Morphological evolution and embryonic developmental diversity in metazoa

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Summary
Most studies of pattern formation and morphogenesis in metazoa focus on a small number of model species, despite the fact that information about a wide range of species and developmental stages has accumulated in recent years. By contrast, this article attempts to use this broad knowledge base to arrive at a classification of developmental types through which metazoan body plans are generated. This classification scheme pays particular attention to the diverse ways by which cell signalling and morphogenetic movements depend on each other, and leads to several testable hypotheses regarding morphological variation within and between species, as well as metazoan evolution.

Key words: Pattern formation, Morphogenesis, Body plan evolution, Evolution of development, Mechanisms of development

Introduction
The conservation of developmental processes, especially that of genes and gene expression patterns (Gilbert, 2006; Carroll, 2001), has traditionally received a lot of attention in evolutionary developmental biology. Differences at the level of genes and gene interactions among metazoan groups have also been studied (Lynch and Wagner, 2008). However, few studies have integrated the available information about different stages of development to understand the commonalities and differences in the overall process of development among metazoa. Earlier work identified gross developmental similarities and differences between metazoan groups that led to their classification into three types of development (Davidson, 1991; Davidson et al., 1995; Wray, 2000). These similarities in development are suggested to relate to similarities in the body plan or in the life cycle of the different species.

This article introduces a classification scheme that incorporates the information about additional species and about later stages of development that has accumulated since the publication of these previous reviews. I also propose new hypotheses about the relationship between signalling and morphogenetic movements in the classification of developmental types. Particular attention is given to the distinction between morphostatic and morphodynamic developmental mechanisms (Salazar-Ciudad et al., 2003). In morphostatic mechanisms, major signalling events occur before the onset of morphogenetic movements, whereas in morphodynamic mechanisms, cell signalling and morphogenetic mechanisms occur at the same time or in a closely interlinked manner (Fig. 1). Previous work (Salazar-Ciudad and Jernvall, 2004) suggests that this distinction has important implications for our understanding of developmental dynamics and for how development affects evolution. However, this previous work focused on individual developmental mechanisms that act only between specific developmental stages. Here, the focus is not on specific stages, but instead on the entire period of development. Thus, the previous classifications are revised to take into account the diversity of events in metazoan over the course of development. On the basis of the relative timing and of the interdependence between major signalling events and morphogenetic movements in early, mid and later development in different metazoan groups, I distinguish five major types of development among metazoans.

I have chosen to define developmental types because many unrelated species show similarities in the relative timing of developmental signalling and morphogenetic movements, and because such developmental types relate to types proposed by other authors (Davidson, 1991). This classification scheme exists, to a large extent, for convenience and does not imply that metazoan development falls into a rigid set of discrete classes without intermediates. In fact, part of the aim of this article is to explain how one developmental type could evolve into others. Note that this classification is not about whether early development is based on autonomous or inductive specification, but about the more general interrelationship between signalling and cell movement throughout development. Note, also, that it only incorporates metazoan groups for which sufficient information about developmental signalling and morphogenetic movements in several stages of development is available.

Developmental mechanisms
For the purposes of this article, developmental mechanisms can be defined as specific gene networks that, by regulating specific cell behaviours (such as cell division, apoptosis, signal or extracellular matrix secretion, changes in adhesion and differentiation), are responsible for the transformation of one spatial distribution of cell types (here, such a distribution is called a ‘pattern’) into another (Salazar-Ciudad et al., 2003). From this perspective, development can be described as a sequence of transformations between patterns, each produced by specific developmental mechanisms that change the pattern in one developmental stage into the pattern of the next stage (Salazar-Ciudad et al., 2003) (Fig. 1).

Basic developmental mechanisms: inductive versus morphogenetic
Three fundamentally different developmental mechanisms, autonomous, inductive and morphogenetic, can be distinguished. In autonomous mechanisms, pattern transformation is achieved by cells changing their expression state without cell signalling (Salazar-Ciudad et al., 2003). For example, a spatially heterogeneous egg produces, after cleavage, a resulting pattern in which different

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daughter cells receive different parts of the egg cytoplasm. In inductive developmental mechanisms, cells change their patterns of gene expression in response to extracellular signals from other cells (Salazar-Ciudad et al., 2003). By contrast, in morphogenetic developmental mechanisms, pattern transformation does not involve signalling, but cells moving or being moved towards different spatial locations (as a consequence, the spatial distribution of cell types, the pattern, is also transformed). Such movements are a consequence of specific changes in cell behaviour, like cell division, adhesion or extracellular matrix secretion. They can involve a small number of cells or the collective behaviour of large groups of cells. Only a few cells are involved, for example, in directed mitosis (Salazar-Ciudad et al., 2003), in which inherited (Bowerman and Shelton, 1999) cytocortical structures mechanically interfere with the mitotic spindle to reorient the direction in which daughter cells bud off. By contrast, a large group of cells is involved, for example, in the invagination of epithelia driven by apical cell constriction (Keller et al., 2003). Although many cells might activate the same molecular chain of events, the mechanical binding between cells and the different mechanical properties at the borders of the invaginating epithelium result in the distinct positioning of cells in the invagination (Fogacs and Newman, 2005). Developmental mechanisms have been classified into several types (see Salazar-Ciudad et al., 2003).

**Combined developmental mechanisms: morphostatic versus morphodynamic**

Most animal species utilise all of the types of developmental mechanism described above. The question then arises of how inductive and morphogenetic mechanisms are combined: does the inductive mechanism occur first, which is also referred to as ‘morphostatic’, or do the inductive and the morphogenetic mechanisms occur together, which is also known as ‘morphodynamic’? The logic of these combinations is very different. In morphostatic mechanisms, inductive mechanisms establish different expression patterns in cells at different locations, and then these patterns trigger specific morphogenetic mechanisms. Thus, the spatio-temporal coordination of cell behaviours required to acquire a final morphology is attained by cells that follow a program independently of later extracellular signals (Fig. 1). By contrast, in morphodynamic mechanisms, cells are signalling while moving (or while being moved). The spatio-temporal coordination of cell behaviours required for proper development is not attained by following a pre-specified developmental program, but instead by cells constantly re-adjusting their behaviour according to the signals they receive in the places to which they move or get moved to, as well as to the signalling and mechanical effects they produce there and along their way.

In addition, there are also morphoautonomous mechanisms, in which different cell types arise by autonomous mechanisms, and later each cell type follows a precisely regulated sequence of activation of morphogenetic mechanisms to produce a resulting pattern. In morphostatic mechanisms, major signalling events occur before the onset of morphogenetic movements, whereas in morphodynamic mechanisms, cell signalling and morphogenetic mechanisms occur at the same time or in a closely interlinked manner. So-called weak morphodynamic mechanisms involve only short-range signalling and modest cell movement, whereas strong morphodynamic mechanisms involve long-range signalling and large cell rearrangements. The colours indicate different cell types (i.e. cells that express different genes). Cells are depicted as circles, and in larger embryos, epithelia and mesenchyma are represented as filled shapes. Black arrows indicate extracellular signal secretion (induction); white arrows indicate cell movements.
that signalling takes place while cells move, channelling can happen several times and result in different outcomes as it takes place in different morphological contexts (taking into account that the morphology of the embryo is changing; Fig. 2E,F). In morphostatic mechanisms, by contrast, signalling occurs early in development, when morphogenetic mechanisms have not yet acted; thus, the morphological context is likely to be relatively simple. The shape and the material properties of territories also channel the spreading of the forces and the relative movements elicited by morphogenetic mechanisms (Belousov, 1998; Keller et al., 2003; Forgacs and Newman, 2005). In general, channelling can make local spatial asymmetries in one part of a pattern have an effect on other parts of a developing pattern (which also explains the fact that parts of a pattern are largely independent in morphostatic mechanisms when compared with morphodynamic mechanisms).

Types of development
In the following, I describe different types of metazoan development on the basis of the overall organization of development in terms of the interdependencies between communication and movement in cell collectives, as described in the previous section.

Type A: nematodes, spiralians and some small phyla
In the roundworm (nematode) C. elegans, the first cell division after fertilisation separates the prospective anterior half of the embryo from a posterior cell, which inherits the so-called P granules from the fertilised zygote (Gönczy and Rose, 2005). These granules are involved in reorienting the direction of the mitotic spindle in a second division (directed mitosis), in which the most posterior cell (P3) inherits the P granules. Meanwhile, the anterior cell, called AB, divides along the anterior-dorsal axis. This leads to a blastomere arrangement in which only one AB daughter cell is in contact with P3, and thus receives a signal expressed by P3. Later, inductive interactions between cells that contain and do not contain P granules (Gönczy and Rose, 2005) lead to additional diversity of fate commitments and mitotic orientation.

During C. elegans gastrulation, two specific epithelial cells (the E cells) constrict their apical side to get internalised into the embryo (Nance et al., 2005) and drag another cell in the same direction. Although the cells involved experience only modest movements of one or a few cell diameters, these movements lead to new spatial arrangements for the cells receiving and sending extracellular signals that allow the induction of subsequent patterns. Thus, early C. elegans embryos employ a morphodynamic mechanism in which inductive mechanisms and morphogenetic mechanisms (either directed mitosis or invagination) are interdependent in the production of pattern transformations. Morphodynamic mechanisms that involve only short-range signalling and modest cell movements are called weak morphodynamic mechanisms in this article (Fig. 1), whereas morphodynamic mechanisms that involve long-range signalling and large cell rearrangements are called strong morphodynamic mechanisms.

Later developmental stages in C. elegans involve the formation of organs by rather modest amounts of cell movement. Meanwhile, the dorsal intercalation of polarized cells (convergent extension), ventral closure due to cell migration, and the extension and contraction-driven elongation of the body produce the typical morphology of the worm (Chisholm and Hardin, 2005). These later stages are often considered to rely on morphogenetic mechanisms that are regulated on the basis of previously established gene expression patterns (Simske and Hardin, 2001). Thus, overall, C. elegans development might be considered to be rather morphostatic.

Fig. 2. Diagrams representing a group of mesenchymal cells that emit a signal (black dots). The different shades of blue (in the mesenchyme) and green (in epithelia) depict different signal concentration thresholds (and thus possibly the induction of different mesenchymal types). (A) The mesenchymal cells are depicted by the black circle. Note that the spatial distribution of the signal at different concentrations is a linear extrapolation of the shape of the signal-emitting tissue. (B) The signal arises from a part (black) of a folded epithelium (green) and diffuses in the mesenchyme (blue) without being able to cross the epithelium. (C) Here, the invaginated epithelium encloses less space, which causes less signal dilution. As a result, larger amounts of epithelium receive high signal concentrations. The same number of dots are depicted in B and C. (D) In epithelia with more complex shapes, the mesenchymal areas are not linear extrapolations of the shape of the signal-emitting tissue or of the diffusion space. Note that the borders of these areas have different curvatures at different distances from the source as a result of the different shapes of the diffusion space. (E, F) In E, diffusion is occurring before the invagination, whereas in F it is occurring afterwards. Morphostatic mechanisms involving signalling and invagination produce the three spatial distributions of mesenchymal types depicted in blue (E). Morphodynamic mechanisms can produce the shapes in E and F and others at intermediate stages of the invagination. Thus, morphodynamic mechanisms can generate a larger diversity and disparity of spatial distributions.

2A). When the space in which the signal is diffusing is simple, then changes in the diffusion rate of the signal (or in its secretion rate or in receptor concentration) lead to simple variations in the spatial distribution of the cells that receive the signal (Fig. 2B,C). However, when the signal is diffusing in a more complex space, then more complex, non-trivial changes in the spatial distribution of the signal will be caused by changes in the diffusion rate of the signal (Fig. 2D). In other words, depending on the shape of the space in which the signal is diffusing, it will be more or less diluted in different directions, effectively ‘channelling’ signal diffusion in specific directions (Fig. 2D). The shape of this space also depends on the relative distances and orientations between the cells that send a signal and the cells that receive it. This channelling is responsible for the complex relationship between genotypic and phenotypic variation and the larger diversity of morphologies attainable by morphodynamic mechanisms. It is also more prominent in morphodynamic mechanisms because here, signalling tends to happen in more diverse and complex morphological spaces. Given
Based on this example, a developmental type A could be defined as using weak morphodynamic mechanisms at early developmental stages, and as using morphogenetic mechanisms at later stages (Fig. 3A, part a).

There is some variation in the orientation of the early cleavage events among nematodes, but given that these differences occur mainly between only distantly related nematode clades, one can postulate that early nematode development is rather conserved (Schierenberg, 2006) when compared with that of arthropods or vertebrates. For example, among all the nematodes studied, only one species displays gastrulation occurring through the introgression of a large number of cells (Schierenberg, 2005), as is normally the case in echinoids, another type A developer.

The development of sea squirts (ascidians) follows a similar sequence to that of C. elegans. Again, an asymmetrically positioned and heritable cytocortical structure produces directed mitosis in the posterior part of the embryo (Kumano and Nishida, 2007; Negishi et al., 2007). In both cases, these successive small-scale cell rearrangements are involved in determining the relative positioning of cells that send and receive signals and, subsequently, in pattern transformation (Nishida, 2005). Later development in ascidians involves convergent extension and elongation in groups of tightly bound cells that lead to the typical ascidian larval morphology (Munro et al., 2006).

Most bristleworms (polychaetes), spoon worms (echiurans), molluscs (except for cephalopods), peanut worms (Sipunculida), Gnathostomulida, polyclad flatworms (polyclad Platyhelminthes), and probably Mesozoans and tubeworms (Vestimentiphera) display a similar, and possibly homologous (Henry 2002; Nielsen, 2005), pattern of cleavage. Their sequence and orientation of cell division, as well as their cell fates, are remarkably similar (Lambert, 2008). Even among closely related species, however, there is evidence of substantial variation in whether the earliest fate decisions during cleavage are due to inductive mechanisms or to autonomous specification (Kingsley et al., 2007; Gilbert and Raunio, 1997). In addition, the later developmental stages of spiralian species are poorly understood, so their classification as type A should be taken as preliminary.

In type A development, early embryos are small, but most cells are epigenetically distinct (i.e. they express different genes). In proportion to their size, they have a large diversity of cell types, and each cell type gives rise to a restricted and largely invariable part of the adult body. Thus, any small variation or error in the induction of a single cell type would produce proportionally large changes in late development. This variation would also probably be amplified, as it could alter the direction of successive mitoses and thus preclude the correct positioning of inducing and inducible cells in later stages. If, on the contrary, induction happens between larger numbers of cells, then variation or induction errors that affect the fate of one or of a few cells would have relatively milder effects on later development.

Therefore, type A development might result in a general entrenchment of early development and in the conservation of this developmental type [although there are instances of early variation in development associated with yolk-rich eggs (Raff and Snake, 2009)]. This entrenchment is likely to be stronger when more induction and movement events are required to accomplish full development (for example, in the production of more complex body plans).

This suggests that, in type A, variation is low in early stages and increases progressively with developmental time. The so-called hourglass model of development proposed that variation in animal development is high in early and late development and low in the middle stages (Ballard, 1981; Slack et al., 1993; Raff, 1996). In other words, species within a clade should be most similar in intermediate developmental stages and less similar in early and late stages (thus providing a link between phylogeny and ontogeny). There is an ongoing debate in the evolutionary developmental biology community about the validity of this model. Some researchers propose instead that variation is the smallest in early development (von Baer, 1828; Arthur, 1997), whereas others suggest that variation is greatest in mid-development (Bininda-Emonds et al., 2003). Within species, type A development does not fit the hourglass model; instead, it fits an inverted pyramid model, as has been suggested for the whole of animal development (von Baer, 1828; Arthur, 1997). The developmental program of very indirect developers (meaning that the adult stage is reached after metamorphosis from a larva that is very different from the adult) could equally be thought of as consisting of two inverted pyramids (one for the larval stage and one for the development of the adult from set-aside cells; see Fig. 3A, part b). Therefore, either the hourglass model does not hold for type A development, or the model fits due to natural selection on variation within species.

**Type B: cnidarians**

Type B development is characterised by extensive cell signalling that appears to occur concomitantly with extensive cell movements (Fig. 3B). In contrast to other types of development, these signalling and cell movement events occur in a relatively simple morphological context, consisting mostly of only two germ layers. Type B development is suggested to occur in cnidarians.

The cleavage and gastrulation of cnidarians has been described as highly variable (Grassé, 1953; Grassé, 1997; Tardent, 1978; Gilbert and Raunio, 1997), even within species (Fritzenwanker et al., 2007; Magie and Martindale, 2007). The morphology of the gastrula seems to be quite variable between individuals in the...
starlet sea anemone *Nematostella vectensis*, and different modes of gastrulation have been suggested within *Nematostella* (Magie and Martindale, 2007).

From early on in *Nematostella* development, two signalling centres exist: one near the presumptive mouth that expresses *fgf8* (Matus et al., 2007), *wnt* (Kusserow et al., 2005), *dpp* and *chordin* (Rentzsch et al., 2006); and a second one at the other extreme of the body that expresses *fgf1* (Matus et al., 2007). These signalling centres thus form an oral-aboral axis.

In *Nematostella*, apical constriction of the oral pole cells initiates the bulging of the ectoderm in the blastocoel (Magie, 2007). These cells develop filopodia with a strong adhesive affinity for the blastocoelic side of the ectoderm. This pulling appears to be the driving force for invagination. Several transcription factors start to be expressed at different levels in the oral-aboral axis, in the directive (dorsal-ventral) axis [a bilateral axis (Finnery et al., 2004)] and in the growing endoderm.

Signalling appears to occur concomitantly with cell movements in cnidarians. In *Hydra* (Bosch and Fujisawa, 2001), it has been proposed that the relative proportion between two signals, one diffusing from the aboral pole and another one diffusing from the oral pole, could be responsible for the specification of intermediate structures along the oral-aboral axis. If this is the case, simple changes in body shape and size might not greatly affect the resulting pattern. It is not clear, however, if such diffusion gradients are present in all cnidarians or only in species with a high regenerative capacity.

Cell movements seem to be more extensive and to involve more cells in type B than in type A development. Apparently, cells in the early embryos of type B developers are not as differentiated from each other as they are in the embryos of type A developers. Accordingly, signalling seems to occur between larger collectives of cells. Thus, it is likely that errors or small variations in signalling will have proportionally milder effects than in type A development. This is consistent with the large variability of early development and with studies (Martin, 1997; Fritsenwanker et al., 2003) indicating that cnidarian embryos are able to withstand substantial rearrangements of cells and cell numbers. Later stages of development are likely to also be variable (at least, there is substantial variation between the adults of different species), and thus cnidarians might fit the hourglass model within species, and possibly also between species.

**Type C: short-germ-band segmentation and sequentially segmenting arthropods**

Type C development is characterised by being morphostatic (or weakly morphodynamic) in its early stages and strongly morphodynamic in later stages and in segment-specific development (Fig. 3C). It is found in some arthropods, as discussed below.

Most arthropods have centrolecithal eggs, meaning that the yolk is located in the centre of the egg cytoplasm. In some species, early karyokinesis occurs without accompanying cytokinesis. Then, most nuclei migrate to the surface of the egg and cellularize (Anderson, 1973), thereby forming an epithelium (blastoderm). In other species, highly asymmetric mitoses directed perpendicularly to the egg surface produce a superficial blastoderm (Anderson, 1973). The blastoderm gives rise to ectoderm and, through a gastrulation process, to mesoderm. The endoderm arises either from the central yolk-rich cells or from the mesoderm (Dawydoff, 1949; Haget, 1977; Campos-Ortega and Hartenstein, 1985).

Gastrulation occurs either by the invagination of a ventral midline in the ectoderm or by individual cell introgression of the mesoderm (Dawydoff, 1949; Anderson, 1973; Haget, 1977). This is accompanied by the proctodeum and stomodeum, invaginations that form the most anterior and posterior parts of the digestive system and that guide the engulfment of the inner yolk mass and the subsequent formation of the midgut. These movements co-occur with signalling and might involve morphodynamic mechanisms.

Species that fit type C development include those arthropods in which several segments become visible more or less at once and in which later segments form progressively in a posterior sequence. Segments form as ventral thickenings of the ectoderm; later on, the ectoderm grows dorsally to displace the non-segmented ectoderm, and the mesoderm grows dorsally in between the ectoderm and the forming endoderm (Anderson, 1973).

In the Malacostraca class of crustaceans, posterior segments arise from a posterior growth zone in which clearly ordered rows of mesodermic and ectodermic teloblasts divide asymmetrically to produce most of the cells in the posterior segments (Scholz and Dohle, 1996). In many non-Malacostraca crustaceans, a conserved free-living stage (nauplius larva) is produced first; subsequently, additional segments arise through the asymmetric division of mesodermic and ectodermic teloblasts in the posterior part of the larva (Weygoldt, 1994). In myriapods (Chipman and Akam, 2008), spiders (Dawydoff, 1949) and short-germ-band insects (Anderson, 1973), segments also arise from a posterior growth zone. Both proliferation and cell intercalation might be involved in segment formation.

In type C developers, segmentation has been suggested to occur through some autonomous or signalling-based clock-like mechanism (Newman, 1993; Salazar-Ciudad et al., 2001; Peel et al., 2005; Choe et al., 2006; Damen, 2007; Pueyo et al., 2008; Choe and Brown, 2009; Pechman et al., 2009). At least in spiders (Schopheimer and Damen, 2005) and myriapods (Chipman and Akam, 2008), the signalling molecules Notch and hairy have been suggested to play a role in periodic segment formation. None of the hypotheses proposed for periodic segment formation is morphodynamic. Appendage development, at least for legs, involves reciprocal signalling between cells co-occurring with intensive cell proliferation during appendage growth (Angelini and Kaufman, 2005), and thus is likely to use strong morphodynamic mechanisms. Thus, type C development is defined as morphostatic (or weakly morphodynamic) in its early stages and as strongly morphodynamic in later and in segment-specific development.

Variation in type C development has not been systematically studied. Which anterior segments form first is variable between species (Anderson, 1973; Haget, 1977). The number and type of segments seems to be relatively conserved within major taxonomic groups of arthropods. The expression patterns of the genes involved in the early stages of segmentation do not seem to be widely conserved (Liu and Kaufman, 2005). By contrast, the segmentation genes themselves have widely conserved patterns of gene expression among arthropods (Gilbert, 2002).

**Type D: long-germ-band insects**

Type D development is similar to type C development except that it is more morphostatic (including appendage development; Fig. 3D). It is found in insects of the orders Hymenoptera, Diptera and Lepidoptera.

*Drosophila melanogaster* and most species of Diptera, Lepidoptera and Hymenoptera have a long-germ-band development, in which all segments form at the same time from a blastoderm that covers the surface of the embryos. In *Drosophila melanogaster*, substantial patterning occurs in the syncytium: transcription factors diffuse between nuclei and activate their own transcription or that of
additional transcription factors (Gilbert, 2006). Pattern transformation occurs by an inductive mechanism, in which maternal genes (expressed in the anterior and posterior of the egg) regulate a lower layer of gap genes (expressed in specific segments along the anteroposterior sequence). These, in turn, regulate pair-rule and segmentation genes, which are expressed as regularly spaced stripes along the anteroposterior axis. Each stripe arises through a combination of positive and negative inputs from genes in the upper layer.

After cellularization, a well-studied hierarchical inductive mechanism leads to the expression of anteroposteriorly oriented stripes along the dorsoventral axis (Moussian and Rovit, 2005). This anteroposterior and dorsoventral patterning occurs without much cell movement. Gastrulation consists of the invagination of a ventral midline along the whole body length, similar to type C development (Leptin, 1999). Extensive folding and movement of the ectoderm also occurs during germ band elongation, retraction and closure (Campos-Ortega and Hartenstein, 1985). Later movements co-occur with cell signalling and could involve morphodynamic mechanisms.

Overall, type D development appears to be more morphostatic than type C development (including appendage development), from which it probably originated.

In insects, examples of type C and type D development can be found even within species of the same genus. In general, most arthropods have a relatively conserved segmented stage, late developmental stages that lead to variable adult morphologies, and early variation in the amount of yolk and in the number of segments formed at once. Thus, the hourglass model, as initially proposed (Ballard, 1981; Slack et al., 1993; Raff, 1996), could hold for variation between species and, perhaps, within species.

**Type E: vertebrates**

Type E development is characterised by extensive cell signalling that appears to occur concomitantly with extensive cell movements (Fig. 3E). In contrast to type B development, strong morphodynamic mechanisms occur in relatively complex morphological contexts (Fig. 2E). Type E development is found in vertebrates.

Compared with type A development, type E development does not employ extensive cell signalling until the embryo has a large number of cells. Even after the first signalling events, the embryo is partitioned into territories that comprise large numbers of equivalent or nearly equivalent cells (in contrast to type A development).

The gastrulation of type E developers involves embryo-wide cell movements. These movements are often associated with and continued by the elongation of the body owing to extensive cell intercalation (Keller et al., 2003). Gastrulation and elongation movements co-occur with extensive cell signalling. During gastrulation in Xenopus (Bouwmeester, 2001), zebrafish (Rohde and Heisenberg, 2007), chicken (Mikawa et al., 2004) and mice (Tam and Loebel, 2007), the expression patterns of multiple signalling molecules and their receptors, such as Wnts (Tada and Kai, 2009), FGFs (Lea et al., 2009), PDGFs (Ataliotis and Mercola, 1997) and nodal (Chea et al., 2005), change over time and space (Heisenberg and Solnica-Krezel, 2008). Thus, it is likely that the spatial distribution of the cells that receive these signals depends on how morphogenetic mechanisms move them, and on how they move and deform the signalling territories (thus affecting, over time, the spatial distribution of the cells that receive a signal). As such, vertebrate gastrulation probably uses strong morphodynamic mechanisms (Shook and Keller, 2008).

The development of later organs, such as the brain, the limbs and the teeth, has also been suggested to rely on morphodynamic mechanisms (Salazar-Ciudad and Jernvall, 2002; Salazar-Ciudad et al., 2003; Salazar-Ciudad, 2008). The use of induction between larger groups of cells might allow early variation in the number of cells that receive a signal to have less dramatic effects on later development (as described), which would make an hourglass pattern of variation between developmental stages feasible. Except for mammals, this variation seems to involve, mainly, the amount of yolk. This does not necessarily have dramatic effects on adult morphology (del Pino and Elinson, 1983; del Pino, 1989; del Pino and Loor-Vela, 1990), although the morphogenetic movements involved can be quite different (Shook and Keller, 2008).

**Other types**

At least cephalopods (Lemaire, 1970; Boletzky et al., 1989; Lee et al., 2003), ctenophores (Freeman, 1976), ciliates (Shankland and Bruce, 1998; Weisblat, 2007), some yolk-poor arthropods (Weygoldt, 1994) and some yolk-rich echinoderms (Raff and Snod Smith, 2009) probably constitute their own developmental types (although not enough information about them is available yet). In spite of these gaps, the classification scheme set out above can be helpful in shedding some light on certain evolutionary questions, as detailed in the next section.

**Developmental types and metazoan phylogeny**

Type A development is found in the three main clades of metazoa: Ecdysozoa (e.g. nematodes), lophotrochozoa (e.g. spiralian) and deuterostomes (e.g. tunicates). This indicates that the common ancestors of types C, D and E might have had type A development. This possibility resembles the turbellarian-like first hypothesis about metazoan phylogeny, according to which a simple small animal with spiralian-like cleavage, as seen in some extant turbellarians, is the ancestor of all bilaterians (Hyman, 1940; Salvini-Plawen, 1978). An alternative hypothesis, not considered in Davidson’s classification, is the gastrea hypothesis (Nielsen and Noerrevang, 1985), which proposes that the origin of Bilateria might be a gastrula-like organism that originated from some cnidarian-like ancestor (presumably a type B developer). This would imply that all developmental types originated from type B, and that type A development would have appeared multiple times as a secondary adaptation to the small body size of planktotrophic and interstitial life-styles that are typical of many current type A developers.

At a coarse descriptive level, there seems to be an association between developmental type and some aspects of the body plan (with several phyla using the same developmental type), and this is the first hypothesis that I propose in this article. Phyla that use type A development tend to be small and to have relatively simple body plans with few cell types, each of which is preferentially localized to one part of the body (Davidson, 1991; Davidson et al., 1995), and with organs composed of one or only a few cell types that are derived from the same germ layer (Bell and Mooers, 1997; Bonner, 2004). Type C and D developers have body plans that can be considered as more complex because they have more cell types (Bell and Mooers, 1997). In addition, each of these cell types is not exclusive to one part of the body, but is distributed in iterated patterns along the anteroposterior axis, and functional organs are often made up of several cell types (with each organ having a specific pattern). The same occurs in type E developers, but with a
less clearly iterated pattern than in type C and D. Type B developers tend to have larger bodies than most type A developers, but have few cell types, and these are generally arranged in only two epithelia.

This first hypothesis could be tested by looking at the development of more species within each group. If the hypothesis is correct, species in the same phylum should have the same type of development. Exceptions would be expected for species with a body plan that is substantially different from that of the rest of the phylum (for example, for cephalopods among molluscs, or for cirripedas among crustaceans). Most phyla with simple and small bodies are still poorly understood at the developmental level. Hypothesis 1 would be falsified if these species do not employ type A development. Note that this requires experimental work on development that not only focuses on identifying genetic interactions, but that also studies morphogenetic movements and how these affect and are affected by signalling.

Davidson's classification (Davidson, 1991) is similar to the one proposed here, but neither the importance of morphogenetic mechanisms nor the distinction between morphodynamic and morphogenetic mechanisms is considered in detail. Davidson's type I is comparable to the type A described here, whereas his type II is similar to types C and D. Additionally, his classification combines vertebrate and cnidarian development; here, these groups are assigned to the separate types E and B.

The second hypothesis that I propose states that species with the same type of development exhibit commonalities in morphological variation and in the genotype-phenotype maps that they produce. The extensive use of morphostatic and weak morphodynamic mechanisms in type A development would allow, in accordance with this hypothesis, gradual variation and a relatively simple relationship between genotype and phenotype. This could facilitate fast responses to small but frequent changes in selective regimes. Thus, type A development might not just be ancestral; it could also be a very adaptive way to generate small body plans in which each part can be changed in a relatively independent way.

Hypothesis two can be empirically falsified by looking at the patterns of morphological variation that arise in groups that employ different types of development. Type E development should produce, within a species, variation that differs more between individuals compared with type C and type D development, and especially compared with type A and type B development. Comparisons between phenotypes that arise through mutation (Driever et al., 1996; Kamath et al., 2003) or between mutation accumulation lines should indicate whether, as expected, type E development produces a more complex genotype-phenotype map than type C and type D development, and especially a more complex one than types A and B.

The third hypothesis that I propose states that different types of development correlate with different amounts of variation at different stages of development. This hypothesis is summarized in Fig. 3 (as discussed in the previous sections) and could be falsified by directly measuring the variation among individuals within a given species at different stages of development and by comparing these patterns of variation between different species with similar and different developmental types. There are some studies partially addressing this question by using discrete characters (Poe and Wake, 2004) but, as of yet, no morphometric data are available.

The evolution of type E development

In principle, large complex body plans, such as those of vertebrates, could be produced through short-range cell-to-cell inductions and through the late activation of morphogenetic mechanisms, as is the case in type A developers. If this is so, then why do vertebrates make such extensive use of morphodynamic mechanisms? The discussion above suggests that morphodynamic mechanisms are able to produce more diverse and also more complex morphologies for a given genetic complexity. Thus, on average, fewer genetic changes are required to attain a (adaptive) pattern with morphodynamic mechanisms than with morphostatic mechanisms. The fourth hypothesis that I propose states, correspondingly, that complex body plans have evolved owing to a gradual transition towards developmental types with a higher interdependence between cell signalling and morphogenesis. Consequently, type E development might not have evolved because of an adaptive advantage, but because it is a simpler way (i.e. one requiring fewer mutations) to produce larger and more complex body plans. In that sense, type E development could have evolved through an increase in the amount of time in which inductive mechanisms act together in a type A development setting, or by allowing their interdependence (if type E evolved from type B). Hypothesis 4 could be falsified by checking whether, among chordates, a simpler morphology (for example, that of lampreys and hagfish) correlates with a more extensive use of morphodynamic mechanisms, especially if this simplicity is not the outcome of secondary evolution from a more complex morphology.

It is interesting to note that, except for molluscs, type A developers tend to have, as mentioned, relatively simple body plans as adults compared with those of type C, D and E developers. Cephalopods are probably among the largest and most complex molluscs; interestingly, they do not seem to use type A development either (Lemaire, 1970; Boletzky et al., 1989).

It has been suggested (Newman et al., 2006) that early metazoa did not use type A development, but morphogenetic and reaction-diffusion-like inductive mechanisms that led to early variable morphologies with a complex relationship between genotype and phenotype and to relatively large sizes, as seen in the Ediacaran fauna (Xiao and Laflamme, 2009). In this scenario, type A development could have evolved as an adaptation to small body size.

The evolution of type C and type D development

The evolution of type C development from type A development might also have been associated with an early increase in cell number and with a relative temporal delay of major early inductive events. The adaptive radiation of arthropods has been suggested to correlate with the specialization of their multiple appendages (Williams and Nagy, 2001; Minelli and Fusco, 2005; Angelini and Kaufman, 2005; Adamowicz et al., 2008). This could correlate with the larger independence between parts that is possible in morphostatic mechanisms and with the use of morphodynamic mechanisms for appendage development (except in type D).

Type D development might have arisen as a morphostatic derivation of type C development. This could correlate, at least in drosophilids, with the relatively small amount of morphological divergence compared with the number of species and the vast time periods since the divergence from common ancestors in each group (Tamura et al., 2004). It has been suggested that new morphostatic mechanisms that arise (or are recruited) through mutations and that are able to produce the morphologies originally produced by morphodynamic mechanisms would be favoured by conservative selection (Salazar-Ciudad and Jernvall, 2004), and thus would lead to the apparent canalization or conservation of drosophilid morphology.
Conclusions
In this article, I suggest that, in spite of the contingent nature of evolution, general inferences about the evolution of development and its effects on morphological evolution might be possible. This work draws some conclusions about how different types of development could influence the patterns of morphological evolution in a group and how the overall structure of development itself might evolve. More detailed analyses of development types and of their phylogenetic distribution, together with analyses of the patterns of morphological variation within groups, will probably become available in the near future and might refute or refine the hypotheses proposed above.

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Competing interests statement
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