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Redesigning the genetic architecture of phenotypically plastic traits in a changing environment

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Normal development depends on specific genetic and environmental inputs. When environments change, entire populations of organisms may simultaneously express maladaptive phenotypes. Selection in the new environment may gradually restore the ancestral phenotype by favouring alleles that counteract the environmental perturbation. This evolutionary process is called genetic compensation, and its effect on the fate of novel phenotypes is opposite to that of genetic assimilation. When genetic compensation occurs along a spatial environmental gradient, it results in the geographic pattern known as countergradient variation. Another place to look for genetic compensation is where human activities are causing environmental changes that affect how traits develop. For example, pollutants with endocrine-disrupting effects are altering the reproductive behaviour of natural populations of animals. If such pollutants persist long enough for genetic compensation to occur, the animals may come to depend on the presence of these chemicals for normal development. Taking genetic compensation into account could enhance our understanding of the role of behaviour in evolution in at least three ways: first, behavioural interactions are often the source of selection against environmentally induced phenotypes; second, behavioural traits themselves may often be targets of genetic compensation; and third, behavioural plasticity can delay or prevent genetic compensation. I present examples to illustrate each of these points, and further explore the ramifications of this understudied and underappreciated evolutionary process. *Biological Journal of the Linnean Society*, 2014, **112**, 276–286.

ADDITIONAL KEYWORDS: behavioural plasticity – climate change – endocrine disruption – genetic accommodation – genetic compensation – phenotypic plasticity – sex determination.

INTRODUCTION

Phenotypic plasticity in general, and behavioural plasticity in particular, may enable organisms to persist in novel environments (Baldwin, 1896; Waddington, 1942; Yeh & Price, 2004; Crispo, 2007; Tuomainen & Candolin, 2011). Adaptive plastic responses may help account for the success of invasive species (Sol & Lefebvre, 2000; Tuomainen & Candolin, 2011; but see Palacio-Lopez & Gianoli, 2011), and may also influence which species persist through periods of rapid climate change (Reed, Schindler & Waples, 2011). Combined with natural selection, plasticity may enable organisms to adapt more rapidly than would be predicted by evolutionary models that do not take plasticity into account (Behera & Nanjundiah, 2004; Lande, 2009; Fierst, 2011). Adaptive plastic responses may, in effect, lead the way and enable organisms not only to persist in new environments but also to reach new adaptive peaks through genetic accommodation (Table 1; Pigliucci & Murren, 2003; Price, Qvarnstrom & Irwin, 2003; West-Eberhard, 2003; Bateson, 2005; Ghalambor *et al*., 2007; Moczek *et al*., 2011).

On the other hand, not all plastic responses are adaptive. Some traits are plastic because of constraints on development or performance

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Table 1. Definitions of key terms

Term	Definition
Genetic accommodation	gene-frequency changes caused by selection in response to environmentally (or genetically) induced changes in the phenotype
Genetic assimilation	a form of genetic accommodation in which environmentally induced phenotypes gradually become canalized and develop in the absence of the triggering environmental stimulus
Genetic compensation	a form of genetic accommodation in which ancestral phenotypes are restored in the presence of a phenotype-altering environmental stimulus

These definitions are taken from Grether (2005). See text for further information on the relationship between genetic assimilation and genetic compensation; see West-Eberhard (2003) for a detailed treatment of genetic accommodation.

(West-Eberhard, 2003). Evolved reaction norms can only be expected to be adaptive within the range of environments that the organism experienced in the past (Ghalambor *et al*., 2007). Evolutionary biologists tend to view maladaptive plastic responses as relatively unimportant. After all, maladaptive phenotypes, by definition, have low Darwinian fitness, and so it is logical to assume that they are evolutionary dead ends. But there are at least two crucial differences between 'environmental mutants' and genetic mutants. First, maladaptive plastic responses cannot be purged by selection as easily as can genetic mutations. Although susceptibility to environmental perturbation may be heritable, the maladaptive phenotypes are only expressed and exposed to selection in individuals that have been exposed to the environmental influence. Second, and more importantly, when environments change, entire populations of organisms may simultaneously exhibit maladaptive plastic responses. This can occur when a species expands its range, the climate changes, the availability or quality of a resource changes, habitat degradation occurs, or the environment becomes polluted, and so on.

When an environmental change that triggers a maladaptive plastic response persists for multiple generations, selection will increase the frequency of alleles that counteract the environmental influence, shifting the population mean of the affected trait back towards the optimum. A general term for this process, which can be applied to environmental change over both time and space, is genetic compensation (Johnson & Black, 1998; Hale, 2000; Grether, 2005); also see Levinton, 1983). When genetic compensation occurs along a spatial environmental gradient, it results in the geographic pattern known as countergradient variation, in which genetic variation counteracts environmental variation, resulting in reduced phenotypic variation along the gradient (Levins, 1968; Conover & Schultz, 1995). When genetic compensation is complete, populations in different environments will differ in the genetic basis of traits that appear to be phenotypically identical. Conover, Duffy & Hice (2009) suggested that genetic compensation is synonymous with the evolution of countergradient variation, but countergradient variation patterns could arise from other processes, and genetic compensation does not necessarily generate a geographic pattern. Both terms are useful, one for describing an evolutionary process and the other for describing a geographic pattern.

Genetic compensation is similar to genetic assimilation (Waddington, 1942, 1953, 1961), in that both processes involve the selective accumulation of alleles that alter the norm of reaction to an environmental factor (Table 1). But they are opposites in terms of their effects on the fate of environmentally induced phenotypes (Grether, 2005). In genetic compensation, the novel phenotype has lower fitness than the ancestral phenotype, and thus selection acts to restore the ancestral phenotype in the new environment (Fig. 1A, B). In genetic assimilation, the novel phenotype has higher fitness than the ancestral phenotype, and thus selection favours alleles that increase the probability of producing the novel phenotype (Fig. 1C, D). Both processes can occur with or without canalization. Canalization leads to the fixation of the optimal trait in the new environment (Fig. 1B, D). Without canalization, the trait remains sensitive to future changes in the environmental factor (Fig. 1A, C).

Genetic compensation is inherently difficult to detect because the pattern that it produces at the phenotypic level is indistinguishable from stasis. 'Common garden' experiments are needed to see whether genetic variation is masking the effects of an environmental gradient (Levins, 1968; Conover & Schultz, 1995). When the environment has changed over time, genetic compensation may be impossible to detect, simply because the ancestral forms no longer exist. Nevertheless, there are ample opportunities to study the process in action. The environment is constantly changing in ways that affect how traits develop, and some of these changes are quite predictable because we humans are causing them. For a well-documented example of genetic compensation in life-history traits in response to anthropogenic

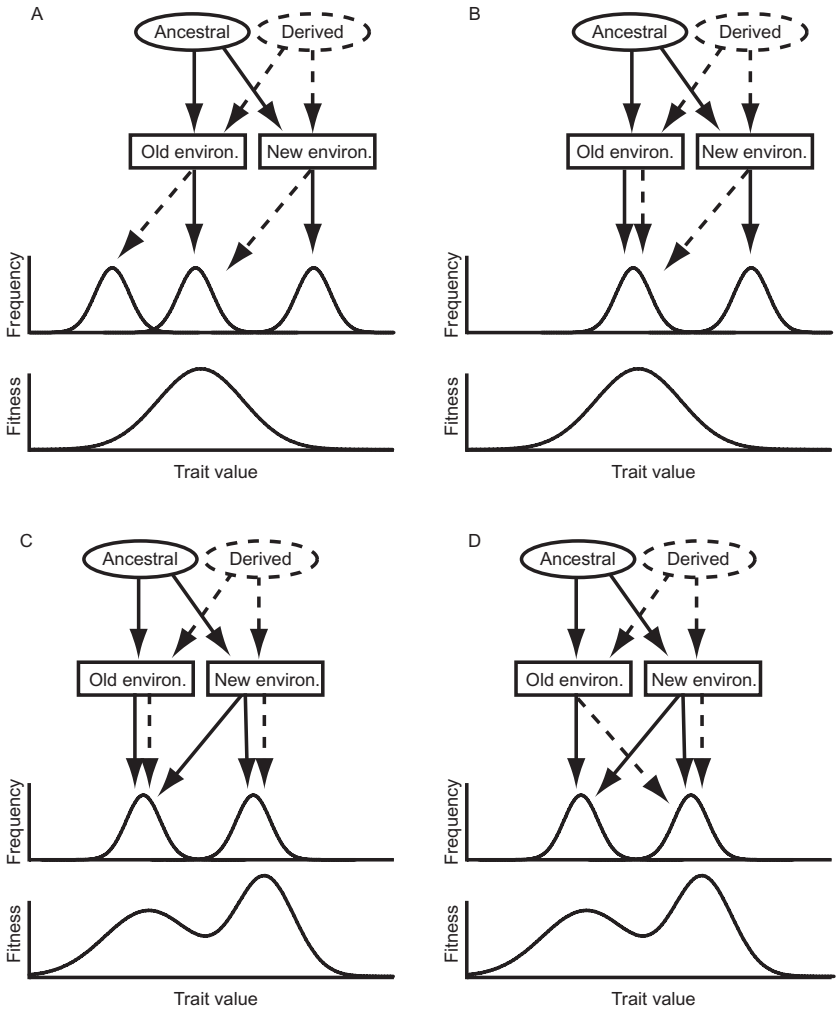

Figure 1. Schematic comparison of genetic compensation without canalization (A), genetic compensation with canalization (B), partial genetic assimilation (C), and full genetic assimilation (D). The upper graph in each panel shows the phenotype distribution under different developmental scenarios, and the lower graph shows the fitness landscape for a trait of interest. Solid arrow pathways show how the ancestral population develops in the old and new environments. Dashed arrow pathways show how development proceeds in the derived population after multiple generations of selection. Under genetic compensation (A and B), the ancestral population develops suboptimally in the new environment. Selection favours genetic changes that shift the mean trait value of the population back towards the fitness peak, thereby restoring the ancestral phenotype. In (A), individuals in the derived population are well adapted to the new environment, but develop suboptimally in the old environment; the level of canalization remains unchanged relative to the ancestral condition. In (B), individuals in the derived population develop the ancestral phenotype in both environments, and thus canalization has increased relative to the ancestral condition. Under genetic assimilation (C and D), the new environment causes some individuals in the ancestral population to develop novel, high fitness-trait values. Selection favours genetic changes that increase the probability of producing the novel trait. In (C), individuals in the derived population reliably produce the novel trait in the new environment, but still produce the suboptimal ancestral phenotype in the old environment. In (D), individuals in the derived population produce the novel trait in both environments. Development is canalized relative to the ancestral condition in both (C) and (D), but more so in (D). Note that in (A) and (B), the ancestral phenotype is favoured in both environments, whereas in (C) and (D) the novel phenotype is favoured in both environments. Figure and legend reproduced from Grether (2005) with permission from the University of Chicago Press.

environmental change, see Carroll *et al*.'s study of the soapberry bug *Jadera haematoloma* (Carroll, Dingle & Klassen, 1997; Carroll, Klassen & Dingle, 1998).

GENETIC COMPENSATION AND THE ROLE OF BEHAVIOUR IN EVOLUTION

Thus far, maladaptive responses to environmental change have largely been left out of the debate about the role of behaviour in evolution. Behaviour can play at least three distinct roles in genetic compensation. First, behavioural interactions are often the source of selection against environmentally induced phenotypes. Second, behavioural development is susceptible to perturbation by environmental change, and thus behavioural traits themselves may often be targets of genetic compensation. Third, behavioural plasticity can delay or prevent genetic compensation by buffering organisms against the effects of environmental change. Below I present examples to illustrate each of these points. The broader goal is to show that taking genetic compensation into account can enrich our understanding of how populations respond to both natural and anthropogenic sources of environmental change.

The first example involves a natural resource gradient in *Poecilia reticulata* (the guppy). In this case, a female mate preference appears to have driven genetic compensation in an environmentally sensitive male secondary sexual character, resulting in reduced phenotypic variation along the gradient. This may reduce gene flow between populations because male migrants have low mating success. Second, I will review evidence that endocrine-disrupting chemicals are adversely affecting the reproductive behaviour and morphology of wild populations of vertebrates. Populations that do not decline to the point of extinction may become dependent on these exogenous chemicals for normal development via genetic compensation. Lastly, I will highlight one of the many ways in which genetic compensation may be relevant for predicting the effects of climate change. The specific issue considered is whether reptiles with temperature-dependent sex determination can adapt rapidly enough to keep pace with anthropogenic temperature change. This is a question about the rate of genetic compensation in thermal reaction norms. To the extent that behavioural plasticity ameliorates the effects of temperature change, it may delay genetic compensation.

Evolutionary responses to changes in carotenoid availability

Male *P. reticulata* have complex and highly polymorphic colour patterns that nearly always include orange spots (Haskins *et al*., 1961; Endler, 1978). Not long ago it was assumed that the orange colour is produced by orange carotenoid pigments, but it is actually produced by a combination of the yellow carotenoid tunaxanthin and the red pteridine drosopterin (Grether, Hudon & Endler, 2001a; Hudon, Grether & Millie, 2003). Drosopterin is synthesized from carbohydrates and amino acids, whereas tunaxanthin is obtained by metabolic conversion of ingested carotenoids (Hudon *et al*., 2003). In the Northern Range of Trinidad, the primary sources of carotenoids for *P. reticulata* are unicellular algae, which grow on rocks in the streambed. Algae availability generally increases in the downstream direction, as rivers widen and make larger gaps in the forest canopy (Grether *et al*., 2001b). Waterfalls restrict dispersal, which enables *P. reticulata* populations to become adapted to the local conditions (Endler, 1995; Reznick *et al*., 1996). The standing crop of algae increases with canopy openness, and carotenoid availability for *P. reticulata* is closely linked to algal standing crops (Grether, Hudon & Millie, 1999). The *P. reticulata* populations at the sites with the highest levels of carotenoid availability ingest the most carotenoids, as measured by gut content analysis, and the males collected at these sites have the highest concentrations of carotenoids in their orange spots. These and other results demonstrate that the coloration of *P. reticulata* is limited by carotenoid availability in the wild (Grether *et al*., 1999).

Population level changes in carotenoid availability, such as occurs when *P. reticulata* colonize new sites, must cause population-level changes in the carotenoid content of the orange spots. Nevertheless, the ratio of carotenoid and drosopterin pigments in the orange spots remains relatively constant across sites along the carotenoid availability gradient (Grether *et al*., 2001a). A common garden experiment showed that geographic variation in drosopterin production is largely genetic (Grether, Cummings & Hudon, 2005). This is a countergradient pattern in that genetic variation in drosopterin production counteracts the effects of the carotenoid availability gradient on the pigment ratio.

The axis of colour variation that is most directly affected by the pigment ratio is the hue of the orange spots (Grether *et al*., 2005). Tunaxanthins and drosopterins have different absorbance spectra, and thus the shape of the orange spot reflectance spectrum depends on the ratio of the two pigments (Grether *et al*., 2001a). To human eyes, the orange spots appear more yellow (and less red) as the carotenoid/drosopterin ratio increases. Geographic variation in the drosopterin content of the orange spots nearly cancels out the effect of the carotenoid availability gradient on a measure of perceived hue based on

P. reticulata vision (Grether *et al.,* 2005). A plausible explanation for this countergradient pattern is that females discriminate among males on the basis of the hue of their orange spots. It has long been known that female *P. reticulata* prefer males with larger and more chromatic orange spots, but a hue preference had not been demonstrated.

To test for a hue preference, Deere *et al*. (2012) arranged for females to choose among males with different carotenoid/drosopterin ratios. To generate males for the mate-choice tests, they crossed females from a low-drosopterin population with males from a high-drosopterin population, and vice versa, and then carried out full-sib crosses in the F_1 generation. F_2 males were raised to maturity on a standardized carotenoid diet so that most of the variation in the pigment ratio was caused by genetic variation in drosopterin production. Compared with the parental populations, the F_1 males were intermediate in drosopterin production, and the F_2 males showed a wide range of variation in drosopterin production (Deere *et al*., 2012). In mate-choice trials, females from the parental populations were asked to choose among F_2 males with differing carotenoid/drosopterin ratios. Females preferred males with intermediate drosopterin levels, and the preferred pigment ratio was nearly the same for both wild populations (Deere *et al*., 2012). This shows that females do not simply prefer males with greater orange spot chroma; instead, the ratio of the pigments, and therefore the hue of the orange spots, also affects male attractiveness.

In the wild, we would not expect females to always prefer males with intermediate drosopterin levels, and especially not if carotenoid availability has recently changed. Consider what must happen when *P. reticulata* colonize new sites above waterfalls, as evidently has happened many times in Trinidad (Seghers, 1973; Endler, 1978). Sites above waterfalls tend to be more heavily shaded by the forest than the downstream sites. This means that the colonists are likely to experience lower carotenoid availability than the site from which they came. Male migrants and their male offspring will develop carotenoid/drosopterin ratios below that preferred by females: a maladaptive plastic response to the change in carotenoid availability. Selection for increases in the ratio would be expected to favour reductions in drosopterin production.

When *P. reticulata* disperse between existing populations that differ in carotenoid availability, male migrants and their offspring are likely to develop suboptimal pigment ratios, and have lower mating success than resident males. Thus, one consequence of genetic compensation is that it may reduce gene flow between existing populations, as appears to be the case in *Oncorhynchus nerka* (Pacific salmon; Craig, Foote & Wood, 2005; Grether, 2005). Many factors are thought to contribute to patterns of gene flow in *P. reticulata* (Russell & Magurran, 2006; Magellan & Magurran, 2007; Sievers *et al*., 2012), but the influence of genetic compensation has not been investigated. Testing for incipient reproductive isolation caused by genetic compensation would require carrying out mate-choice tests on migrants and their offspring in the field, or mimicking the effects of the relevant environmental changes in the laboratory (e.g. the change in dietary carotenoid levels).

Evolutionary responses to endocrine-disrupting pollutants

Effects and prevalence of endocrine-disrupting chemicals

There is an extensive literature on the effects of endocrine-disrupting chemicals (EDCs) in the environment (Colborn, vom Saal & Soto, 1993; Crews, Willingham & Skipper, 2000; McLachlan, 2001; Sumpter & Johnson, 2005; Crews & McLachlan, 2006; Wingfield & Mukai, 2009; Carere *et al*., 2010). Many endocrine disruptors mimic or block endogenous hormones by binding hormone receptors. Others stimulate hormone synthesis or degradation. Most of the documented phenotypic effects can be described as feminization or de-masculinization of males, or masculinization of females. Most studies of endocrine disruption focus on physiological or morphological traits, but behaviour is disrupted as well (e.g. Palanza *et al*., 1999; Bell, 2001; Clotfelter, Bell & Levering, 2004; Garcia-Reyero *et al*., 2009; Partridge, Boettcher & Jones, 2010; Saaristo *et al*., 2010; Frederick & Jayasena, 2011; Shenoy & Crowley, 2011; Tuomainen & Candolin, 2011).

Hundreds of studies have shown endocrine-disrupting effects of common pollutants in aquatic animals (reviewed by Scholz & Mayer, 2008). One of the most potent endocrine disruptors is synthetic oestrogen (ethynylestradiol), which is used in birth control pills, and many other EDCs also have their effects by binding oestrogen receptors (McLachlan, 2001). The pesticide dichlorodiphenyltrichloroethane (DDT) is an endocrine disruptor (Fry & Toone, 1981), as are many of the pesticides still in wide use (Colborn *et al*., 1993; Palanza *et al*., 1999). Compounds in plastics, paint, and industrial waste of various kinds also make their way into the environment, and can have chronic endocrine-disrupting effects on populations of animals, including humans (Colborn *et al*., 1993; Patisaul & Adewale, 2009; Carere *et al*., 2010). Some of these compounds mainly affect marine or aquatic animals, but others, such

as the common industrial pollutant methylmercury, bioaccumulate and move up the food chain. One important difference between endocrine disruptors and other types of pollutants is that, in the case of EDCs, there may be no threshold level below which the chemical has no negative effect because the threshold is already exceeded by the endocrine system itself (Crews *et al*., 2000). Any increase or decrease in hormone titres is likely to have a phenotypic effect.

Specific examples of endocrine disruption

To set the stage for discussing the evolutionary consequences of chronic exposure to endocrine disruptors, I briefly review five illustrative examples.

1. In *Gasterosteus aculeatus* (the three-spined stickleback), oestrogenic compounds and anti-androgens, such as the pesticide fenitrothion, reduce the production of a glue protein (spiggin) that males use in nest building (Sebire *et al*., 2009). This results in reductions in nest building and courtship behaviour.
2. Fish populations downstream from wastewater treatment plants are exposed to a cocktail of endocrine-disrupting chemicals, with potentially synergistic effects. In a study carried out in England, *Rutilus rutilus* (the roach) raised in effluent from a wastewater treatment plant almost all developed as females (Lange *et al*., 2011). The sex-reversed fish were capable of reproducing as females, but they had much lower reproductive success than genetic females, especially in the presence of genetic females.
3. In a study on the effects of methylmercury on *Eudocimus albus* (the white ibis), over 50% of exposed males paired up and nested with other males (Frederick & Jayasena, 2011). Males in homosexual pairs exhibited male-typical courtship behaviour, but they were less active in courtship and less aggressive to male intruders than the unexposed controls. Among the males that formed heterosexual pairs, males exposed to methylmercury were less active in courtship and had lower reproductive output (number of offspring fledged) than the controls (Frederick & Jayasena, 2011).
4. The herbicide atrazine is a potent endocrine disruptor that reduces the synthesis, secretion, and circulation of androgens in vertebrates (Hayes *et al*., 2011). Male *Rana pipiens* (leopard frogs) exposed to just 0.1 $\mu g\ L^{-1}$ atrazine develop oocytes in their testes, in addition to sperm (Hayes *et al*., 2003), a condition referred to as 'intersex'. The fitness consequences of intersex have not been examined in *Rana pipiens*, but in other species, such as *Pimephales promelas* (fathead minnows), intersex males lose out in competition with normal males (Martinović *et al*., 2007). A field survey of *Rana pipiens* in the USA showed that even populations in non-agricultural areas (where atrazine is not used) were exposed to atrazine at levels of 0.2 $\mu g\ L^{-1}$ or higher, and had the same sorts of gonadal abnormalities as frogs exposed to atrazine in the lab (Hayes *et al*., 2002).
5. The population-level consequences of endocrine disruption are debated, especially in cases in which EDCs convert males into reproducing females. In theory, converting males into females could increase the growth rate of a population, but it also reduces the effective population size, and may limit responses to selection (An *et al*., 2009; Cotton & Wedekind, 2009). To test for population-level effects of endocrine disruption on fish populations, synthetic oestrogen was added to a lake in Ontario for three consecutive years (Kidd *et al*., 2007; Palace *et al*., 2009). All four species of fish in the lake showed physiological signs of endocrine disruption: increased production of vitellogenin (VTG), which is a protein normally synthesized by females during egg maturation; intersex males were found in two species; and three species showed population declines. By all measures, the population most strongly affected was that of the *Pimephales promelas*, which collapsed in the second year of treatment, and did not rebound for at least 2 years after the chemical treatment ended (Kidd *et al*., 2007; Palace *et al*., 2009). Why this species was affected more strongly than the others is not known.

Evolved resistance to endocrine disruption

Whereas the population-level consequences of endocrine disruption may be difficult to predict, any disruption of the normal hormonal balance that alters morphology and behaviour is likely to reduce the fitness of affected individuals. Thus, chronic endocrine disruption should select for resistance to these chemicals (Crews *et al*., 2000; Hayes *et al*., 2003; Crews & McLachlan, 2006; Carere *et al*., 2010; Shenoy & Crowley, 2011). There are several ways that resistance might evolve. Hormone receptors could evolve greater ligand specificity, such that they continue to bind endogenous hormones but stop binding synthetic hormones and other chemicals with hormone-like properties (Crews *et al*., 2000). Most documented cases of endocrine disruption involve oestrogen receptors. Oestrogen receptors have rather low binding specificity, so there may be some scope for enhanced receptor specificity (Crews *et al*., 2000). Perhaps the most likely way for resistance to EDCs to evolve is for hormonal set points to adjust to the level

of endocrine disruptors in the environment until normal development is restored. Such adjustments might involve changes in endogenous hormone production, in receptor numbers, or in the pathways that link receptor outputs to development. For example, in the case of *Gasterosteus aculeatus* (see above), selection in the presence of oestrogenic chemicals might act to restore the optimum level of spiggin production and nest-building behaviour, thereby masking the effects of the chemicals. Hormonal set points clearly can evolve, because closely related species often have very different hormone titres. This may be one of the reasons that EDCs affect some species more strongly than others (Crews *et al*., 2000). Evolved shifts in hormonal set points could result in a situation in which populations in polluted areas become dependent on external sources of hormones for normal development. The extent to which this is happening, or has already happened, is unknown. In amphibians, another possible route to evolving resistance would be to delay gonadal development until after the aquatic phase. Indeed, *Rana pipiens* populations exposed to atrazine show high levels of gonadal dysgenesis (Hayes *et al*., 2003), which is essentially a failure of the gonads to differentiate during the larval phase. Gonadal dysgenesis might be an evolved mechanism for postponing sexual differentiation until after the animals metamorphose and leave the polluted water (Hayes *et al*., 2003).

Any evolutionary response that reverses the phenotypic effects of endocrine disruption would qualify as genetic compensation. An evolved increase in receptor specificity would be an example of genetic compensation with canalization, whereas an evolved shift in hormonal set points would be an example of genetic compensation without canalization (see Fig. 1).

Genetic compensation could potentially have been detected in the whole-lake experiment with synthetic oestrogen (see above). Not all male *Pimephales promelas*s had oocytes in their testes, and even during the population collapse, some fish managed to reproduce (Kidd *et al*., 2007), which suggests individual variability for selection to act upon. A comparison of sensitivity to synthetic oestrogen before and after this intense bout of selection might have revealed a response to selection. Detecting evolved responses to endocrine disruption may not be quite so straightforward, however, because some endocrine disruptors have transgenerational effects via mechanisms such as DNA methylation (reviewed by Crews & McLachlan, 2006). To separate evolved responses from epigenetic effects, it may be necessary to raise animals from exposed and unexposed sites through multiple generations in a common environment before testing for differential responses to EDCs.

Evolutionary responses to climate change

Climate change could trigger genetic compensation in a multitude of ways (Grether, 2005; Baumann & Conover, 2011). Consider the effects of changes in temperature on reptiles with temperature-dependent sex determination (TSD). Several long-term studies of species with TSD have shown that sex ratios co-vary with annual temperature (e.g. Janzen, 1994; Wapstra *et al*., 2009). What will happen to these species when temperatures rise outside the range to which the species is adapted? Assessing the ability of TSD species to adapt to rapid climate change has been identified as an important conservation research priority (Wapstra *et al*., 2009; Mitchell & Janzen, 2010).

There is some evidence that TSD thresholds are heritable (McGaugh *et al*., 2011; Rhen *et al*., 2011), but the best evidence that sex-determining mechanisms can evolve in response to climate change comes from species distributed along altitudinal gradients. In *Niveoscincus ocellatus* (the snow skink), lowland populations have TSD but highland populations have genetic sex determination (GSD) (Pen *et al*., 2010). When females from the lowland population were housed under temperatures representative of warm years, they produced mostly daughters with early birthdates, but when they were housed under temperatures representative of cool years, they produced mostly sons with late birthdates. In contrast, females from the highland population produced approximately 50 : 50 sex ratios under both temperature regimes. Pen *et al*. (2010) showed that it is adaptive for lowland females to produce mostly daughters in warm years, and mostly sons in cool years, because females born early in the year have higher age-specific fecundity than those born later in the year. This is not true for the highland population, perhaps because the activity season is much shorter, birth dates are more synchronized, and growth rates are slower in the highlands. Furthermore, TSD would be selected against at the highland site because a high variation in temperature across years would lead to extreme sex ratios (Pen *et al*., 2010). If we assume that the lowland form represents the ancestral condition, and that the highlands were colonized from the lowlands, it is easy to see this as a genetic compensation scenario. In the low-temperature highland environment, females arriving from the lowlands would have produced mostly sons. Sex ratio selection would be expected to restore a 50 : 50 sex ratio, on average, either by shifting the TSD threshold downwards or by eliminating it altogether. A mathematical model parameterized for this species and taking into account the temperature variation across years showed that GSD readily evolves from TSD in this

scenario (Pen *et al*., 2010). This outcome represents genetic compensation with canalization.

In a 10-year study of another skink with TSD (*Bassiana duperreyi*), females compensated for rising temperatures behaviourally, by nesting deeper, and through shifts in the timing of oviposition. Behavioural compensation was not complete, however, and towards the end of the study the species had crossed the thermal threshold beyond which sex determination is purely genetic (50 : 50; Telemeco, Elphick & Shine, 2009). This illustrates the interplay between behavioural compensation and genetic compensation. As long as animals can adjust behaviourally, this may forestall selection, but once a behavioural limit is reached, genetic variation in the sex determination mechanism will be exposed to selection and a new thermal threshold may evolve. Alternatively, maternal temperature regulation behaviour itself might evolve, unless a true performance limit has been reached. Either way, the expected evolutionary outcome would be a reversal of the effects of climate change on the offspring sex ratio.

CONCLUSIONS

Whereas maladaptive phenotypes themselves may be hopeless monsters, the evolutionary responses they evoke can have some important consequences. Genetic compensation provides a route for the evolution of different developmental pathways to the same phenotype. In repeated cycles of environmental change and genetic compensation, the developmental pathway to a given phenotype may diverge even between populations subject to the same environmental fluctuations, because different mutations and allele combinations are likely to arise in different populations (Mani & Clarke, 1990). In effect, the genetic architecture of phenotypically plastic traits is continuously being redesigned by natural selection. Although genetic compensation causes phenotypic stasis in the short term, it may facilitate further local adaptation by reducing the fitness of interpopulation migrants and thereby slowing gene flow between populations, and may ultimately result in a cryptic form of ecological speciation (*sensu* Schluter, 2009). Finally, understanding how organisms adapt to environmental change is increasingly pertinent to conservation, and the policy recommendations might not always be intuitive. For example, if an endangered species became adapted to an endocrine disrupting pollutant, it might be unwise to suddenly ban the chemical. Controlling the use of such chemicals before they have evolutionary effects would be the prudent course of action.

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