rates (Appendix B: Table B8). Factors that favored mosquito populations or disease transmission, including adult mosquito survival, larval development, and biting rates, were also important in bird population declines in mid-elevation forests. In mid-elevation forests, bird demographics (fecundity, proportion of breeding adults, and carrying capacity) had secondary influences on population patterns. Amakihi at low elevations, with higher tolerance to malaria, were sensitive to population demographics

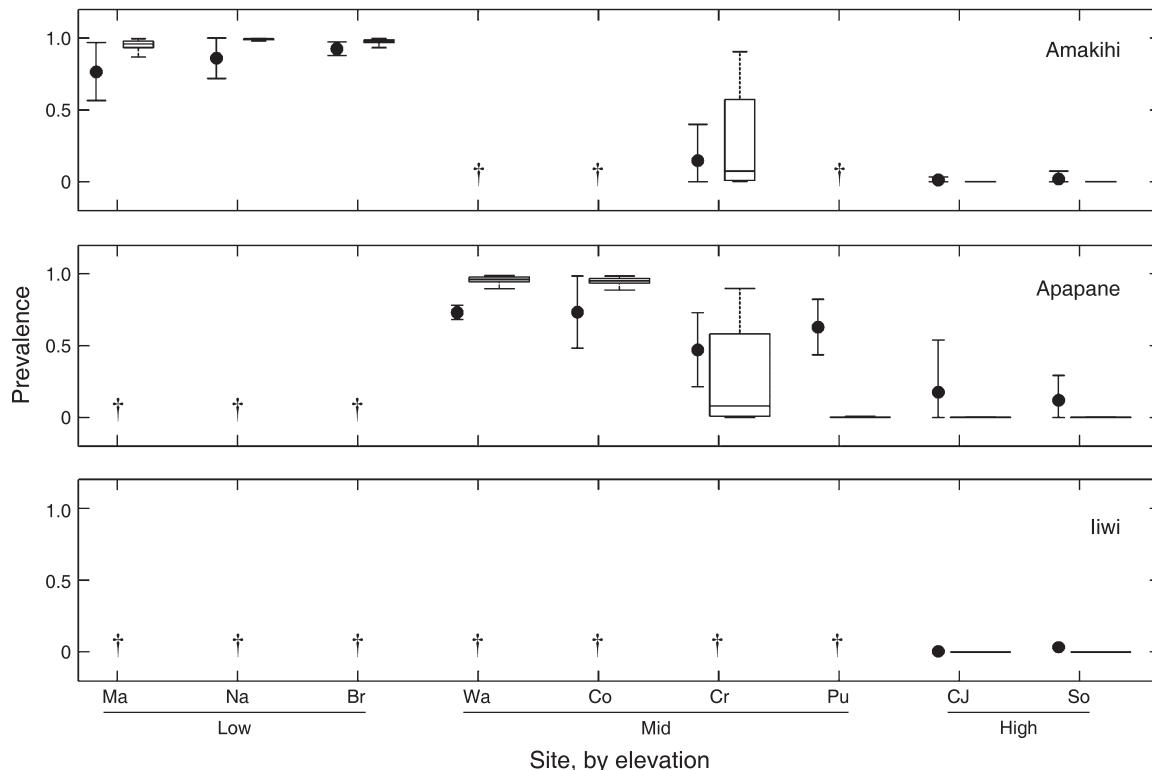


FIG. 5. Annual malaria prevalence for three Hawaiian honeycreepers as predicted by the model (boxplots with mean, 2.5th, 25th, 75th, and 97.5th percentiles) and observed (solid dots with 95% confidence intervals) at nine study sites in low-, mid-, and high-elevation forests. Model predictions were based on the last year of the simulation period. Prevalence was based on both infectious and recovered birds. A dagger (†) indicates that field data were inadequate or not available.

(reproduction and natural mortality), as well as disease mortality and recovery.

Adult mosquito abundance was strongly influenced by the larval maturation ($d(T)$), so higher temperatures

produced more mosquitoes, especially at low and mid elevations (Appendix B: Table B7). Larval carrying capacity (K_L) also had a strong positive influence on mosquito density. Variables with important negative

TABLE 1. Rank correlation coefficients (r) of model predictions and field data for model variables.

Variable	r	N	P
Density			
HAAM	0.22 (0.74†)	9 (8)	0.58 (0.037)
APAP	0.52 (0.62)	9 (8)	0.15 (0.10)
IIWI	0.70† (0.68†)	9 (8)	0.038 (0.062)
JAWE	0.22 (0.31)	9 (8)	0.58 (0.46)
Prevalence			
HAAM	...‡ (0.93†)	...‡ (7)	...‡ (0.0025)
APAP	0.82† (0.77†)	7 (6)	0.023 (0.072)
IIWI	0.87 (...§)	3 (...§)	0.33 (...§)
JAWE	0.013 (-0.06)	9 (8)	0.97 (0.89)
Relative abundance M	0.64† (0.90†)	9 (8)	0.061 (0.0024)
Prevalence L_m	-0.26 (-0.7)	6 (5)	0.62 (0.19)
Prevalence I_m	0.45 (0.42)	9 (8)	0.23 (0.30)

Notes: N indicates the number of study sites used in the analysis. P values indicate the probability of obtaining r under the null hypothesis that model predictions and field data are not correlated. Values in parentheses represent the correlation results when the site Pu'u was excluded. Abbreviations are: HAAM, Amakihi; APAP, Apapane; IIWI, Iiwi; JAWE, Japanese White-eye; M , density of adult mosquitoes; L_m , density of latent adult mosquitoes; and I_m , density of infectious adult mosquitoes. Model parameters are defined in Appendix B.

† Statistics were significant at the $P = 0.10$ level.

‡ No prevalence data were available for Pu'u.

§ Prevalence at the remaining two field sites was the same.

impacts on adult mosquito abundance included drought conditions (threshold dry days), adult mortality ($\mu(R)$), and larval mortality ($\mu_L(D)$).

DISCUSSION

Previous researchers have hypothesized that avian malaria played a key role in the decline and elevational distribution of native forest birds because of their high susceptibility in experimental studies (Warner 1968, van Riper et al. 1986, Atkinson et al. 1995). Our model of avian malaria, which also agrees with studies on transmission and survival of native Apapane in mid-elevation forests (Atkinson and Samuel 2010), suggests that malaria is likely a key factor in causing declines, restricting the distribution, and preventing recovery of many vulnerable Hawaiian species. Van Riper et al. (1986) proposed a static model based on observed abundance of mosquito vectors and presence of malaria parasites in mid- and low-elevation forests to explain why native forest birds were generally restricted to high elevation. Our model reproduces this elevational pattern, but, beyond that, it shows that avian malaria is a dynamic process that can significantly reduce the diversity and abundance of susceptible Hawaiian honeycreepers in low- and mid-elevation forests. Our model reproduces several key attributes of the malaria-forest bird system in Hawaii (van Riper et al. 1986, Atkinson et al. 2005, Woodworth et al. 2005, Atkinson and Samuel 2010), including infection patterns (Fig. 3) characterized by: (1) high transmission in low-elevation forests with minor seasonal or annual variation; (2) episodic transmission in mid-elevation forests with site-to-site, seasonal, and annual variation depending on mosquito dynamics and bird susceptibility; and (3) disease-free refugia in high-elevation forests with only slight risk of infection during summer when climatic conditions are briefly favorable for pathogen and mosquito development. The model demonstrates these infection patterns are driven by the effects of temperature and rainfall on mosquito dynamics across an elevational gradient and the availability of larval habitat, especially in mid-elevation forests.

In low-elevation forests, the model illustrates that climate is consistently favorable for mosquitoes and larval habitat is sufficient to produce a high abundance of infectious mosquitoes (Appendix C: Figs. C3 and C4) leading to the absence of susceptible native species (Fig. 4) and a high rate of chronic infection in the native birds that remain (Fig. 5). However, in mid-elevation forests abundance of infectious mosquitoes is lower; seasonal disease transmission is driven by climate and affected by available larval habitat, which varies among forest sites. Together these factors show the absence of most native birds in low-elevation forests, that malaria-tolerant Amakihi can persist at low elevations (Woodworth et al. 2005), and variation in species abundance among mid-elevation forests. A major difference between our results and patterns observed by van Riper et al. (1986)

is the persistence of malaria-tolerant Amakihi in low-elevation forests. Our model results are also consistent with previous studies that native Hawaiian birds are an important reservoir of malaria because native birds that survive acute infection acquire immunity, become reservoirs for transmission to mosquitoes that can infect susceptible birds (Atkinson and LaPointe 2009a).

A variety of conservation programs have been proposed for saving Hawaiian forest birds, including removal of introduced avian-disease reservoirs, predator control, enhanced disease tolerance in native birds, mosquito control, and habitat restoration or conservation (Pratt et al. 2009). Some of these programs can be evaluated qualitatively using our modeling framework. For example, introduced birds such as the highly abundant Japanese White-eye probably play a limited role in malaria transmission and may buffer malaria epidemics (Dobson 2004, Ahumada et al. 2009). However, these introduced birds have short periods of malaria transmission to mosquitoes, and our sensitivity results suggest that changes in abundance of Japanese White-eye have limited potential impact on native species. Predator control has also been suggested as a conservation strategy to improve survival of Hawaiian birds (Lindsey et al. 2009). Model sensitivity analysis indicates that in the absence of avian malaria, adult and juvenile survival rates are two of the most important factors affecting native bird densities, and therefore improvement in these survival rates by predator reduction would likely enhance bird abundance. However, according to the model, when malaria is present, disease processes (malaria recovery and mortality rates) are the most important parameters affecting native bird abundance; consequently, conservation programs that reduce malaria transmission or mortality would likely have a larger impact on bird abundance than predator reduction.

Some have suggested the reintroduction, translocation, vaccination, fostering genetic tolerance, or facilitation of malaria-tolerant birds are viable conservation strategies (Kilpatrick 2006, Atkinson and LaPointe 2009a, LaPointe et al. 2009). Because Amakihi are currently the only species suspected to have malaria tolerance (Woodworth et al. 2005, Foster et al. 2007), it may be unrealistic to assume other species have tolerant genotypes. Thus, further evaluation of the potential for successfully fostering genetic tolerance by increasing population abundance through predator reduction (Kilpatrick 2006) is warranted. In addition, it is important to evaluate the potential impacts of translocation programs on native bird species with different levels of malaria susceptibility, because, as the model suggests, reintroduction or translocation of disease-tolerant species to other elevations could increase the reservoir of chronically infected birds and therefore transmission to susceptible species.

Habitat loss and degradation, including feral ungulates, invasive plants, and introduced pests, have undoubtedly taken their toll on the historical abundance

and distribution of native Hawaiian birds (van Riper and Scott 2001, Banko and Banko 2009, Pratt et al. 2009). Our model suggests that improving habitat for native birds could increase abundance when malaria is not present. However, with malaria, bird populations may remain far below carrying capacity, suggesting that restoration or expansion of forest habitat should first be concentrated in high-elevation forests and those mid-elevation forests where malaria transmission is absent or at low levels. An important exception may be the management of feral pigs, which are an important source of mosquito larval cavities in many Hawaiian forests. Reducing pig density could both increase bird carrying capacity and reduce malaria through the control of larval mosquito habitat (Ahumada et al. 2009, LaPointe et al. 2009). According to model predictions, pig control would likely be most beneficial in mid-elevation forests where reducing mosquito larval habitat could have the greatest influence on mosquito populations. Further evaluation of this strategy is needed to understand where and how much pig control would be most beneficial, as well as the size of control areas needed to improve bird populations.

Our model can be useful in identifying areas where scientific data is absent or more accurate data would improve model predictions. Model predictions are reasonably precise for measures of mosquito abundance (Appendix C: Fig. C4) and disease prevalence in birds (Fig. 5) and mosquitoes (Appendix C: Fig. C4), but are imprecise for bird abundance and malaria infection (Figs. 3 and 4). Further research including model simplification and better precision of model parameters is needed to improve some model predictions. Our model does not consider how movement of birds or mosquitoes would impact transmission or potential source/sink dynamics for either vectors or birds. In addition, little is known about mosquito feeding preferences among bird species, host defensive behavior, or biting rates on non-avian hosts. Thirdly, environmental effects are particularly important for mosquito population dynamics. Rainfall is predicted to affect adult mosquito mortality, larval development/survival, and larval carrying capacity; however, data related to these factors is limited. Finally, our model does not consider avian pox, which is an additional disease threat to native Hawaiian birds, nor do we consider forested riparian systems, which are also important for native birds throughout the Hawaiian Islands. Further research is needed on all these topics to improve our understanding of vector-borne disease threats to the endemic Hawaiian avifauna.

Historically, avian malarias were the first models of the disease in humans and provided key tools in biological, immunological, and chemotherapeutic research and the successful development of an antimalarial program during World War II (Slater 2005). While our research has specific importance for understanding the ecology of avian malaria in Hawaiian avifauna, it may

also facilitate an evaluation of biotic and abiotic factors on vector-borne diseases such as human malaria (Pascual et al. 2006), dengue (Effler et al. 2005), and West Nile virus (Barker et al. 2009), which affect humans, domestic animals, and wildlife (Daszak et al. 2001, Harvell et al. 2009, Randolph 2009). Avian malaria in Hawaii provides a relatively simple natural system for understanding the interaction of disease, landscape, climate, and biotic factors on disease dynamics and host populations. In the absence of human intervention, this natural system facilitates the assessment of climate and non-climate effects on fundamental properties of vector-borne diseases, which are also crucial in interpreting the more complex patterns seen in human and domestic animal systems (Pascual and Bouma 2009, Dobson 2009). Recent studies of human disease have reached similar conclusions about the importance of climate and landscape on the dynamics of human malaria, and raised concerns about global warming on future disease transmission (Harvell et al. 2002, Patz et al. 2005, Patz and Olson 2006). In addition, many of the population and disease processes in our model could be applied to other vector-borne diseases of wildlife conservation concern, including West Nile virus in Sage Grouse (Naugle et al. 2004) or Yellow-billed Magpie (Crosbie et al. 2008), and avian malaria in the Galápagos (Levin et al. 2009).

Our mathematical model of avian malaria in Hawaiian forest birds integrates disease, climate, epidemiology, and population processes to understand how these components contribute to disease dynamics and host demographics. Our model indicates that avian malaria has the potential to severely reduce the abundance and limit the distribution of susceptible Hawaiian birds. The model provides a framework for the evaluation of conservation programs to control disease epidemics and evaluate future risks. Under current climate patterns, high-elevation forests serve as a disease-free refuge for susceptible birds. However, because mosquito dynamics are strongly controlled by temperature and rainfall, future climate warming will likely have negative impacts on native bird populations in both high- (Benning et al. 2002, Atkinson and LaPointe 2009b) and mid-elevation forests.

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APPENDIX A

Equations describing the susceptible, exposed (latent), and infectious (SEI) model for mosquitoes and the susceptible, acutely infected, and recovered (SIR) model for each bird species (*Ecological Archives* A021-134-A1).

APPENDIX B

Data for study sites, description of model parameters, and model sensitivity results (*Ecological Archives* A021-134-A2).

APPENDIX C

Figures describing bird breeding cycles, study site map, predicted mosquito population dynamics, and comparison of predicted vs. observed mosquito abundance and prevalence (*Ecological Archives* A021-134-A3).