

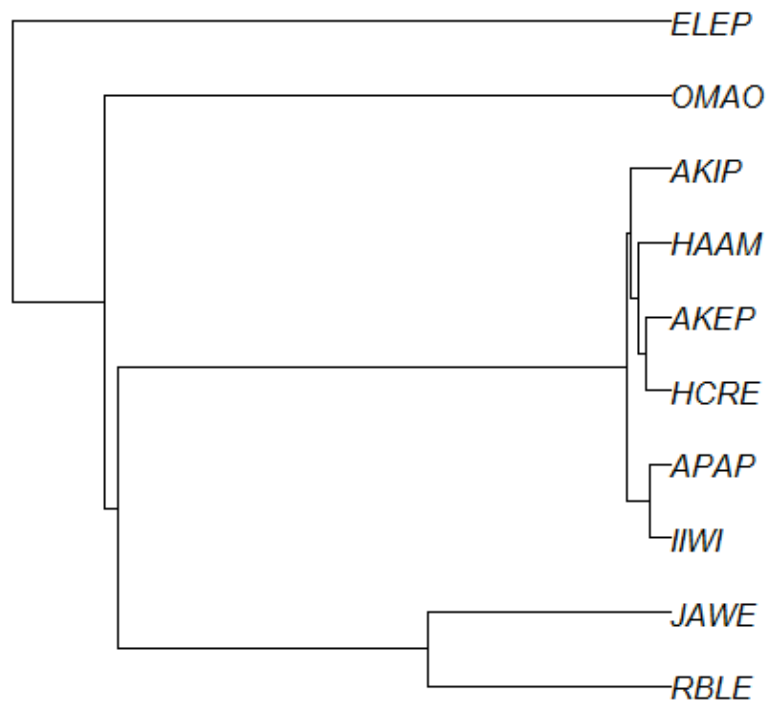
Supplementary material

Appendix. 1 Phylogeny and phylogenetic signal. A composite phylogenetic tree was obtained by integrating the information from published work (see Fig. A1.1 below). First, the divergence between the Hawai'i 'Elepaio, a monarch flycatcher part of the core Corvoidea and the rest (all 'Passerida') was dated at ~ 50 MYA (Barker et al. 2004; their Fig. 2). After their separation from the *Picathartidae* and *Petroicidae* (Barker et al. 2004), the ancestors of modern Passerida underwent an early explosive divergence as demonstrated by extremely short internodes at the base of the group (e.g., Nabholz et al. 2010), starting ~ 43 MYA (Barker et al. 2004). We adopted the topology obtained by Nabholz et al. (2010) showing that Muscicapoidea, including the 'Ōma'ō, diverged first, followed by a split between Sylvioidea (including Red-billed Leiothrix and Japanese White-eye) and Passeroidea (including all six Hawaiian honeycreepers) that we arbitrarily dated ~1 MY later. Divergence between *Zosteropidae* (including Japanese White-eye) and the core babblers (including Red-billed Leiothrix) was estimated at 16.1–21.0 MYA by Moyle et al. (2012), and was taken here to be ~ 18.5 MYA. Finally, we used the topology obtained by Lerner et al. (2011) to describe phylogenetic relationships between our six species of Hawaiian honeycreepers, starting by a split dated at ~3.36 MYA between I'iwi and 'Apapane on one hand, and the remaining four species on the other hand (their Fig. 2).

Blomberg's K (Blomberg et al. 2003) and Pagel's λ (Pagel 1999), were used to test for the presence of phylogenetic signal in our data (tested specifically for ϕ , r , λ and S). To account for parameter uncertainty in our demographic estimates, they were calculated as follows: (i) a posterior sample was drawn at random for each species; (ii) Blomberg's K and Pagel's λ were calculated using the topology described above; steps (i) and (ii) were repeated 1,000 times to obtain the distribution of these statistics. For both statistics, a value close to zero indicated a lack

of phylogenetic signal (phylogenetic independence) while a value close to one indicated that species' traits were distributed as expected under a Brownian motion model of trait evolution.

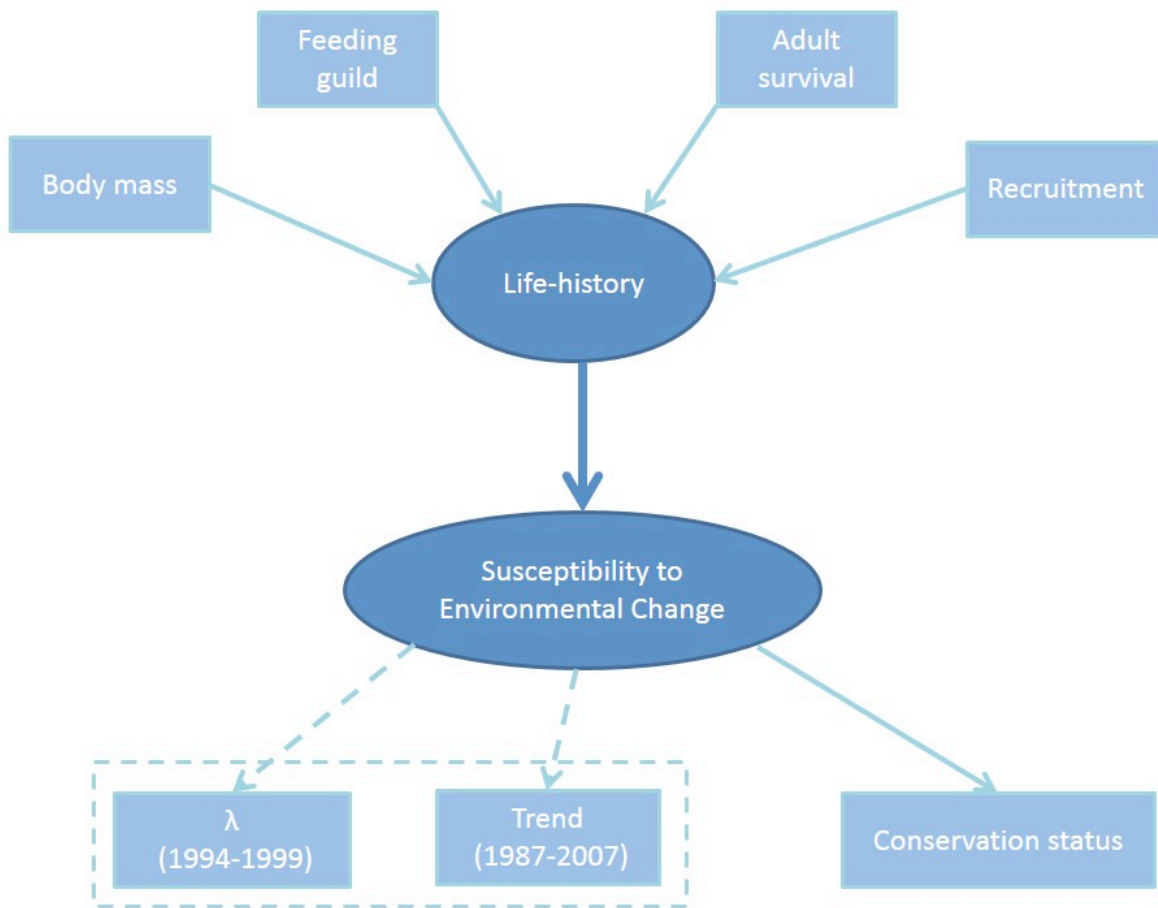
Fig. A1.1. Phylogenetic tree. Species: AKIP = ‘Akiapōlā‘au, AKEP = Hawai‘i ‘Ākepa, HCRE = Hawai‘i Creeper, IIWI = ‘Iiwi, ELEP = Hawai‘i ‘Elepaio, OMAO = ‘Ōma‘o, APAP = ‘Apapane, HAAM = Hawai‘i ‘Amakihi, JAWE = Japanese White-eye, RBLE = Red-billed Leiothrix.



Appendix. 2 Partial least squares path model. We used partial least squares (PLS) path modeling (Sanchez 2013) to test the hypothesis that a species' susceptibility to environmental change might be predicted by its life history strategy (Jiguet et al. 2007, Reif et al. 2010). Because these two factors were complex and integrative, they were treated as two latent variables indirectly measured by the following indicators. First, body mass, feeding guild, adult survival and recruitment were used as formative indicators of life history; in other words, we assumed that life history was, at least in part, determined by the combination of these formative factors. Second, the population growth rate λ , the long-term (1987-2007) trend estimate in the open forest section of Hakalau (Cramp et al. 2010, their Table 1), and the global conservation status were used as reflective indicators of a species' susceptibility to environmental change; in this case, reflective indicators were the consequence, not the cause, of the underlying latent variable. Following Sanchez (2013), unidimensionality of reflective indicators was tested by performing an eigenanalysis of the correlation matrix (if a block is unidimensional, the first eigenvalue should be $\gg 1$ whereas the second eigenvalue should be < 1), and by calculating Cronbach's alpha, Dillon-Goldstein's rho, and correlations between latent variables and their indicators (also called loadings) (for all three, values greater than 0.7 are considered acceptable). Loadings were obtained by running a single analysis taking as input the average of the posterior sample for adult survival and recruitment. However, the path coefficient (result of the inner regression between latent variables), which was our main parameter of interest, was obtained by adopting the following procedure accounting for parameter uncertainty: (i) a posterior sample of adult survival and recruitment was drawn at random for each species; (ii) the path coefficient was estimated; steps (i) and (ii) were repeated 1,000 times to obtain the distribution of the path coefficient.

Unidimensionality of reflective factors in our PLS path model was rejected: Cronbach's $\alpha = 0.51$, first eigenvalue of the correlation matrix = 1.73, second eigenvalue = 1.21, and the correlation between the population growth rate λ and its latent factor was 0.50 for the 'constant' approach and null for the 'best CMR' approach. Only the Dillon-Goldstein's rho was acceptable (0.75). As it turns out, our three potential reflective indicators were either not correlated, or show evidence of a negative association. For instance, vulnerable species at the global scale tended to have more favorable trends during the 1987-2007 period in the open-forest section of Hakalau (linear regression between trend and status: $t = 3.01$, $P = 0.017$), but the local (Nauhi) population growth rate was not related to long-term population trends ($t = -0.74$, $P = 0.48$) or global vulnerability ($t = 1.05$, $P = 0.32$). Because our objective was to determine whether a species' life history strategy could play a role in species' decline and vulnerability observed beyond the apparent refuge area of Hakalau, we ran a new analysis where only 'status' was used as a reflective factor of a species' susceptibility to environmental change. The latter was the analysis presented in the main text.

Fig. A2.1 Graphical display of our full path model comprising two submodels: the inner model shows the relationship between latent variables (in circles); the outer model shows the relationships between each latent variable and its block of indicators (in squares). Two variables potentially reflective of the susceptibility to environmental change were either included or excluded from the analysis: the Nauhi population growth rate during the 1994-1999 period (this study), and the long-term population trend (1987-2007) in the whole open-forest section of Hakalau (Cramp et al. 2010). See text for details.



Appendix. 3 Recapture rate estimates derived from integrated population models. We give the estimates (Est.) based on $\phi_1 p_1 r_1$ (the 'constant' approach = c.m), the arithmetic mean calculated across 'best CMR' models only (b.m), and the DIC-based weighted average (w.m) inferred across the full set of converged models (n.m), together with the corresponding (total) standard deviation (c.s, b.s and w.s, respectively). See Table 2 for additional information on the models used. See text for further explanations.

Species	Est (mean)			Est (SD)		
	c.m	b.m	w.m	c.s	b.s	w.s
‘Akiapōlā‘au	0.663	0.678	0.604	0.145	0.140	0.286
Hawai‘i ‘Ākepa	0.428	0.428	0.451	0.119	0.119	0.120
Hawai‘i Creeper	0.361	0.366	0.363	0.077	0.076	0.078
‘I‘iwi	0.180	0.268	0.180	0.025	0.104	0.025
Hawai‘i ‘Elepaio	0.341	0.452	0.346	0.042	0.191	0.042
‘Ōma‘o	0.343	0.334	0.343	0.082	0.084	0.082
‘Apapane	0.136	0.290	0.136	0.067	0.253	0.067
Hawai‘i ‘Amakihi	0.230	0.308	0.239	0.023	0.114	0.088
Japanese White-eye	0.219	0.405	0.219	0.073	0.112	0.073
Red-billed Leiothrix	0.210	0.377	0.214	0.037	0.230	0.045

Appendix. 4 JAGS code for the 'constant' integrated population model (the 'constant' approach = c.m: $\phi_1 p_1 r_1$). Note that the code allows to simultaneously estimate the mark-recapture parameters (survival = surv.C; recapture rate = p.cap.C) independently of the abundance (count) data.

model

{

#-----

PRIORS AND CONSTRAINTS

#-----

for(i in 1 : n.ind) {

for(t in f[i] : (T.CMR -1)) {

s[i,t] <- surv

p[i,t] <- p.cap

s.C[i,t] <- surv.C

p.C[i,t] <- p.cap.C

}

}

surv ~ dunif(0, 1)

surv.C ~ dunif(0, 1)

p.cap ~ dunif(0, 1)

p.cap.C ~ dunif(0, 1)

Recruitment

rec ~ dunif(0,10)

Precision

tau ~ dgamma(0.0001, 0.0001)

sigma <- 1/sqrt(tau)

Intial population sizes

N.1[1] ~ dnorm(5000, 0.0001)I(0,)

N.ad[1] ~ dnorm(5000, 0.0001)I(0,)

#-----

DERIVED PARAMETERS

#-----

for(t in 1 : (T.count + T.predict - 1)) {

```
lambda[t] <- N.breed[t+1] / N.breed[t]
```

```
}
```

```
#-----
```

```
# LIKELIHOOD FOR IPM
```

```
#-----
```

```
#-----
```

```
# For census data
```

```
#-----
```

```
#-----
```

```
# System process
```

```
#-----
```

```
for (t in 2 : (T.count+T.predict) ) {
```

```
  esp.n.juv[t] <- rec * N.breed[t-1]
```

```
  N.1[t] ~ dpois(esp.n.juv[t])
```

```
N.ad[t] ~ dbin(surv, round(N.breed[t-1]))
```

```
}
```

```
for(t in 1 : (T.count+T.predict) ) {
```

```
N.breed[t] <- N.1[t] + N.ad[t]
```

```
}
```

```
#-----
```

```
# Observation process
```

```
#-----
```

```
for(t in 1 : T.count) {
```

```
count[t] ~ dnorm(N.breed[t], tau)
```

```
}
```

```
#-----
```

```
# For capture-recapture data
```

```
#-----
```

```

# CJS model

for(i in 1 : n.ind) {
# define latent state at first capture
z[i, f[i] ] <- 1
      for(j in (f[i] + 1) : T.CMR) {
        # state process
z[i,j] ~ dbern(mu1[i,j])
mu1[i,j] <- s[i,j-1] * z[i,j-1]
        # observation process
CH[i,j] ~ dbern(mu2[i,j])
mu2[i,j] <- p[i,j-1] * z[i,j]
      }
}

#-----
# LIKELIHOOD FOR CMR ONLY
#-----

# CJS model

for(i in 1 : n.ind) {

```

```

# define latent state at first capture
z.C[i, f[i] ] <- 1
    for(j in (f[i] + 1) : T.CMR) {
        # state process
        z.C[i,j] ~ dbern(mu1.C[i,j])
        mu1.C[i,j] <- s.C[i,j-1] * z.C[i,j-1]
        # observation process
        CH.C[i,j] ~ dbern(mu2.C[i,j])
        mu2.C[i,j] <- p.C[i,j-1] * z.C[i,j]
    }
}

} # End Model

```

Appendix 5. Parameter estimates derived from integrated population models (complement to Table 2). For each species, we give the global conservation status, the number of models that satisfied our convergence criterion (n.m, the 'converged' models), and the number of converged models used to estimate parameter value for the 'best CMR' models (n.b, max = 2). For 3 parameters (adult survival, ϕ , recruitment, r , and population growth rate, λ), we give the estimates (Est.) based on $\phi_1 p_1 r_1$ (the 'constant' approach = c.m), the arithmetic mean calculated across 'best CMR' models only (b.m), and the DIC-based weighted average (w.m) inferred across the full set of converged models (n.m), together with the corresponding (total) standard deviation (c.s, b.s and w.s, respectively). Note that the contribution of $\phi_t p_t r_t$, for which identifiability issues are expected on the last year of the study, was always null for c.m (by definition) and b.m ($\phi_t p_t$ was never a component of the best model; see Table 1 and below), and negligible in the calculation of w.m (all DIC weight $< 4 \times 10^{-28}$; not shown). Other notes: (^) for 'Ākepa, n.b was constrained to be one, as we only kept $\phi_1 p_1 r_1$ while excluding $\phi_1 p_1 r_t$ because of a lack of suitable data to estimate time-dependent recruitment estimates (not shown); (*) for 'Ōma'ō and 'Apapane, none of the two potential 'best CMR' models satisfied our convergence criterion (i.e., n.b = 0), so we used the 2nd best model for 'Apapane ($\phi_1 p_t$, Akaike weight = 0.223; compare with Table 1), and the 3rd best model for 'Ōma'ō ($\phi_1 p_1$, Akaike weight = 0.228). Conservation status: E = Endangered, V = Vulnerable, LC = Least Concern. See text for further explanations.

Species	Status	n.m	n.b	Par	Est (mean)			Est (SD)		
					c.m	b.m	w.m	c.s	b.s	w.s
'Akiapōlā'au	E	12	2	φ	0.680	0.648	0.657	0.112	0.102	0.115
				r	0.250	0.297	0.273	0.124	0.202	0.127
				λ	0.928	0.937	0.928	0.089	0.169	0.090
Hawai'i 'Ākepa	E	11	1^	φ	0.817	0.817	0.733	0.112	0.112	0.187
				r	0.354	0.354	0.444	0.190	0.190	0.198
				λ	1.172	1.172	1.179	0.167	0.167	0.241
Hawai'i Creeper	E	12	2	φ	0.830	0.822	0.833	0.082	0.080	0.083
				r	0.216	0.239	0.213	0.086	0.119	0.087
				λ	1.045	1.060	1.045	0.033	0.081	0.033
'I'iwi	V	5	1	φ	0.601	0.638	0.601	0.048	0.055	0.048
				r	0.427	0.390	0.427	0.049	0.055	0.049
				λ	1.028	1.028	1.028	0.010	0.010	0.010
Hawai'i 'Elepaio	V	4	1	φ	0.836	0.889	0.844	0.045	0.054	0.045
				r	0.180	0.127	0.172	0.049	0.057	0.049
				λ	1.016	1.016	1.016	0.023	0.022	0.023
'Ōma'ō	V	4	2*	φ	0.583	0.598	0.583	0.076	0.086	0.076
				r	0.418	0.405	0.418	0.076	0.100	0.076
				λ	1.000	1.002	1.000	0.009	0.042	0.009
'Apapane	LC	4	1*	φ	0.407	0.195	0.407	0.114	0.059	0.114
				r	0.622	0.833	0.622	0.114	0.060	0.114
				λ	1.029	1.029	1.029	0.016	0.017	0.016
Hawai'i 'Amakihi	LC	8	1	φ	0.703	0.775	0.672	0.036	0.047	0.036
				r	0.283	0.210	0.314	0.037	0.048	0.037
				λ	0.986	0.986	0.986	0.012	0.011	0.012
Japanese White-eye	LC	8	2	φ	0.531	0.746	0.531	0.109	0.087	0.109
				r	0.442	0.230	0.442	0.112	0.117	0.112
				λ	0.972	0.976	0.972	0.030	0.066	0.030
Red-billed Leiothrix	LC	10	2	φ	0.763	0.813	0.757	0.063	0.075	0.063
				r	0.249	0.204	0.255	0.066	0.106	0.066
				λ	1.012	1.017	1.012	0.025	0.064	0.026