Modeling Effects of Environmental Change on Wolf Population Dynamics, Trait Evolution, and Life History

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Supporting Online Material

www.sciencemag.org/cgi/content/full/334/6060/1272/DC1
Materials and Methods
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Modeling Effects of Environmental Change on Wolf Population Dynamics, Trait Evolution, and Life History

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Environmental change has been observed to generate simultaneous responses in population dynamics, life history, gene frequencies, and morphology in a number of species. But how common are such eco-evolutionary responses to environmental change likely to be? Are they inevitable, or do they require a specific type of change? Can we accurately predict eco-evolutionary responses? We address these questions using theory and data from the study of Yellowstone wolves. We show that environmental change is expected to generate eco-evolutionary change, that changes in the average environment will affect wolves to a greater extent than changes in how variable it is, and that accurate prediction of the consequences of environmental change will probably prove elusive.

Populations of the same species living in different environments often differ genetically or phenotypically. For example, the frequency of the genotype that determines whether a gray wolf (*Canis lupus*) has a black or gray coat varies with forest cover throughout North America (*1*). Similarly, wolves that predominantly feed on large prey are typically larger than those that specialize on smaller species (*2*). Numerous studies of a range of species also have reported that population dynamics and life history can vary across populations living in different environments (*3, 4*). In addition to these cross-population differences, environmental change within a population can generate rapid change in life history parameters such as generation length, in phenotypic trait and genotype distributions, and in population dynamics (*5, 6*). The eco-evolutionary consequences of environmental change are sometimes repeatable (*7*) but are frequently not (*8*). The wide range of population responses means that predicting likely dynamics has become one of the greatest challenges currently facing biology (*5*). This is particularly true for species, such as the gray wolf, that play important roles in structuring ecosystems, because their response to environmental change can have cascading effects across trophic levels (*9*). Given that environmental change can lead to potentially complex genetic, phenotypic, life history, and demographic responses, how can its likely consequences be explored? We show how integral projection models (IPMs) (*10*) provide a powerful framework to simultaneously investigate the ecological and evolutionary consequences of environmental change. We developed, applied, and analyzed one to explore how Yellowstone wolves may respond to environmental change.

Yellowstone National Park has experienced substantial environmental change in recent decades, with elk numbers declining, bison numbers increasing, and woody vegetation regenerating in some areas. These changes have been attributed variously to climate change, fluctuations in culling rates, and the reintroduction of wolves (*11*–*14*). Change is ongoing, with elk and bison numbers still trending in the same directions and further climate change being predicted (*15*). The

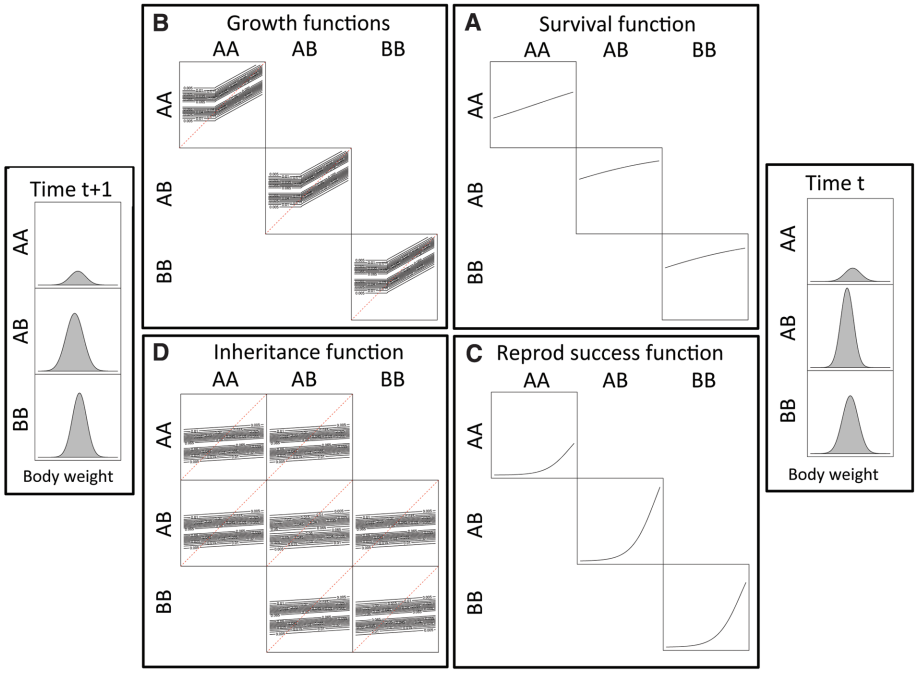

Fig. 1. (A to D) Graphical representation of the IPM that maps the bivariate distribution of genotype and body weight at time *t* to a new distribution at time *t* + *1*. Functions (B) and (D) are probability density functions showing the range of *y* values for each *x* value; both of these functions are identical across genotypes. Associations between body weight and both survival and reproductive success varied with genotype, whereas growth rates and inheritance did not. Equations for these functions and parameter values can be found in tables S1 and S2. The body weight and genotype distributions at times *t* and *t* + *1* are, respectively, on the right and left of the functions to provide a graphical representation of the mathematical structure of the IPM (SOM).

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Yellowstone wolf population has been extensively monitored since its introduction in 1995–1996 (*16*). We used survival and reproductive success data, body weights, and genotype at the K locus (*CBD103*, a β-defensin gene that has two alleles and determines coat color) collected from 280 radio-collared wolves living in the park between 1998 and 2009. Body weight and genotype at the K locus vary across U.S. wolf populations, and both traits influence fitness (*1, 2, 17*).

We constructed an IPM (Fig. 1) describing the temporal dynamics of the bivariate distribution of body weight and genotype [supporting online material (SOM)]. The model consists of functions (Fig. 1) describing how density dependence and environmental variation influence associations between body size and genotype at the K locus and (Fig. 1A) annual survival, (Fig. 1B) the probability of a surviving individual growing from weight z at time t to weight z' at time $t+1$ (the growth function), (Fig. 1C) annual reproductive success, and (Fig. 1D) the probability that a parent of body weight z at time t produces an offspring with body weight z' at time $t+1$ when the offspring recruits to the population (the inheritance function). Plasticity is captured by the growth and inheritance functions (Fig. 1), which capture how individuals of identical genotypes and body weight at time t can develop to different sizes at $t+1$ and produce recruiting offspring of different sizes. The functions constituting the IPM describe how "mass" of the genotype–body weight distribution is added, removed, and transformed by the fundamental biological processes of reproduction, inheritance, survival, and development (*10*). IPMs are a very general class of model, because all populations can be characterized as fluctuating distributions of phenotypic traits and genotypes, and because adding, removing, and transforming mass are the only ways to change the shape of a distribution or its size (the area under the distribution) (*18*). Because of their generality, it is possible to calculate many population biology parameters of both ecological and evolutionary interest from IPMs (*18–22*). We calculated population size, the mean and variance of body weight, the strength of viability and fertility selection on body weight, and genotype frequencies at each time step in a 500-year simulation and the means and variances in lifetime reproductive success and generation time for each cohort (*18*). Although we report results for populations at equilibrium, IPMs can be used to investigate transient dynamics.

IPMs can be parameterized for any system where repeated phenotypic measurements are taken from marked individuals, survival and reproductive rates are recorded, and the phenotype is measured across parents and offspring (*10*). Complete population coverage is not necessary, and biases in data can be statistically corrected (*20*). Stochastic IPMs require data collected from multiple censuses and are straightforward to parameterize (SOM). We used generalized linear mixed models (*23*) to statistically identify the survival, annual reproductive success, growth, and inheritance functions. The function describing how body weight and genotype influenced annual reproductive success (Fig. 1) is the product of two functions: one describing how body weight and genotype influenced the probability of reproducing (fertility function), and one describing the number of offspring produced conditional on successful reproduction (offspring number function). The growth function consists of two probability density functions, one each for wolves <41.7 kg and ≥41.7 kg. Survival and annual reproductive success functions differed with genotype; growth and body weight inheritance functions did not (Fig. 1). Population density was retained as a fixed effect in all functions (table S1 and fig. S1), and year was always retained as a random effect (SOM). Each function includes an intercept (for the average year) and an associated standard error describing how the intercept varies with time as the environment fluctuates. In Yellowstone wolves, such fluctuations are caused in part by temporal variation in snow depth, prey availability, and disease (*24–26*). We explored the consequences of environmental change by altering the means and standard deviations of the intercept distributions. Increasing the value of the mean intercept for the survival function, for example, mimics the effect of environmental change that improves average annual survival rates, whereas increasing the standard error of the distribution mimics environmental change that increases temporal variation in survival rates. We initially assumed no correlation in intercepts across functions. However, by imposing covariation between intercepts across functions, we explored how both positive and negative correlation in the values of function intercepts affects conclusions (SOM).

The model performed well in predicting key features of the wolf population (Table 1A) and provided insight into the dynamics of the coat color genotype. The IPM predicts that black heterozygotes have higher annual survival rates and annual reproductive rates, longer generation times, and greater lifetime reproductive success than either of the homozygotes (Table 1B). The substantial difference in fitness between black heterozygote and black homozygote wolves suggests that coat color per se might not be the cause of the heterozygote advantage—camouflage cannot explain the maintenance of the polymorphism. Presumably some other function of the gene, perhaps via its role in cellular immunity, determines the fitness differences (*27*).

Altering the mean environment affected all of the population biology parameters we calculated, with different parameters being most sensitive to changes in the mean value of intercepts of different functions (Fig. 2). For example, population size was most sensitive to perturbation of the intercept for the fertility function; coat color frequency was most sensitive to perturbations of the survival function intercept; the strength of viability and fertility selection was most sensitive to perturbation of the intercept of the body weight growth function for wolves ≥41.7 kg; and generation length was most sensitive to perturbation of the inheritance function. The way a population responds to environmental change, and which ecological or evolutionary parameters are most affected, depends on which functions are altered.

The direction of change in pairs of parameters can differ depending on the function intercepts that are perturbed (Fig. 2), demonstrating that different types of environmental change can

Table 1. Model performance. (**A**) Comparison between parameters estimated directly from data and those predicted from the baseline model. (**B**) Genotype-specific predictions of demographic rates and selected life history parameters.

A

Population biology parameter	Observed	Predicted
Mean population size	104.83	111.23
Minimum population size	59.00	93.72
Maximum population size	174.00	149.25
Frequency of gray coat	0.56	0.62
Generation length	5.05	4.70
Dispersion of reproduction	10.13	9.87
Mean body weight	44.25	45.15
Strength of viability selection	0.27	0.24
Strength of fertility selection	4.89	4.06

B

Genotype	AA	AB	BB
Phenotype	Black	Black	Gray
Annual survival rate	0.47	0.77	0.75
Annual recruitment rate	0.08	0.28	0.24
Generation length	2.4	4.91	4.5
Mean lifetime reproductive success	0.031	2.35	1.83
Mean frequency	0.02	0.36	0.62

generate a wide range of eco-evolutionary responses. For example, perturbing the mean intercept of the fertility function reduces the strength of viability selection and increases mean body weight, whereas perturbing the growth rate function for wolves ≥41.7 kg increases both the strength of viability selection and mean body weight. These results help explain why such a wide range of eco-evolutionary responses to environmental change is observed in nature (*5, 6*): the consequences of environmental change depend on whether survival, reproduction, development, or inheritance is most affected.

What are the consequences of altering how variable the environment is? Perturbing the standard deviation of the intercept distributions for each function, and the correlation in intercepts across functions, had little effect on all population biology parameters (Fig. 2). In a population model, it is straightforward to independently perturb the mean environment or how variable the environment is (*28*). In reality, environmental change alters both means and variances of year effects. However, our results suggest that changes in the average environment are likely to affect Yellowstone wolves to a much greater extent than changes in environmental variability.

Why do we see these results? Environmental variation causes the shape and size of the distribution to change from one time step to the next, but density dependence means that no part of the distribution consistently grows or shrinks with time—the genotype–body weight distribution attains a stationary stochastic distribution. When a function is changed, a new stationary stochastic distribution is attained, and the number of individuals at each genotype–body weight combination changes. As the shape and size of the stationary stochastic distribution change, so do the summary statistics that population biologists use to characterize aspects of the distribution, whether these parameters are calculated for each time step or for each cohort (Fig. 2). Perturbing different functions changes the stationary stochastic distribution that the population converges to.

If dispersal can be ignored, simultaneously predicting the dynamics of individual genotypes and phenotypes, life history parameters, and population dynamics only requires the identification of survival, reproductive success, development, and inheritance functions. There are many systems where such models could be constructed (SOM). Despite this, accurately predicting eco-evolutionary responses to environmental change for density-dependent populations living in variable environments is challenging. Environmental drivers that influence functions need to be identified. Biologists have made progress in characterizing how the environment can influence parameters in some of the functions that constitute

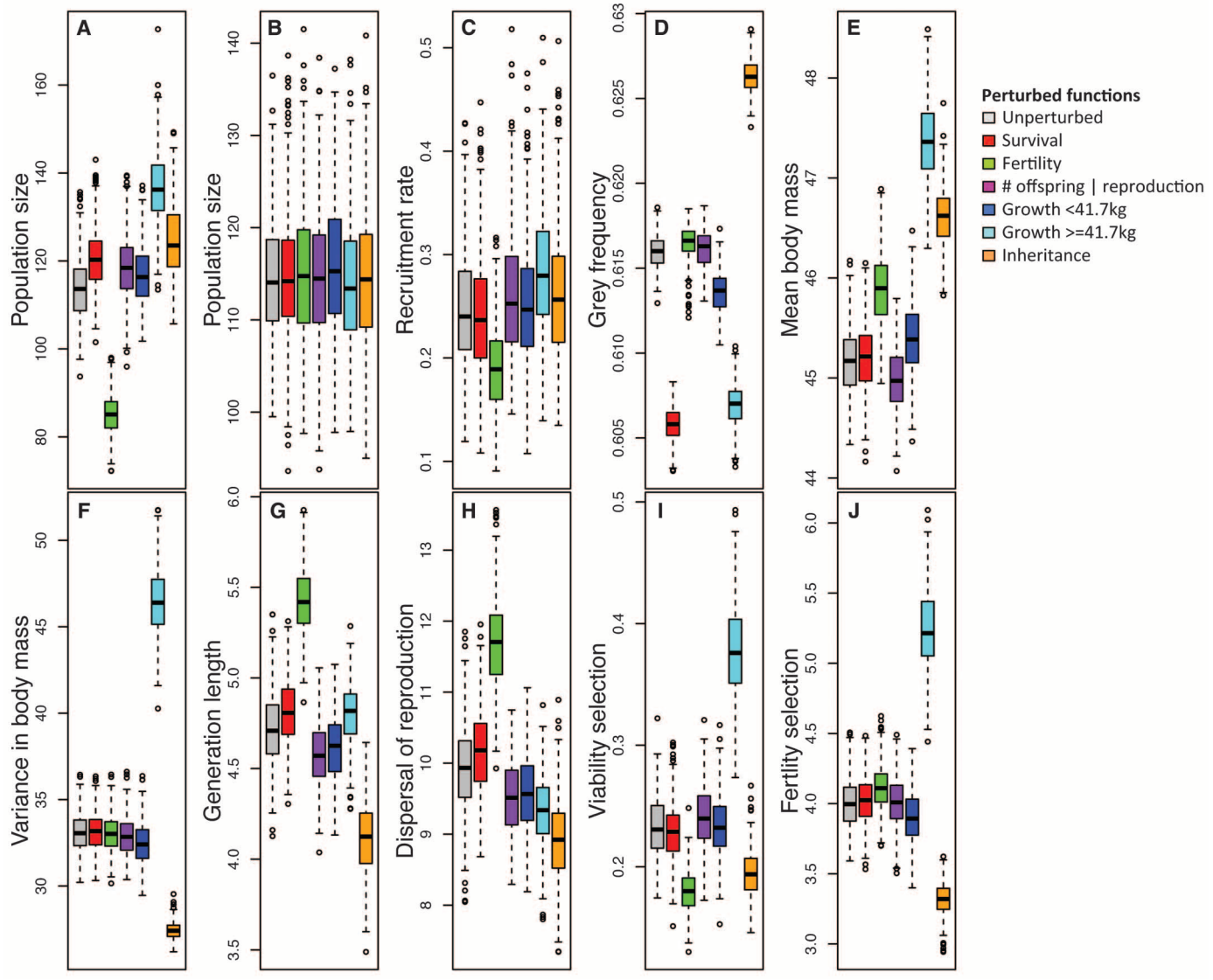

Fig. 2. Consequences of perturbing the mean value of function intercepts (**A**) and (**C** to **J**) and the standard deviation of the intercept distribution (**B**) on the distribution of various population biology parameters. The gray distributions represent values from a simulation with no function perturbed, and the colored distributions are from simulations in which one intercept distribution was perturbed. The dispersion of reproduction is the variance in generation length (SOM).

an IPM (*29*), but we are unaware of any field studies where drivers have been identified for all functions. Even if environmental drivers are identified, predicting how they may change in the future is currently unfeasible, because the environment that populations experience is complex, consisting of abiotic and biotic drivers that can interact, sometimes nonlinearly (*30*). Currently, the best that can probably be done is to explore the consequences of environmental change scenarios. For example, if we assume changes that reduce the mean of each intercept by 10%, we predict decreases in mean population size and the strength of both viability and fertility selection; no change in coat color frequencies; and increases in the variance in population size, mean body size, and generation length. In reality, we have little idea of the extent to which environmental change will affect each function, because key environmental drivers have yet to be identified for all functions, and the dynamics of those that have been identified are not well understood (*24*–*26*).

Although accurate prediction is currently not possible, our results do reveal that, for Yellowstone wolves, (i) environmental change will inevitably generate eco-evolutionary responses; (ii) change in the mean environment will have more profound population consequences than changes in the environmental variance; and (iii) environmental change affecting different functions can generate contrasting eco-evolutionary dynamics. Because IPMs are sufficiently general and because density dependence and environmental variation affect most populations, these conclusions are likely to extend to other systems. The construction and analysis of IPMs across a range of systems may provide support for this proposition. In addition to providing a tool to explore eco-evolutionary dynamics, IPMs have also been extended to include spatial variation and to identify evolutionarily stable strategies (*21, 22*), giving them potential to unify several subdisciplines of population biology, including population ecology, quantitative genetics, population genetics, and life history theory. They have not yet been extended to incorporate processes that generate novel genetic variation; the results we report arise via the shuffling of existing phenotypic and genetic variation via selection and plasticity. Our findings suggest that existing phenotypic and genetic variation within Yellowstone wolves is sufficient for environmental change to generate substantial evolutionary change that will occur in tandem with shifts in wolf life history and population dynamics. Although accurate prediction of the eco-evolutionary consequences of environmental change is currently unfeasible for most natural populations, our results help explain why it so widespread, and perhaps inevitable.

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Supporting Online Material

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Inhibition of Pyruvate Kinase M2 by Reactive Oxygen Species Contributes to Cellular Antioxidant Responses

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Control of intracellular reactive oxygen species (ROS) concentrations is critical for cancer cell survival. We show that, in human lung cancer cells, acute increases in intracellular concentrations of ROS caused inhibition of the glycolytic enzyme pyruvate kinase M2 (PKM2) through oxidation of Cys^{358}. This inhibition of PKM2 is required to divert glucose flux into the pentose phosphate pathway and thereby generate sufficient reducing potential for detoxification of ROS. Lung cancer cells in which endogenous PKM2 was replaced with the Cys^{358} to Ser^{358} oxidation-resistant mutant exhibited increased sensitivity to oxidative stress and impaired tumor formation in a xenograft model. Besides promoting metabolic changes required for proliferation, the regulatory properties of PKM2 may confer an additional advantage to cancer cells by allowing them to withstand oxidative stress.

Control of the intracellular concentrations of reactive oxygen species (ROS) is critical for cell proliferation and survival. In cells treated with growth factors, transient increases in ROS concentrations are implicated in enhanced cell proliferation through inhibition of phosphotyrosine phosphatases and PTEN, which allows amplification of tyrosine kinase and phosphatidylinositol-3 kinase (PI-3K) signaling pathways (*1*). However, high concentrations of ROS can also damage cellular components and compromise cell viability (*2*). Tumor suppressor and oncogenic pathways frequently mutated in cancer commonly result in increased accumulation of ROS (*3*–*7*). Furthermore, conditions associated with tumorigenesis such as hypoxia, matrix detachment, mitochondrial dysfunction, and inflammation can all lead to excess production of ROS (*8*–*12*). Therefore, cancer cells are particularly challenged in dealing with oxidative stress (*2*, *13*).