PROCEEDINGS OF THE ROYAL SOCIETY B

Proc. R. Soc. B (2011) **278**, 2705–2713
doi:10.1098/rspb.2011.0971
Published online 15 June 2011

Review

The role of developmental plasticity in evolutionary innovation

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Explaining the origins of novel traits is central to evolutionary biology. Longstanding theory suggests that developmental plasticity, the ability of an individual to modify its development in response to environmental conditions, might facilitate the evolution of novel traits. Yet whether and how such developmental flexibility promotes innovations that persist over evolutionary time remains unclear. Here, we examine three distinct ways by which developmental plasticity can promote evolutionary innovation. First, we show how the process of genetic accommodation provides a feasible and possibly common avenue by which environmentally induced phenotypes can become subject to heritable modification. Second, we posit that the developmental underpinnings of plasticity increase the degrees of freedom by which environmental and genetic factors influence ontogeny, thereby diversifying targets for evolutionary processes to act on and increasing opportunities for the construction of novel, functional and potentially adaptive phenotypes. Finally, we examine the developmental genetic architectures of environment-dependent trait expression, and highlight their specific implications for the evolutionary origin of novel traits. We critically review the empirical evidence supporting each of these processes, and propose future experiments and tests that would further illuminate the interplay between environmental factors, condition-dependent development, and the initiation and elaboration of novel phenotypes.

Keywords: genetic accommodation; genetic assimilation; novelty; developmental plasticity

1. INTRODUCTION

Identifying the factors that promote the origin of complex, novel traits is among the most intriguing and enduring problems in evolutionary biology [1]. It is intriguing because it lies at the heart of what motivates much of evolutionary biology: to understand the origins of exquisite adaptations, and the transitions and radiations that they fuelled. It is enduring because it embodies a fundamental paradox. On the one hand, Darwin's theory of evolution is based on descent with modification, wherein everything new, ultimately, must come from something old [2]. On the other hand, biologists are captivated by complex novel traits precisely because they often lack obvious homology to pre-existing traits [3]. How, then, does novelty arise within the confines of ancestral developmental patterns and variation?

In this review, we describe how the study of developmental plasticity can offer significant insights into the origins of evolutionary innovation. We define evolutionary innovation broadly, ranging from the expression of traits or trait variants that are themselves novel to the expression of existing traits in new behavioural, physiological or morphological contexts. Developmental plasticity, in turn, is defined as a single genotype's ability to alter its developmental processes and phenotypic outcomes in response to different environmental conditions. Such environmental effects on trait expression can range from modest adjustments to growth rate or tissue allocation in response to resource levels, to dramatic polyphenic switches by which a single genotype can give rise to discrete and often radically different alternative phenotypes [4]. Intriguingly, many innovations of macroevolutionary significance also occur as facultatively expressed alternatives in related lineages (figure 1; electronic supplementary material, table S1). This raises the central questions our article aims to address: can major novel traits originate as plastic, environment-dependent alternatives to already established, ancestral phenotypes? If so, what are the mechanisms by which developmental plasticity may mediate the initiation and subsequent elaboration of incipient novel traits?

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Electronic supplementary material is available at http://dx.doi.org/10.1098/rspb.2011.0971 or via http://rspb.royalsocietypublishing.org.

Received 9 May 2011
Accepted 24 May 2011

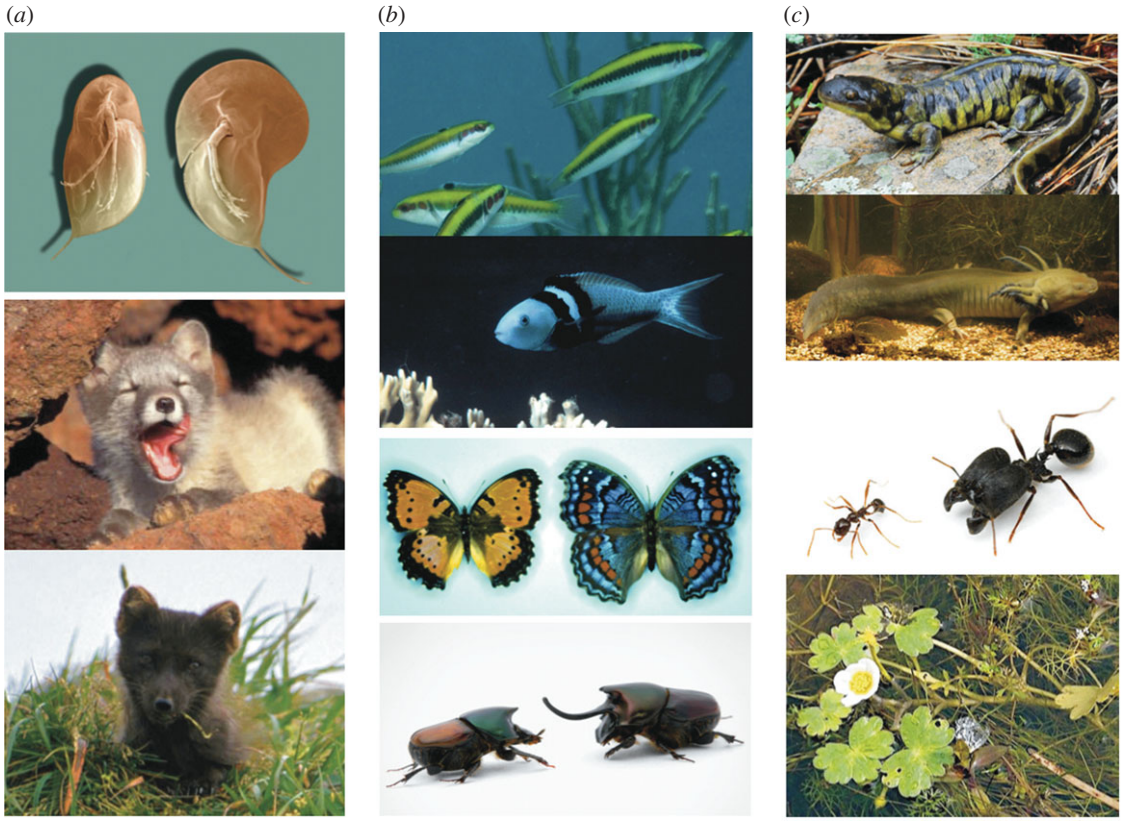

Figure 1. Environmentally dependent polyphenism in various taxa. (*a*) The water flea *Daphnia longicephala* develops protective crests and tail spines in response to its water bug predator, *Notonecta*. Differences in coat colour and texture are produced in Arctic fox (*Vulpes lagopus*) in response to seasonal change. (*b*) When a bluehead wrasse (*Thalassoma bifasciatum*) male (blue morph) is removed from his harem, a female (yellow morph) will change phenotype completely and become a male. The gaudy commodore, *Precis octavis*, is seasonally dimorphic. In the wet season, it has an orange wing and in the dry season the wings are bluish purple in colour. *Onthophagus nigriventris* dung beetles metamorphose as horned major males or hornless sneaker males in response to ample or insufficient larval feeding resources, respectively. (*c*) The tiger salamander (*Ambystoma tigrinum*) only metamorphoses if its aquatic environment becomes uninhabitable. Larval nutrition determines major and minor worker development in *Pheidole rhea*. The morphology of white water-buttercup (*Ranunculus aquatilis*) leaves depends on their environment. Submerged leaves are branched into 20 or more thread-like segments. Floating or exposed leaves are scalloped.

The notion that plasticity promotes innovation is not new. Indeed, researchers have suggested for over a century that developmental plasticity is crucial in the formation of evolutionary novelties (reviewed in [5]). What is new, however, is that we are finally beginning to grasp the underlying mechanisms by which developmental plasticity might promote innovation. Our goal is therefore to integrate knowledge of these mechanisms with theory and thereby explain how developmental plasticity promotes innovation. We begin by reviewing the causes, mechanisms and consequences of genetic accommodation, a process by which environmentally induced phenotypes can become subject to heritable modification [5–7]. We then explore the means by which developmental and genetic mechanisms associated with environmentally induced alternatives influence the subsequent evolutionary potential of a lineage. Finally, we investigate the developmental genetic architectures that underlie environment-dependent trait expression and discuss their implications for the evolutionary origin of novel traits.

2. GENETIC ACCOMMODATION AND INNOVATION

Genetic accommodation is adaptive genetic change owing to selection on the regulation and form of a mutationally or environmentally induced novel phenotype [5,8,9]. Genetic accommodation does not require new mutations to occur, but it might incorporate such mutations along with standing genetic variation, including variants that were formerly cryptic, neutral or rare in a population. Genetic accommodation improves the function and integration of novel traits, and diminishes harmful pleiotropic effects. Genetic accommodation can also promote the persistence of developmental plasticity, refine the conditions under which alternative traits are expressed and enhance the precision of environmental matching. In extreme cases, such as when a population is exposed to a novel but relatively invariant environment, the novel phenotype can become constitutive, a phenomenon referred to as genetic assimilation [10]. Below, we briefly discuss the properties of development that fuel evolution by genetic accommodation. We then highlight empirical studies that advance our understanding of the significance of evolution by genetic accommodation.

(a) *Developmental and genetic mechanisms underlying genetic accommodation*

Organisms have evolved a diverse array of homeostatic mechanisms to buffer or canalize development against environmental perturbations. These mechanisms are best

understood in metabolic and physiological systems, but are also beginning to be elucidated in developmental genetic systems. Such mechanisms include feedback regulation, duplicate or redundant pathways, a balance between antagonistic processes and switch-like behaviour [11,12]. Several partially redundant homeostatic mechanisms may be at work simultaneously in a given system, a redundancy that further stabilizes the phenotype. Importantly, these same mechanisms can also protect a developing organism from genetic perturbations owing to mutations [13,14] (but see [15]). By acting as a phenotypic buffer against both environmental and genetic perturbations, homeostatic mechanisms permit the accumulation of greater genetic variability than would be possible in their absence. Cryptic genetic variation that accumulates in this manner is a component of, rather than separate from, the standing genetic variation in a population. Specifically, it represents standing variation that is phenotypically unexpressed under certain environmental or genetic circumstances and, as such, contributes to the potential for either genotype-by-environment or epistatic interactions to influence the evolutionary process.

The expression and rapid evolution of novel phenotypes become possible when the phenotypic effects of accumulated genetic variation become expressed though a change in the environment or a sensitizing mutation. Once expressed, such formerly cryptic genetic variation does not differ fundamentally from standing genetic variation for constitutively expressed traits. However, being unexpressed under a subset of conditions allows cryptic genetic variation that is neutral or even deleterious in some environments to persist in a population, analogous to models for recessive alleles.

How then does evolution by genetic accommodation differ from adaptive evolution as traditionally understood? In many ways, evolution by genetic accommodation provides a shift in emphasis, rather than a radically new view of adaptive evolution. Traditional neo-Darwinian perspectives on adaptive evolution generally envision a 'waiting for a mutation' process [16], by which adaptations emerge from the gradual accumulation and fixation of mutations that change phenotype expression in a direction favoured by selection. In such models, standing genetic variation is usually presented in the context of an equilibrium between new mutations and removal by selection (mutation–selection balance). Environmental conditions are important, because they determine the nature and direction of selection, whereas development provides the means by which genotype is translated into phenotype.

Although both genetic variation and the selective role of the environment remain key factors, evolution by genetic accommodation differs from this traditional model in two critical ways. First, it ascribes the additional role to the environment of releasing novel phenotypes that express previously accumulated genetic variation. In other words, the environment plays a formative as well as a selective role. Environmental perturbations can operate immediately on the level of populations and may persist for generations, potentially releasing substantial heritable variation to confront new conditions. Second, evolution by genetic accommodation emphasizes the role of developmental processes in determining which genetic variants will be manifested in selectable, phenotypic differences and under what environmental circumstances this will occur [5]. Critically, environment-dependent development permits genetic variants to be neutral under a larger set of circumstances, and thus to be hidden from selection, and allowed to drift and accumulate in natural populations. Evolution by genetic accommodation therefore expands beyond a traditional neo-Darwinian model by recognizing that the interplay between environment and development provides a mechanism for both the accumulation and the rapid release of genetic variation in the face of novel environmental challenges.

But what evidence exists to suggest that genetic accommodation can indeed yield novel, adaptive phenotypes under new conditions, and that this process shapes the evolutionary trajectories of natural populations?

(b) *Artificial selection experiments demonstrate genetic accommodation*

The earliest demonstration of evolution by genetic accommodation through artificial selection was Waddington's study on cross-vein expression on *Drosophila* [17]. Cross veins contribute to torsional stiffness of the wing, and vary in presence/absence and position within the Diptera [18]. When exposed to ecologically relevant temperature stress during development, flies expressed phenotypic variation for loss of cross veins, otherwise observed at low frequency in natural populations (0.5%). Using artificial selection, Waddington demonstrated that this variation was heritable, and that the initially induced phenotype could rapidly become constitutively expressed in a population. Waddington and others further demonstrated that a variety of phenotypes could become genetically assimilated under artificial selection [19]. Subsequent work demonstrated that unexpressed standing genetic variation was responsible [20], and that segregating variation was widespread in natural populations [21]. Similar results for plants were obtained by Huether [22,23], who demonstrated that the rare expression of flower morph variants in *Linanthus* was, in part, the result of environmental stress experienced by plants in the field. Huether then demonstrated that such stress-induced variation was indeed heritable via artificial selection, suggesting that here, too, environmental conditions were responsible for revealing selectable heritable variation.

More recently, laboratory studies on a broad array of organisms (including *Drosophila* [15,24], *Arabidopsis* [25], fungi [26] and Lepidoptera [8]) have focused on the role of temperature stress and heat shock proteins as a means of releasing selectable phenotypic diversity (but see [27]). In these studies, environmental stress resulted in a remarkable increase in the amount of selectable phenotypic variation, mediating rapid responses to artificial selection—including some reminiscent of naturally evolved phenotypes [8]. Artificial selection experiments have thus demonstrated unequivocally that developmental systems confronted with challenging environments can expose novel phenotypic variants, which in turn provide sufficient substrate for rapid, selective evolution of novel forms.

(c) *Genetic accommodation in natural populations*

Demonstrating that genetic accommodation has occurred in natural populations is considerably more challenging than demonstrating that it can occur in the laboratory.

If genetic accommodation has played a role in the evolution of a particular novel trait, then we would predict that patterns of plasticity in ancestral populations should resemble the constitutively expressed trait differences observed in derived populations. A major impediment to testing this prediction is that ancestral populations are usually no longer available for study, making it difficult to characterize ancestral reaction norms. The best systems for testing this prediction are therefore those in which ancestral populations are extant [28–30]. Below, we describe several studies in which genetic accommodation has been inferred in natural populations.

Our first example comes from the house finch (*Carpodacus mexicanus*). *Carpodacus mexicanus* has colonized a remarkable range of environments during its recent invasion of North America, with resulting populations exhibiting extensive differentiation in physiological responses to environmental variation, including the induction of incubating behaviour and associated hormones in response to temperature variation. Available data indicate that such responses have been fine-tuned from plastic ancestors to produce local adaptation, giving rise to populations with divergent reproductive attributes after only 14 generations [29]. Systems that have undergone such recent and rapid evolution (see also [31]) provide excellent opportunities to accurately describe ancestral patterns of developmental plasticity.

Comparisons of longer-separated populations allow us to determine whether ancestral plasticity can contribute to greater novelty than that observed during contemporary evolution. An example comes from the most recent diversification of three-spine stickleback fish initiated as glaciers retreated 12 000 years ago. As oceanic stickleback invaded shallow lakes, giving rise to bottom-feeding (benthic) populations, and deep lakes, giving rise to planktivorous (limnetic) populations, differences in habitat use favoured differentiation of suites of functionally integrated traits including trophic morphology, body form and behaviour. Experiments reveal that ancestral, oceanic populations exhibit phenotypic plasticity that parallels differentiation among independently replicated freshwater benthic and limnetic ecotypes, but which are of lesser magnitude [32,33]. These results are consistent with the possibility that ancestral plasticity has guided the evolution of more extreme features characteristic of the derivative ecotypes. Combined, these examples demonstrate how ancestral plasticity can be refined or enhanced in derived populations.

When a single aspect of the phenotype is strongly favoured, canalization of an initially inducible response can also evolve rapidly. For example, introduction of salmonid predators to alpine lakes inhabited by the zooplankter *Daphnia melanica* has led to a loss of plasticity in an antipredator defence [34]. Melanin protects *D. melanica* from UV light but renders them conspicuous to piscine predators. Following the introduction of salmonid predators to two lakes, *D. melanica* exhibited a substantial decline in UV-mediated plasticity of melanin production relative to that expressed in predator-free populations. Where predators were introduced, *Daphnia* exhibited constitutive upregulation of the arthropod melanin gene *ebony* and *Ddc* (dopa decarboxylase), both responsible for the adaptive reduction of melanin production. Reduced plasticity has also evolved in populations of three-spine stickleback from geologically recent (post-glacial) freshwater lakes in the expression of sodium–potassium ATPase (ATP1A1) [35] with adaptation to fresh water, and in New World spadefoot toad species that exhibit constitutively short larval development as a result of their short natal pond durations [36]. Additional evidence of genetic assimilation is found in the apparent loss of ancestral polyphenisms across diverse taxa (electronic supplementary material, table S1).

Two important insights arise from the preceding examples. First, comparisons of 'ancestral' and derived populations may vary with respect to how long such populations have diverged, presenting a potential trade-off between the accuracy of assessing ancestral reaction norms, and the uniqueness of a novel, derived trait. Secondly, although these examples demonstrate patterns consistent with those we would expect from genetic accommodation [5,10], the fundamental features of this process—that environmental stimuli initiate genetic and selection processes—make it impossible to discriminate cases of natural selection on environmentally dependent versus constitutively expressed variation once natural selection has occurred [37]. Nevertheless, the evidence for an environmentally dependent origin of novelty is, in such cases, as strong as that for an origin based on constitutively expressed standing genetic variation.

3. DEVELOPMENTAL PLASTICITY AND EVOLVABILITY

Developmental plasticity can increase the evolutionary potential, or 'evolvability', of developmental systems in three important ways, thereby increasing a lineage's potential for diversification and innovation. We discuss each of these three ways separately below.

(a) *Developmental plasticity provides new targets for evolutionary processes*

Once environmentally mediated development has evolved, the underlying mechanisms can promote evolutionary diversification by increasing the points in ontogeny at which change can potentially arise, thus increasing the degrees of evolutionary freedom [38]. A consensus is emerging that diversity in multicellular organisms primarily reflects changes in the regulatory interactions that shape gene expression [39–41]. Highly complex regulatory interactions are precisely what characterize plastic phenotypic expression [42]. In plastic developmental systems, environmental conditions influence development at various points in ontogeny via multiple external and somatic signals. External signals are transduced into cellular ones by means of hormones, metabolites, receptor molecules, nervous signals, osmotic changes and physical interactions among cells. This broad and diverse regulatory dimensionality dramatically increases the potential evolutionary change points. Additionally, because these regulatory systems are highly epistatic, change in any one genetic element can lead to novel phenotypic effects [38].

Furthermore, the different components underlying plastic regulatory systems can evolve independently of one another, thereby diversifying the evolutionary trajectories available to a lineage, including those that may eventually lead to novel, adaptive phenotypes. Such diverse evolutionary opportunities are exemplified by the many cases of threshold evolution in insects [4,19,43], evolved

divergences in response cues and response mechanisms in plants [44,45], and timing and magnitude of plastic responses in amphibians [46,47].

(b) *Plasticity promotes novelty by providing 're-usable' building blocks for development*

Plastic developmental systems also promote evolutionary novelty because shared regulatory modules—including both the transduction or switch mechanism and the downstream pathways of phenotypic expression—can be re-used and recombined in new ways in different descendent taxa and environmental circumstances. Several recent studies reveal how a common transduction event can activate divergent phenotypic responses. In plants, for instance, phytochromes are a family of photo-convertible molecules found in above-ground plant cells that initiate the complex signalling pathways involved in shade plasticity [48]. Phytochromes are activated by specific wavelengths of transmitted and reflected light that stimulate sensitive and rapid growth adjustments, such as stem and petiole elongation that lifts leaves away from shade cast by neighbouring plants—a 'shade-avoidance syndrome' shown to be adaptive [49]. Interestingly, plants have evolved to use the phytochrome sensory system to switch on an entirely different suite of plastic responses: the production of defensive compounds in response to herbivory via the jasmonate signalling pathway [50]. Both shade avoidance and defence plasticity use this diffuse sensory system, which can read environmental conditions at any of the plant's leaves or branches to initiate either elongation or biosynthetic responses within minutes. Similarly, in insects, the same endocrine machinery plays a critical role in coordinating alternative reproductive decisions (whether to invest in growth and maintenance or reproduction), alternative developmental decisions (moulting and metamorphosis) and polyphenic development (facultative diapause, host switch, caste and morph expression [51]). Re-use and recombination of developmental machinery underlying plastic responses have also been implicated in nematode evolution, where dafachronic acid (DAF-12)-mediated induction of *dauer*-stage formation (an adaptive response to food shortage widespread across nematodes) has become co-opted to mediate the induction of alternative feeding morphologies in at least one species, *Pristionchus pacificus* [52].

Conversely, different environmental cues and transduction events can make use of a shared hormonal pathway or other common downstream module, 're-using' that response pathway to produce a similar plastic outcome in a novel ecological situation [42]. For instance, the plastic 'shade avoidance' response mentioned above consists largely of stem and petiole elongation. Rapid elongation of these same structures is also an essential plastic response to a plant's submergence under water (which can occur episodically in wetland habitats [53]). Both shade and flooding elongation responses are governed by shared hormonal pathways that interact with the DELLA family of growth-restraining proteins and expansin genes that affect cell-wall extensibility [48,54,55]. Yet these shared developmental pathways are initiated by entirely different environmental switches: light spectral composition in the case of shade avoidance and submergence-induced build-up of the gaseous hormone ethylene in case of flooding elongation [55].

(c) *Developmental plasticity creates novel trait interactions*

Patterns of phenotypic correlation among developmentally or functionally related traits vary from one environment to another when some or all of the constituent traits express plasticity [56,57]. As a result, plastic developmental systems can give rise to new trait interactions, trait covariances and fitness trade-offs that contribute to evolutionary diversification, as reported for learning ability in cabbage white butterflies [58] and diet-induced horn expression in beetles [59]. However, plasticity does not always result in a trade-off between traits: environmentally induced morphologies may simply act as a platform for the modification of additional traits that work well as a suite. For example, a shrimp diet can produce a short-gut morphology in species of spadefoot toads that do not normally consume shrimp. In other species, however, this environmentally induced change in gut morphology is accompanied by a suite of functionally integrated traits that jointly comprise a distinct ecological response [60]. The phylogenetic relationships of these lineages suggest that diet-induced gut plasticity in spadefoots was followed by the evolution of these drastic modifications of behavioural, morphological and physiological plasticity. Plastic traits that differ among related species can also interact with constitutive species-specific traits to shape environment-specific fitness outcomes [56].

These examples illustrate that, just as plasticity can contribute novel targets for evolutionary change, it may also help generate novel trait interactions. Accordingly, developmental plasticity may cause species and populations to diverge in many more traits than those specifically targeted by a given evolutionary mechanism. Such trait interactions can pose pleiotropic constraints on adaptive evolution, but also have the potential to shift the evolutionary trajectories available to lineages into phenotypic and ecological space that otherwise would remain unexplored.

4. DEVELOPMENTAL GENETIC BASIS OF PLASTIC TRAITS: MECHANISMS AND CONSEQUENCES

The developmental genetic basis of conditional traits is just beginning to be explored, yet it is already clear that diverse mechanisms underlie environment-dependent trait expression [61]. Here, we briefly examine the implications of two extremes in a continuum of developmental control architectures. At one end of this continuum, the same developmental genetic network can mediate the expression of alternative phenotypes across environments by altering the nature of interactions between network components through environment-specific regulatory elements. For example, comparative gene expression data suggest that winged and wingless ant castes are produced developmentally through caste-specific interruption of the same wing-patterning network [62]. Although the points of interruption may differ among different wingless castes of the same species (as well as between species), the same network is involved in each case. Similarly, in horned beetles the same developmental mechanism—programmed cell death—is involved in generating both sexual and alternative male dimorphisms in horn expression [63], and recent microarray studies show that sexes and morphs overlap substantially in patterns of gene expression [64]. In such pleiotropic systems, the independent evolution of

alternative phenotypes can be constrained, as evolutionary changes affecting expression of one phenotype will affect other phenotypes regulated by the same developmental genetic network. These constraints would be relaxed only during periods when a given alternative morph was rare or absent.

At the same time, shared mechanisms can maintain a developmental system's ability to express environment-specific traits even during prolonged periods of environmental stasis when certain alternatives are not elicited. In this case, re-expression of such traits in descendent lineages, or their co-option into novel contexts, may become feasible with only minor evolutionary changes in the underlying developmental genetic network. Indeed, loss and recurrence of complex traits has been demonstrated in a number of cases [65], and co-option of ancestral developmental networks during the genesis of novel complex traits appears to be a ubiquitous feature of developmental evolution [66]. However, it remains unclear whether developmental plasticity and polyphenic development enhance retention and co-option of developmental pathways, or whether both emerge simply as a product of the integrated nature of development in general.

At the other end of the mechanistic continuum, distinct genes and gene networks may mediate the expression of alternative environmentally contingent phenotypes. Context-specific gene expression is extremely widespread [67] and may have evolved under selection to supersede the pleiotropic constraints discussed above, permitting organisms to fine-tune gene expression in each environmental context. Additionally, environment-specific gene expression can have unique and fundamentally important evolutionary consequences not shared by other types of context-specific expression. While tissue- and stage-specific expression occurs in every individual in a population, environment-specific expression is restricted to those individuals within a population and generation that encounter a given environment. If selective environments are coarse-grained (i.e. each individual encounters only one environment during its lifetime), then environmental frequencies determine the proportion of individuals within a population that expresses a given set of environment-specific phenotypes and underlying gene networks. Genes for which expression is restricted to a subset of individuals in each generation are predicted to experience relaxed selection, because mutations occurring in gene copies that reside in individuals who do not express these genes are hidden from selection. Mutations thus accumulate faster in these genes than they do in genes that are expressed in every individual [68].

Relaxed selection on components of environment-specific gene-regulatory networks provides a population-genetic mechanism by which developmental plasticity can contribute to the evolution of new traits. Specifically, population-genetic models predict that (i) the extent of mutation accumulation should scale with the proportion of unexpressed gene copies in a population [69]; (ii) conditionally expressed genes may diverge many times faster between species than similar genes for which expression is condition-insensitive [70]; and (iii) during prolonged periods of environmental stasis, genes that are *not* expressed may undergo rapid degradation and loss of function owing to continued mutation accumulation [67]. (iv) Additionally, periods of environmental stasis (and consistent selection) should allow genes that have become constitutively expressed to undergo rapid bursts of adaptive evolution, enabled, in part, by mutations accumulated during prior periods of relaxed selection on those genes.

The first three of these predictions are supported by a growing body of empirical evidence (reviewed in [67]). For instance, bacterial quorum-sensing genes, induced only when certain population densities are reached, show increased levels of variation within species when compared with similar, constitutively expressed genes [68]. In horn-polyphenic beetles, genes that are more specific to alternative morphs show greater divergence than genes for which expression is shared across morphs [64]; and in aphids, where sexual and asexual generations alternate, such that males are often expressed only once every 10–20 female generations, male-specific genes exhibit greatly accelerated divergence more consistent with relaxed selection than positive selection [71]. Studies on microbes also provide substantial support for the third prediction (i.e. that unexpressed genes should rapidly accumulate mutations and degrade during periods of environmental stasis [72]).

But what about the converse? As we propose above, genes that become constitutively expressed during periods of stasis should be subject to the full strength of positive selection rather than relaxed selection, such that mutations and mutation combinations accumulated during prior periods of relaxed selection on such genes can now promote their rapid adaptive evolution. Although little direct evidence is presently available to test this hypothesis, numerous studies have highlighted the importance of cryptic genetic variation that can be released during shifts into novel or stressful environments [73,74] to facilitate rapid adaptive evolution through genetic accommodation. Relaxed selection on environment-specific genes may provide a key mechanism by which such variations may accumulate.

We have discussed shared versus alternative developmental genetic networks as extremes along a continuum of models for the regulation of plastic trait expression. In real organisms, both types of regulatory architecture are probably involved, depending on the organism, trait and level of biological organization in question. Indeed, gene-expression surveys provide ample evidence that both environment-shared and environment-specific expression patterns are widespread [67]. Moreover, both types of regulation can apply to the same trait at different levels of a developmental genetic network: upstream regulators such as transcription factors tend to be highly pleiotropic, whereas their downstream targets may be expressed in a highly context-specific manner, and thus more likely to become subject to relaxed selection. Both regulatory models can even apply simultaneously to different parts of the same gene: protein-coding regions may be transcribed across environments, while the action of promoters may be environment-specific. A similar situation may apply in cases of context-specific splicing of exons (e.g. [75]).

Clearly, further integration of molecular, developmental and evolutionary mechanisms of conditional trait expression will require a much more detailed understanding of the developmental genetic machinery that underlies plasticity. Here, traditional as well as emerging model systems in developmental and evolutionary genetics have the

potential to make important, cross-fertilizing contributions. For instance, the role of dafachronic acid signalling has been studied in detail in the regulation of *dauer*-stage formation in the nematode and genetic model system *Caenorhabditis elegans*, and recent work has begun to explore the developmental co-option of the same pathway in the regulation of derived alternative feeding morphologies in related genera [52]. Similarly, a combination of population genetic and mapping studies on pea aphids permitted the identification of the *aphicarus* locus (which influences both sex- and environment-specific wing expression [76]), the regulatory role for which is currently being studied using candidate genes and pathways identified primarily through studies on *Drosophila* wing development [77]. Finally, the increasing availability and affordability of genetic and genomic techniques permit their application directly onto organisms famous for their developmental plasticity, such as water fleas [78] or honeybees [79].

5. CONCLUSIONS AND FUTURE DIRECTIONS

Developmental plasticity has long been posited to play a key role in the origin and diversification of novel traits. With recent theoretical and technical advances, it is now possible to critically test this broad hypothesis in the laboratory and field. However, a number of key questions are as yet unanswered. Below, we highlight five specific questions that provide fruitful avenues for future research into plasticity's role in innovation.

First, *do most novel traits indeed begin as conditionally expressed alternative phenotypes?* Recent theoretical considerations [5] suggest that novel, complex traits probably start out as alternative phenotypes within populations. However, more empirical studies are needed to assess the generality of plasticity's role in the origins of novelty. An effective approach is to assess patterns of ancestral plasticity in lineages that have given rise to taxa expressing derived novelties to evaluate whether ancestral plasticity might have provided the raw material for these novel traits. A broad range of such studies will also reveal whether these transitions are more often moderate and quantitative or macroevolutionary in nature.

Second, *how is developmental plasticity stabilized to produce novel phenotypes*? Genetic accommodation occurs when evolutionary processes act on quantitative genetic variation underlying environmentally dependent traits, thereby enhancing or diminishing plasticity. However, we know very little about the developmental and genetic mechanisms enabling plastic responses to be stabilized as novel traits.

Third, *what is the nature of genetic variation that fuels evolution by genetic accommodation?* Studies are needed to determine the degree to which evolution by genetic accommodation is fuelled by: (i) constitutively versus conditionally expressed genetic variation; (ii) novel mutations versus standing genetic variation; (iii) rare versus common allelic variants; (iv) differential expression of the same gene networks versus separate regulatory gene networks; (v) changes in upstream regulator genes versus downstream target genes; (vi) changes in promoter versus coding regions; (vii) changes in *cis*-regulation or *trans*-regulatory factors; and (viii) few or many genes of either large or small effect.

Fourth, *how common is genetic accommodation in natural populations?* Although genetic accommodation has been demonstrated in the laboratory [8], the frequency and importance of genetic accommodation in nature is unclear. Studies in the wild are especially relevant, given that many natural environments are undergoing dramatic and rapid changes owing to global climate change, habitat degradation and the increased presence of invasive species. At the same time, genetic and genomic screening techniques, from bar-coding to next-generation sequencing, are now available well outside molecular model systems. Such methods would permit population-wide changes in phenotypic variation to be correlated with genome- or transcriptome-wide surveys of variation patterns at DNA and transcript levels, as populations encounter, respond and adapt to profound environmental changes.

Finally, *can we develop models that realistically integrate developmental plasticity into a population genetics framework?* As evolutionary biologists use qualitative and quantitative models to explore the role of environmental trait induction and its influence on the direction and rate of evolution, future research needs to test the assumptions and predictions of these models. For instance, most current models make implicit and explicit simplifying assumptions about the developmental genetic architecture underlying plastic traits, about how environments can influence trait expression, and about the co-variation between the roles of environment as inductive and selective agents. Empirical verification of these assumptions will allow for a robust theoretical framework to be developed to complement and motivate empirical studies.

This paper grew out of a working group sponsored by the National Evolutionary Synthesis Centre (NESCent), organized by D.W.P. and A.P.M. We thank the other members of our working group (M. J. West-Eberhard, E. Snell-Rood, T. Cruickshank, C. Schlichting and M. Wund) for stimulating discussions and helpful suggestions on the manuscript, and three anonymous reviewers for constructive comments on earlier versions. For allowing us to use their images we would like to thank C. Laforsch (*Daphnia longicephala*), J. and K. Hollingsworth and K. Morehouse (*Vulpes lagopus*, USFWS), K. Clifton (*Thalassoma bifasciatum*), R. Babb (*Ambystoma tigrinum*), A. Wild (*Pheidole rhea*, *Onthophagus nigriventris*), and J. Crellin, FloralImages (*Ranunculus aquatilis*).

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