SYMPOSIUM

The Nature of Nurture and the Future of Evodevo: Toward a Theory of Developmental Evolution

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Synopsis This essay has three parts. First, I posit that much research in contemporary evodevo remains steeped in a traditional framework that views traits and trait differences as being caused by genes and genetic variation, and the environment as providing an external context in which development and evolution unfold. Second, I discuss three attributes of organismal development and evolution, broadly applicable to all organisms and traits that call into question the usefulness of gene- and genome-centric views of development and evolution. I then focus on the third and main aim of this essay and ask: what conceptual and empirical opportunities exist that would permit evodevo research to transcend the traditional boundaries inherited from its parent disciplines and to move toward the development of a more comprehensive and realistic theory of developmental evolution? Here, I focus on three conceptual frameworks, the theory of facilitated variation, the theory of evolution by genetic accommodation, and the theory of niche construction. I conclude that combined they provide a rich, interlocking framework within which to revise existing and develop novel empirical approaches toward a better understanding of the nature of developmental evolution. Examples of such approaches are highlighted, and the consequences of expanding existing frameworks are discussed.

Introduction

In an important paper written over two decades ago, Nijhout (1990) discussed how interpretations of genes as controllers of development and of genomes as blueprints for organisms and their traits are, when taken too literally, distorting the realities of organismal development and misdirecting research in unprofitable directions. Supporting his arguments with quotes from widely recognized textbooks and reviews, mostly dating from the 1980s, Nijhout wrote:

> The concepts that genes control development and morphology, that genomes contain developmental information, and that development follows a genetic program pervade modern thinking in molecular, developmental, and evolutionary biology. The genome is assumed to encode higher levels of organization. Genes and their products are seen as the causative agents of differentiation, and controlled gene expression is seen as the driving force of progressive change in development. The crucial regulatory role attributed to genes is emphasized by the widespread acceptance of the notion that a substantial number of genes are specifically concerned with the orderly progression of events during development. As a consequence, it is assumed that an understanding of the mechanisms of gene regulation and of the detailed structure of the genome are not only fundamental to an understanding of development but virtually sufficient for this understanding.

Instead, he argues, genes and genomes contain neither instructions nor a program for development. Rather, they are "passive sources of materials upon which a cell can draw." Further, genes do not "code"

for form, instead form emerges out of an interaction between gene products and environment (Nijhout 1990). Rather than causing or controlling development, genes enable it to take place.

To begin this essay I would like to examine how our views of what causes and controls the development of organisms and their traits have changed in over two decades since the writing of Nijhout's essay. What follows are representative quotes taken mostly from popular textbooks written for college-level and graduate-level courses:

> The instructions for making and maintaining an organism are encoded in its hereditary material—the molecule called deoxyribonucleic acid, or DNA. (Freeman and Heron 2007, 144).

> The molecule DNA (deoxyribose nucleic acid) provides the physical mechanism of heredity in almost all living creatures. The DNA carries the information used to build a new body, and to differentiate its various body parts. (Ridley 2004, 22).

> Life depends on the ability of cells to store, retrieve, and translate the genetic instructions required to make and maintain a living organism [. . .]. These instructions are stored within every living cell as its genes, the information-containing elements that determine the characteristics of a species as a whole and of the individual within it. (Alberts et al. 2008).

> The hereditary basis of every living organism is its genome, a long sequence of DNA that provides the complete set of hereditary information carried by the organism. [. . .] It is the sequence of the individual subunits, or bases, of the DNA that determines development. (Krebs et al. 2008, 3).

Examining these quotes it seems we remain rather convinced that organisms, traits, and differences in traits reside in, and are controlled by, genes and genetic variation. At least this is what we teach incoming students who we wish to become biologically literate. Are these perspectives also shared by textbooks written to contribute to, among others, the field of evolutionary developmental biology? Below are several examples from widely used references:

> Genomes need to be seen not just as collections of individual genes and other DNA sequences, but as complex sets of instructions and procedures of making a phenotype, written in a digital form. (Pagel and Pomiankowski 2008, 4).

> The sequence content, arrangement, and other aspects of the organization of these modular control elements are the heritage of each species.

They contain the sequence-specific code for development; and they determine the particular outcome of developmental processes and thus the form of the animal produced by every embryo. In evolution, the alteration of body plans is caused by changes in the organization of this core genomic code for developmental gene regulation." (Davidson 2006, 2).

If morphological diversity is all about development, and development results from genetic regulatory programs, then is the evolution of diversity directly related to the evolution of genetic regulatory programs? Simply put, yes. But to understand how diversity evolves, we must first understand the genetic regulatory mechanisms that operate in development. In other words, what is the genetic toolkit of development and how does it operate to build animals? (Carroll et al. 2005, 13).

What is a genome? Life is specified by genomes. Every organism, including humans, has a genome that contains all of the biological information needed to build and maintain a living example of that organism. NCBI (National Center for Biotechnology Information), A Science Primer 2011—A Basic Introduction to the Science Underlying NCBI Resources: www.ncbi.nlm.nih.gov/About/primer/genetics_genome

Clearly, the latter set of quotes presents a more nuanced view of what controls development, and thus what must be modified if development is to evolve, but implicit in all of them remains the basic notion that the essences of organisms, traits, and trait differences ultimately reside in genes and genetic variation and that development is determined and directed by genes or their immediate products. So it seems we have not changed our views all that much regarding what drives the development and evolution of traits since Nijhout's writing.

For the remainder of the current essay I will argue that such a change remains necessary. In fact, I posit that such a change is inescapable if evodevo is to continue to provide meaningful ways of thinking about the nature of developmental evolution. In the next section I begin my thesis by highlighting three key observations, broadly applicable to all organisms and traits, that highlight why gene- and genome-centric views of development and developmental evolution are unrealistic and unproductive. I then focus on the main aim of this essay and ask: what conceptual and empirical opportunities exist that would permit evodevo research to rephrase the questions it asks and revise the approaches it takes toward the development of a more comprehensive and realistic theory of developmental evolution?

Genes and genetic variation are insufficient to explain developmental outcomes

If genes and genomes "...harbor complex sets of instructions and procedures of making a phenotype, written in a digital form" (Pagel and Pomiankowski 2008), we should eventually be able to explain, and predict, the emergence of biological diversity through our knowledge of genes operating during development. Such predictions can be made with a high degree of accuracy for any trait influenced by alleles of major effect, such as the Mendelian traits we highlight in introductory courses, "genetic" diseases, or master regulatory genes such as Hox genes. In each case, genetic variation or alteration reliably result in profound and predictable phenotypic consequences. This does not mean we necessarily understand how a particular genetic variant becomes manifest in a particular phenotype, merely that the association is reliable. However, Mendelian inheritance and alleles of large effect are overall rare and non-representative of the diversity of traits organisms possess. Instead we have come to appreciate that most traits are influenced by variation at hundreds to thousands of loci, and that variation at many loci influences far more than a single trait (Lynch and Walsh 1998). This realization does not necessitate that that we abandon the view that genes make traits, only that the way genes determine traits is far more complicated than Mendelian genetics might initially suggest. Other observations, however, suggest that even this refined view may be inadequate.

For instance, some of our most thorough examinations of the genetic basis of complex traits have been executed in the context of human diseases. In most of them we can discern a clear signature of genetic contributions, predisposing certain genetic backgrounds to be more, or less, likely to give rise to a disease phenotype (Gibson 2009). Similarly, the growing number of genome-wide association studies published in recent years has successfully linked variation at hundreds of loci to variation in phenotype expression. Whatever trait or disease we investigate, genes and genetic variation clearly matter. However, the fraction of phenotypic variation explainable by the detected genetic variation has been surprisingly modest. From diabetes, asthma, and late-onset Alzheimer's disease to schizophrenia, depression, or obsessive-compulsive disorder, genetic variation rarely explains more than a few percent of the variation in disease phenotypes (Levinson 2006; Kato 2007; Gibson 2009; Nestadt et al. 2010; Alzheimer's Association 2010).

The study of human diseases, however, is often limited to finding associations between genotype and phenotypes without the benefit of experimental manipulations. What about traits in which the genetic regulation of development can be studied and manipulated experimentally? Here, great progress has been made, particularly in traditional model systems and traits such as the fly leg (e.g., Kojima 2004) or the nematode vulva (e.g., Wang and Sternberg 2001; Sommer 2001). On one side, these efforts have further confirmed the highly polygenic nature of developmental regulation of complex traits. Furthermore, they have given us an appreciation of how the interactions of developmental pathways to which genes contribute can result in the emergence of complex developmental properties, such as spatial or temporal information. On the other side, few if any have succeeded in the development of predictive models whereby a complex trait could be produced from knowledge of the genetic constitution of an organism alone. Focusing on morphological traits, Angelini and Kaufman (2005) summarized our current situation as: "We are still far from an explanation of biological diversity in which morphology may be unambiguously described by our knowledge of ontogenetic pathways."

Our ability to predict developmental outcomes from our knowledge of associated genes and their products alone thus remains surprisingly modest. One could argue that this lack of predictive power arises because the genes underlying most traits have yet to be identified and their contributions characterized, and will thus improve over time. This is probably correct. But the truly critical question is: is it correct to think that once all genes, genome regions, and their interactions have been identified that contribute to a complex trait of interest we will have really unearthed all we need to know to understand what controls the development and evolution of that trait?

The contingent nature of genetic contributions to development and evolution is substantial

Environmental conditions provide the context within which gene products contribute to developmental functions. Environmental conditions therefore have the potential to influence this contribution, and we see this potential manifest in a great diversity of contexts. The penetrance of mutant phenotypes, even of genes of major effect, is a function of environmental conditions, and often decreases in more benign, less stressful environments (e.g., Shields and

Harris 2000; Cook et al. 2005; Martin and Lenormand 2006; Beckmann et al. 2007). Trait heritabilities, or the fraction of phenotypic variation due to additive genetic variation, also change greatly with environmental conditions (Gibson and Dworkin 2004; Schlichting 2008). Similarly, the degree and nature to which multiple traits co-vary and influence each other's development and evolution can change considerably, depending on environmental context (e.g., Stearns 1989).

The environmentally contingent nature of genetic contributions to development and evolution is ubiquitous and has rightfully received renewed attention in evolutionary biology in general and evodevo in particular. This is especially obvious in the growing number of review articles (e.g., Pfennig et al. 2010; Beldade et al. 2011), edited volumes (e.g., Pigliucci and Müller 2010), and monographs (e.g., Schlichting and Pigliucci 1998; West-Eberhard 2003) devoted to the field of developmental (phenotypic) plasticity, as well as, for instance, the renaissance enjoyed by concepts such as the norm of reaction. Originally coined by Woltereck (1909) over 100 years ago, a norm of reaction is commonly defined as the range of phenotypes produced by a genotype over a range of environments. It is now firmly established as a tool with which to describe a given genotype's extent of plasticity in a quantitative genetic framework, and to model the evolution of plasticity in natural or laboratory populations. This framework is blind to the actual developmental mechanisms by which plastic responses are generated, but can of course be enriched by their understanding. For example, much work has been done on the endocrine regulation of plastic developmental responses in insects, from the regulation of the timing of metamorphosis to caste- and morph-determination in polyphenic insects (Nijhout 1994), and several insightful studies have now successfully managed to explore these developmental phenomena within a quantitative genetic framework (reviewed by Zera et al. 2007). Similarly, recent attention has turned to the role of environment-biased gene expression as a mechanism by which different environmental conditions, possibly transduced via endocrine mechanisms, elicit differential developmental responses (Snell-Rood et al. 2010). A growing body of literature now supports that environment-biased gene expression is indeed widespread. The role of differential methylation in transcriptional regulation has received particular attention in this context, highlighting that patterns of methylation are heritable across cell divisions, can persist across generations, and may be altered in response to a range of environmental factors (reviewed by Jablonka and Raz 2009). These few examples are not enough to do justice to the increasing richness of the field of developmental plasticity, but they suffice to highlight how much we have come to appreciate the environment as an important source of information and signals, which developing organisms exploit, even depend on, to guide their development. Clearly, genes and genotypes do not produce phenotypes in the absence of environmental conditions, but in interaction with them.

Despite this progress, some fundamental perspectives have remained unaltered. First, whatever it is we consider environmental, it remains external to and separable from an organism's genotype. In the absence of the latter, the former still exists. Second, while we have come to appreciate the environment and its signals as important, often critical, we still view them as passive. Instead, it is assumed that the ability to perceive and respond to environmental conditions resides in genes and genotypes. It is genes that change their expression or methylation signatures, and genotypes that exhibit a norm of reaction, all in response to changes in an environment that exists separate from them. The evolution of novel or different environmental responses similarly resides in genes and genotypes: populations diverge in average reaction norms or in the composition of their methylome. It seems, we now acknowledge that organisms, traits, and traits differences may not completely pre-exist their development residing in genes and genomes; instead we view genes and genomes as possessing the *added ability* to adjust or alter their function depending on the environmental circumstances in which they find themselves. The key question now before us is: after having bestowed environmental sensitivity onto genes and genotypes, have we now arrived at a realistic view of the nature of development and of developmental evolution?

The contingent nature of development precludes a meaningful separation of genetic and environment contributions to trait formation

It is common to partition environmental and genetic effects in development. We consider them separable, albeit interactive. This concept works well when used to investigate sources of variation; when clonal replicates develop in different environments, phenotypic variation among them is inferred to have arisen due to the environmental effects on development. A closer look at development, however, suggests that this perspective only applies well under very limited circumstances, and becomes especially unproductive

when applied to individual traits and their components.

For instance, transcription and translation of genes take place in a specific nuclear and cellular environment. These environments include complex cellular machineries, diverse resources from tRNAs to nutrients, signals from neighboring cells, and signatures from developmental decisions made earlier, such as the current position in the cell cycle, cell size, shape, etc. Importantly, while many of these components of the nuclear and cellular environment ultimately somewhere earlier in development required genes to be expressed, at the current time they collectively make up an environment that defines the current developmental context within which a given cell finds itself and to which it responds by adjusting its transcriptional or translational activity. Thus, already at this stage it becomes not at all straightforward to separate exactly what is a genetic and what is an environmental contribution to phenotype formation (Moss 2001).

This interdependency between genes and the environment continues, in fact increases, as we move up the levels of biological organization. As cells differentiate into types and give rise to tissues and organs, and as organs coordinate their actions within individuals, and individuals within groups, more and more opportunities emerge for genes and their products to contribute to environmental conditions that influence gene function in other contexts. It is the environment of the cell type, the organ, the developmental stage, the partner, or the social group that influences the activities of genes and their products. At the same time it is the activities of genes and their products that contribute to the creation of each of these environments. Viewed this way it becomes insufficient to describe the relationship between genes and environment as merely interactive. In addition, throughout development genes and environment become interdependent, both cause and effect of each other (Oyama 1985; Keller 2010). Similarly, partitioning the relative contributions of genes and environment in the making of traits yields little meaningful insight. Instead, traits emerge as the integral of developmental processes over space and time, enabled through the interdependent contributions of genes and environment. Or put another way, "a trait begins with a gene only if we choose to start our investigation at this point" (Oyama 1985).

It is worth emphasizing that many of the perspectives highlighted in this essay up to this point are not new. Similar arguments were put forward eloquently by prominent writers decades ago (e.g., Waddington 1959; Lewontin 1983; Oyama 1985) and have been expanded upon and refined in several more recent publications (e.g., Gilbert 2002; Gilbert and Epel 2009; Keller 2010). Moreover, many of the same issues and arguments are central components of developmental systems theory, a comprehensive field formalized by the works of Oyama et al. (2001), although perhaps with modest impact on the remainder of evolutionary and developmental biology thus far.

What is new, however, is that recent, and largely separate, conceptual developments in evolutionary biology, ecology, and evodevo are now providing us with starting points to better understand how development links genotype and environment in the formation and evolution of traits and organisms. What these conceptual frameworks are, how they relate to each other, and how their further integration and development may enable the formulation of a realistic and productive theory of developmental evolution, is therefore the focus of the second half of this essay. I begin by highlighting what it is we hope to accomplish in the process.

A theory of developmental evolution: what we need to accomplish

A meaningful theory of developmental evolution needs to adequately incorporate the following components:

(1) Traits emerge as the integral of developmental processes. A theory of developmental evolution needs to provide us with a thorough understanding of the developmental mechanisms that characterize organismal development, their interactions, consequences, and emergent properties;

(2) Development proceeds through the interdependent contributions of genes and environment. A theory of developmental evolution needs to fully incorporate the contingent nature of developmental processes;

(3) The evolution of traits requires heritable changes in the developmental processes that produce traits. A theory of developmental evolution needs to provide a framework within which evolutionary change arises through heritable changes in developmental systems enabled by environmental and genetic contributions;

(4) A theory of developmental evolution needs to provide opportunities to move beyond a descriptive and towards a predictive theory of developmental evolution.

Below I introduce three theories that have been developed largely independently in evolution, ecology, and evodevo. I posit that collectively, they provide us with valuable starting points to formulate a comprehensive theory of developmental evolution able to meet the challenges listed above. I will begin with the theory of facilitated variation.

The theory of facilitated variation

Formulated by Kirschner and Gerhart (2005) and Gerhart and Kirschner (2007, 2010) the theory of facilitated variation provides a framework for understanding how genetic variation is transformed into phenotypic variation via the agency of development, and the emergent properties of this transformation for the process of evolution. At a general level it provides a framework for understanding the nature and direction of phenotypic variation that emerges from random genetic variation. Specifically, it posits that the development and operation of traits is enabled through a number of conserved core processes such as gene regulation, transcription, translation, vesicular trafficking, microtubule formation, cell–cell signaling, and muscle-, neural-, and vascular-system development. Across phyla, these core processes are highly conserved, as are the genes whose products enable these processes. This extreme level of conservation reflects strong selection against evolutionary changes in the processes themselves.

Many of these processes share a propensity for what Gerhart and Kirschner (2007, 2010) call exploratory behavior, which in turn enables somatic selection of the most functional states. For instance, microtubules grow and shrink randomly into cytoplasmic space until polarized by stabilizing signals, such as those coming from neighboring cells or cell-internal gradients that select and stabilize certain microtubule states over others. Even though tubule formation is highly conserved, it enables the attainment of a great diversity of potential cellular morphologies. Cell shape emerges as highly adaptable and de-constrained, due to the exploratory nature of its highly conserved underpinnings.

Much the same applies for many other core processes. The neural, muscular, and vascular systems all select and stabilize certain states over others following periods of exploratory behavior (reviewed by Alonzo et al. 2011; Kovach et al. 2011; Herring 2011; see also Gerhart and Kirschner 2010 and references therein). Muscle precursors migrate randomly, but select positions relative to bones. Motor neurons are produced in great abundance during early developmental stages but are maintained into

later stages only if they manage to innervate muscles. Those that fail to do so are lost like unstabilized microtubules. Similarly, the vascular system simply expands into empty space, stabilized subsequently through its attraction to hypoxic conditions. In each instance, a complex developmental process adapts to local demands, enabling a high level of adaptability. This adaptability does not require genetic changes, rather it emerges when highly conserved core processes explore developmental space and somatic selection stabilizes those states that are most appropriate, given current conditions, and eliminates those that are not.

At the same time, conserved core processes are characterized by what Kirschner and Gerhart refer to as weak linkage to the signals that regulate their activity as well as other developmental processes with which they interact, causing any specific signal to have only a weak (meaning *easily altered*) relationship to the specific developmental outcome it solicits. For instance, a great diversity of sensory inputs can entrain, via the same highly conserved neuronal machinery, a great diversity of motor function outputs. Similarly, deconstrained input–output relations exist for instance in endocrine physiology (Nijhout 1994; Hartfelder and Emlen 2005) and cell–cell signaling (Alberts et al. 2008), where a rich diversity of inputs, via the use of a highly conserved signaling machinery, solicits a rich diversity of output responses.

The theory of facilitated variation proposes that the combination of exploratory behavior and weak linkage, together with other developmental phenomena such as compartmentation, enable developmental processes to be adaptably responsive to conditions. Development thus *facilitates ontogenetic change* because it allows adjustments to developmental context. Development *facilitates evolutionary change* because it enables random genetic variation to give rise to non-random, functional, integrated, and on occasion adaptive, phenotypic variations. Due to the highly constrained nature of its constituent core processes, their respective specific developmental functions are ensured regardless of context. Due to their exploratory behavior and weak linkage, the genesis of adaptive phenotypic variation is deconstrained. As a consequence, evolutionary change is facilitated by the phenotypic variation enabled through the nature of development.

The theory of facilitated variation makes several important contributions towards a theory of developmental evolution. First, it views the genesis of traits and trait variation as rooted in development rather than in genes and genetic variation

(Component 1 above). The latter clearly matter, they make a difference, but they do not make traits. As such it begins to fill an otherwise abstract genotype–phenotype map with biological reality. Second, it provides a framework for understanding the mechanisms by which random and modest genetic changes can elicit substantial and well integrated phenotypic changes, chaperoned by the facilitating nature of development (Components 2 and 3). As such facilitated variation provides a powerful new way of thinking about the mechanisms underlying and enabling developmental evolution.

The theory of facilitated variation has been criticized (Schlichting 2006), and dismissed by some (Charlesworth 2005), for failing to contribute toward a predictive theory of developmental evolution (Component 4). While a predictive theory of developmental evolution may, as discussed in more detail below, eventually be our goal, this criticism detracts from what is most needed at this stage in evodevo: a better understanding of what matters most in determining why and how developmental systems function and evolve the way they do. It is worth noting that the theory of evolution by natural selection proposed by Darwin was similarly non-predictive in nature at its inception. But by focusing on what he saw as the key mechanism enabling evolutionary change—natural selection—Darwin provided a foundation on which evolutionary biologists could eventually build a predictive framework. There is no reason why evodevo cannot do the same.

An additional, and particularly important contribution of the theory of facilitated variation is the explicit acknowledgement of the conditional nature of development and developmental evolution. Environment matters in determining developmental outcomes and in delineating phenotypic variation upon which selection or neutral processes can act. Both perspectives are also central to the theory of evolution by genetic accommodation, discussed next.

The theory of evolution by genetic accommodation

The theory of evolution by genetic accommodation, developed by West-Eberhard (2003, 2005a, 2005b), posits that environmental changes can elicit, via the agency of development, phenotypic transformations that can subsequently be stabilized genetically through selection operating on genetic variation in a population. Genetic accommodation does not require new mutations to occur, but will take advantage of them alongside standing, including conditionally neutral, genetic variation. On one side, evolution by genetic

accommodation is firmly rooted in a traditional understanding of the role of genetic variation in enabling evolutionary change. On the other, it critically extends the roles of development and environment in the evolutionary process. It extends the role of development by emphasizing its ability to determine which genetic variants will be manifest as selectable, phenotypic differences. It extends the role of the environment by emphasizing its ability to interact with developmental processes, and release novel phenotypes and selectable genetic variation in the process (reviewed by Pfennig et al. 2010).

The concept of genetic accommodation is perfectly compatible with, yet extends in critical ways, the theory of facilitated variation. It is compatible because both frameworks emphasize developmental processes as the nexus in the creation of heritable phenotypic variation (Components 1, 2, 3). It extends it because, at least so far, genetic accommodation has lent itself more easily to the formulation of specific tests of its assumptions and predictions (Criterion 4). For instance, genetic accommodation is thought to be enabled by the conditional release of genetic variation. Ample evidence now exists that conditionally neutral genetic variation is widespread, releasable under novel or stressful environmental conditions, and sufficient to fuel the rapid, selective evolution of novel forms (Rutherford and Lindquist 1998; Queitsch et al. 2002; Cowen and Lindquist 2005; Suzuki and Nijhout 2006). Similarly, genetic accommodation theory predicts that many novel traits or variants were expressed initially as environmentally induced, conditional alternatives to established traits. A growing body of evidence from a diversity of taxa now supports the notion that novel, or more extreme, forms have arisen through refinement of ancestral patterns of plasticity (reviewed by Moczek et al. 2011). Modeling studies have provided additional support for the facilitating function of plasticity in the evolution of novel traits (Lande 2009; Chevin and Lande 2010; Chevin et al. 2010; Espinosa-Soto et al. 2011a, 2011b).

Many other aspects of evolution by genetic accommodation remain to be explored, however. For instance, we know little about the nature of the genetic variation that enables evolution by genetic accommodation. Similarly, we need to learn more about the degree to which trait evolution enabled by genetic accommodation is generally modest and quantitative, or macroevolutionary in nature. Nevertheless, by complementing and extending the theory of facilitated variation, genetic accommodation provides valuable opportunities to frame investigations into how phenotypic variation and

evolution are enabled through developmental processes and their genetic and environmental inputs. Moreover, both theories also provide room for thinking of genes and environment not just as separate, albeit interacting contributors to phenotype construction, but *as interdependent causes and effects of each other*. Explicit, and quantitative, examination of this last consideration is what especially distinguishes the third and last theory I discuss, the theory of niche construction.

Niche-construction theory

Niche-construction theory focuses on the interplay between organisms and their niches, which are traditionally thought of as existing separate from each other; organisms evolve to fill niches, offered to them by the environment. Niche-construction theory overturns this dichotomy and instead argues that organisms actively construct their niches, which in turn affect organisms' development and evolution (Lewontin 1983; Odling-Smee 2010). Niche construction is defined as the process whereby "organisms, through their metabolism, their activities, and their choices, modify their own and/or each others niches" (Odling-Smee et al. 2003). Such niche construction is obvious in the manufacturing of dams by beavers or pupal cases by insects, the alteration of soil properties by fungi or earthworms, or the modification of fire regimes by plant communities. Similarly, any form of parental care can be considered a form of (temporary) niche construction by parents for their offspring. Niche-construction theory comes with two major conceptual consequences. First, it allows the selective environment of individual organisms to be understood as constructed, influenced by the organism's own actions. In other words, the selective environment experienced by individuals does not exist separately from them, but instead is shaped and modified by the organisms themselves. As such, the selective environment represents an extended phenotype that itself has a heritable component and can evolve. Second, niche construction occurs across generations, as is especially evident in the context of parental care. Niche-modifying behaviors occurring in one generation affect the selective environments experienced by members of the current, or subsequent, generations. Living organisms and their selective environment are thus shaping each other across generations (Odling-Smee 2010).

Several important consequences have emerged from these perspectives. First, niche-construction theory allows adaptation to be understood as

emerging not just from organisms *responding* to the environment, but *modifying* their environment in ways that suit their responses. Second, niche-construction theory allows selective environments to be understood as being moving targets, evolving in concert with a population of organisms that is adapting to them (Laland et al. 2001). As such, niche-construction theory has already resulted in an expansion of evolutionary theory by modeling selective environments as co-evolving due to the evolution of environment-modifying phenotypes (Laland et al. 1996, 1999; Laland and Sterelny 2006). These efforts have shown that adding niche construction to evolutionary models can change predicted dynamics and alter realized evolutionary trajectories.

On the surface it may appear that niche-construction theory has relatively little in common with the theories of facilitated variation and evolution by genetic accommodation, in part because much of niche-construction theory has been applied to ecosystem-level processes (e.g., Laland et al. 1999, but see Laland et al. 2008). Yet there is no reason why niches and environments must exist outside the body or why their construction cannot occur during any stage of development. In fact, the active construction of selective environments suitable for subsequent developmental events matches precisely the type of thinking explicit in the exploratory behavior of core processes and the demand-based nature of development envisioned in the theory of facilitated variation. In both frameworks, organisms, or their parts, actively construct environments that enable subsequent adaptive responses. The only expansion is one of scale: niche-construction theory traditionally focuses on the environment-constructing abilities of individuals or groups of organisms and their effects on subsequent generations; facilitated variation extends this ability to all levels of biological organization within a single generation, from organelles to cells, tissues, and organs. Regardless of scale, niche construction facilitates the production of adaptive phenotypes by improving the match between developmental products and the selective contexts within which they function.

The concept of genetic accommodation is at least partly congruent with the concept of niche construction. While genetic accommodation does not emphasize the environment-creating role of organisms, it does highlight the role of environmental conditions, as transduced through the organism's own actions (i.e., development) in determining the amount and nature of heritable phenotypic variation exposed to evolutionary processes. Although niche-construction theory does not inform our understanding of the

developmental processes that produce traits in development (Component 1), when combined with genetic accommodation it provides a powerful way of understanding and perhaps analyzing (see below) the contingent nature of development (Component 2) and developmental evolution (Component 3). Most importantly, it has already proven its ability to extend traditional quantitative models in evolutionary ecology, thereby raising the possibility it could make a similar contribution to evodevo (Component 4).

What remains to be done

Much work lies ahead in creating a unifying theory of developmental evolution. Yet important advances have been made in delineating what such a theory must incorporate in order to be useful, and how this might be accomplished. Specifically, I have argued above that for a theory of developmental evolution to be meaningful and productive it needs to (1) be firmly rooted in an understanding of the developmental processes that produce traits, (2) incorporate the contextual nature of developmental processes, (3) allow evolutionary change to arise through heritable changes in developmental systems enabled by environmental and genetic contributions, and (4) provide opportunities to move toward a predictive theory of developmental evolution. All three theories discussed above, albeit to different degrees, contribute toward meeting these four challenges. To move farther, however, will require an adjustment of the current priorities of evodevo research. Below I highlight three focal areas I consider especially relevant.

Too many genes, too little development

Traits do not reside in genes but emerge during development. A theory of developmental evolution needs to provide us with a thorough understanding of the developmental processes that enable organismal development. We need to know the interactants, including genes and their products that support these processes, and the emergent properties of the developmental system they themselves enable. Here, the highly conserved nature of core processes, highlighted by the theory of facilitated variation, provides a framework that could guide and organize such a characterization by focusing our attention on core processes and how linkage between processes (and their inputs and outputs) is established and altered. To do so, however, evodevo research must focus more on characterizing the evolution of developmental processes and less on cataloging and characterizing developmental genes. The latter is a great starting

point toward the former, but will never substitute for it. Here, the study of focal traits in traditional developmental model systems (for which we know as much about the genetic contribution to trait development as can be hoped) alongside close relatives with divergent (or currently diverging) traits is likely to provide important contributions to our understanding of how traits and trait differences emerge in development and evolution.

The contingent nature of development and developmental evolution

Development proceeds through the interdependent contributions of genes and environment. Traits thus begin with a gene, gene product, or a specific environmental change only if we start our investigation at this point. Similarly, evolutionary change depends on the phenotypic variation enabled by development, which through its environmental interdependencies determines which genetic variations will be manifest in selectable phenotypes, and which will not. It is time that evodevo research more heavily confronts the contingent nature of development and developmental evolution, for several reasons. First, great conceptual advances have been made that permit the development of hypothesis-driven research into the role of developmental plasticity and niche construction in developmental evolution (e.g., Ledon-Rettig et al. 2010; McCairns and Bernatchez 2010; Scoville and Pfrender 2010). Second, many natural environments are undergoing dramatic and rapid changes due to global climate change, habitat destruction, and the increased presence of invasive species. Consequently, the number of species and populations confronting profoundly altered selective environments has never been greater in the history of biological research. This provides truly unprecedented opportunities to document developmental evolution in nature and in action, and to test model predictions in the field. Third, genetic and genomic screening has become available and affordable well outside traditional molecular model systems (e.g., Colbourne et al. 2011). This puts us in a position to evaluate how much, and what type of, genetic and environmental variation and interdependencies enable heritable, population-wide responses to changes in the environment.

Toward a predictive theory of developmental evolution

Providing new ways of thinking about biological phenomena is a critical step in the formulation of new theories, especially if they provide new ways of

addressing questions that existing frameworks have been unable to answer or successfully integrate. For instance, the modern synthesis has yet to provide a satisfying way to explain the origin of novel traits or resolve the lack of correspondence between dramatic phenotypic diversification and genetic conservation seen across taxa (Pigliucci and Müller 2010). It is here that new frameworks, such as those portrayed in this essay should be seriously considered. Eventually, however, new theories, including ones we hope to formulate for developmental evolution, must transition from providing a new way of *thinking* about developmental evolution and move toward a better way of *predicting* it. This time has come for evodevo.

On one side, evodevo is positioning itself to develop its own theoretical, predictive framework. The three theories outlined above provide instructive examples. For instance, the theory of evolution by genetic accommodation predicts that developmental plasticity enhances speciation by facilitating character displacement, which is supported by comparative studies of species diversity in plastic and non-plastic sister clades (reviewed by Pfennig et al. 2010). The same framework predicts that many novel traits start out as environmentally induced alternatives that become genetically accommodated over time. A growing body of studies investigating derived populations with extreme or novel phenotypes suggests that their evolution was enabled through the developmental plasticity of ancestral populations (reviewed by Moczek et al. 2011).

In addition, all three theories have great potential to productively revise and extend already existing theoretical models developed by other disciplines. For instance, population geneticists have begun to model the impact of environmental induction of novel traits on the direction and rate of evolution (e.g., Lande 2009). Other models have been expanded to include the effect of conditional gene expression on relaxed selection, mutation accumulation, and the rate of adaptive evolution, many predictions of which are matched by empirical findings (Demuth and Wade 2007; Cruickshank and Wade 2008; Van Dyken and Wade 2010). In all of these cases, insights into aspects of the developmental basis of traits allowed population-genetic models to be made more biologically realistic. Similarly, ecological-genetic models have been extended productively through the integration of viewpoints derived from niche-construction theory (Laland et al. 1996, 1999; Laland and Sterelny 2006).

Ultimately, however, our ability to understand and predict developmental evolution will likely only be as good as our understanding of developmental processes, including the roles of context and contingency therein. A comprehensive understanding of developmental evolution across levels of biological complexity, from cells to organs to bodies, therefore still lies in the distant future. But there is much reason to be hopeful that evodevo has the knowledge, tools, and frameworks necessary to embark on the journey.

Conclusions

The "blueprint" and "program metaphors" for development have long outlived their usefulness, yet continue to bias evodevo's view of the nature of developmental evolution. In this essay I have argued that it is time for evodevo to cut the conceptual umbilical cord to its parent disciplines, to breathe on its own, and to take advantage of several rich conceptual frameworks that have emerged in its midst. Doing so will allow us to formulate a more nuanced and realistic understanding of what enables development and evolution and holds the promise to lay the foundation for the formation of a comprehensive and predictive theory of developmental evolution.

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