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Review Article

The origin of higher taxa: macroevolutionary processes, and the case of the mammals

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Abstract

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The origin of a new higher taxon is characterized by a long-term phylogenetic trend, involving evolutionary changes in a large number of characters. At this phylogenetic level, the conflict between internal integration of the phenotype and its evolvability can be resolved by the correlated progression model, in which many disparate traits evolve by a sequence of small increments in loose correlation with one another, rather than by the modularity model. The trend leading to the new higher taxon implies the existence of a long ridge in an adaptive landscape. An evolutionary lineage tracking it requires adaptive changes in broad biological characteristics, involving many traits. Species selection is a possible additional driver of the trend. These conclusions are tested against the synapsid fossil record of the origin of mammals. The reconstructed sequence of acquisition of mammalian traits supports the correlated progression model. The adaptive ridge involved is postulated to have been a sequence of overlapping niches requiring increasing ability to remain active in daily and seasonally fluctuating environments by means of increasing internal regulation. An inferred speciation bias in favour of relatively small, relatively more progressive carnivores indicates that species selection was also involved in driving the trend. Palaeoenvironmental evidence indicates that ecological opportunity probably played a role at certain points along the lineage.

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Introduction

A higher taxon is one of those biological entities that are easier to recognize than to define. It is an arbitrary construct in so far as it is only recognizable as such by a subjective assessment of the degree of morphological disparity between its contained species and those that constitute any other higher taxon: different higher taxa occupy widely separated regions of morphospace. As with other issues concerning relative degrees of overall similarity and difference between organisms and taxa, the lack of an objective measure of this property of disparity has tended to obscure the biologically interesting question of how new higher taxa arise (e.g. Gould 1991; Foote 1997).

The essence of a higher taxon relevant to the present work is that its evolutionary origin included changes in many phenotypic characters, over a large morphological distance. If an evolutionary lineage leading from some early ancestral stage to the basal-most member of the new higher taxon is abstracted from the cladogram in which it occurs, straightened out so to speak, and inspected in isolation, then it inevitably takes on the appearance of a long-term evolutionary trend. Successive points on the lineage represent species with ever-increasing numbers and states of the characters that define the higher taxon. Any lineage within the branching tree (Fig. 1A) could be taken as an example of a trend; those recognized as leading to a new 'higher' rather than a new 'lower' taxon are merely those seen to have travelled the furthest through morphospace (Fig. 1B). However, the longer the trend, and the higher the number of characters involved, the greater the interest in and mystery about how such a trend could be maintained. There is a scale-effect here worthy

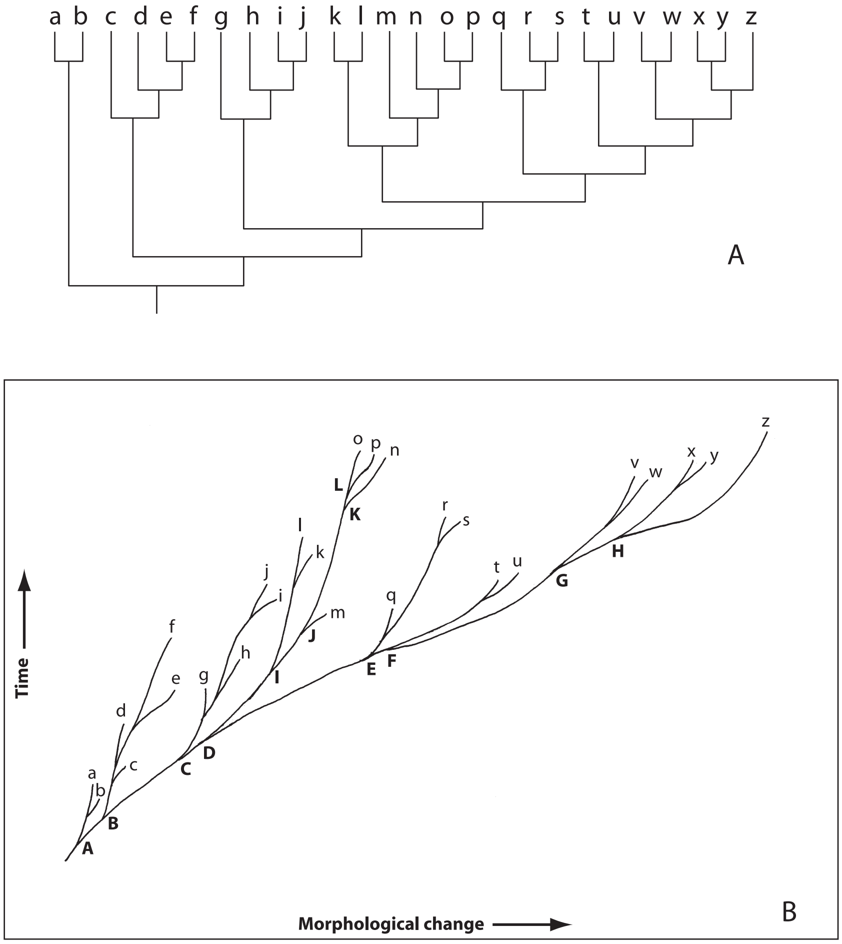


Fig. 1—Extracting a long-term phylogenetic trend from a cladogram. —**A**. Formal cladogram of 26 taxa. —**B**. The same phylogeny plotted against time and an arbitrary measure of morphological disparity, showing that the trend of hypothetical ancestors A, B, C, D, I, J, K, L is the same cladistic length as that of A, B, C, D, E, F, G, H, but traverses much less morphospace. Subjectively, taxon 'z' may be said to constitute a new higher taxon, but taxon 'p' does not.

of more careful attention than it has received in recent years: that the evolutionary process can result in large phenotypic changes, in many characters, as a result of long-continued, more or less unidirectional trends. Within the vertebrates, lineages from a hypothetical agnathan-grade fish to the teleosts or to the elasmobranchs, from an ancestral sarcopterygian to the tetrapods, from a basal amniote to the mammals or to the birds, are all examples of such trends. Within the invertebrates, every progressive phylum presumably was also the culmination of such a trend.

The overarching question addressed here is whether the origin of major new phenotypic structure and function, as manifested by a new higher taxon, is a consequence of normal microevolutionary processes acting in normal environments for enough time, or is a consequence of special genetic processes and/or unusual environmental circumstances. There are two obvious corollaries of the inferred long-term trend. One is that the evolving lineage of organisms must be assumed to have maintained the necessary internal integration between the phenotypic parts throughout, despite many of these individual parts having been radically modified by evolution. The second is that an evolutionary trend leading to a new higher taxon runs in an at least roughly consistent direction through a very large tract of morphospace, but on a time scale that must inevitably have seen highly varying ecological conditions. Over the tens of millions of years that it takes, there are climatic and biotic fluctuations of a magnitude that is, on the face of it, inconsistent with a simple, unidirectional selection force acting on the lineage.

These two issues are first addressed from a general point of view. The ensuing conclusions about how a new higher taxon might arise are then tested, so far as it is possible, against the best fossil record currently available for elucidating this particular level of macroevolution, namely that relating to the origin of mammals.

Functional integration versus evolvability

The concept that an organism is a highly integrated entity, in which its structures and processes work harmoniously together to create the functions of the whole organism, is as old as biology, and can be found famously explicated in the writings of, to name but a few, Goethe, St Hilaire, Cuvier and Owen. The appreciation that this property of integration tends to conflict with the property of evolvability, which is the ability of the organism to change separate component parts over time, is a more recent issue that has been receiving a good deal of attention lately, as molecular details of the underlying developmental processes responsible for evolutionary change emerge (Wagner and Altenberg 1996; Kirschner and Gerhart 1998; Hansen 2003; Hansen and Houle 2004; Merilä and Björklund 2004; Schwenk and Wagner 2004; Griswald 2006). To maintain the high level of integration of the organism during the course of evolutionary change, it would be expected that a high level of co-variation between many parts would be necessary. But an evolutionary change can only occur by mutation in an individual gene, which affects only one part, or by means of pleiotropy a few parts, of the phenotype. It might be supposed therefore that any mutation causing more than the most trivial change in the phenotype is likely to reduce the integration, and therefore the fitness, of the organism as a whole. Yet organisms are evolvable to a degree far beyond the trivial, and the origin of new higher taxa exposes the most profound level of expression of the paradox.

Several ways of resolving the conflict between integration and evolvability have been proposed, one of little more than historic interest, one undoubtedly a part, but nowhere near the whole explanation, and two that are currently serious contenders.

Structural revolution

Theories proposing the instant origin of major new kinds of organisms have existed in several guises. Schindewolf's typostrophism, published in detail in 1950 (see Schindewolf 1993; for an English translation) is the most familiar example. This kind of idea was predicated on an extreme view of the strength of integration of an organism, to the extent that any significant perturbation of one of its characters would lead to an unstable and therefore inviable organism. Only a spontaneous revolution of the whole organization, involving many characters, could cause a shift to a new, stable configuration. This mode of thinking has been abandoned in the face of all the evidence that has accrued showing that no possible mechanism for such change exists, and furthermore need exist. (It is nevertheless meet that such possibilities should continue to occupy a small corner of the corporate mind of biologists. How many of today's commonplaces were mid-20th century absurdities – DNA was too simple and stable to be the genetic code; there was no possible mechanism for continental drift; computers can never match the playing ability of grandmaster chess players?)

The closest modern version of revolutionary change comprises Kauffman's ideas (Kauffman 1993; Depew and Weber 1995) about the rules of spontaneous self-organization in complex systems. These appear to be more relevant to molecular systems associated with the origin of life and function within cells, but they do provoke speculation about aspects of the evolution of phenotypes, insofar as these are also examples of highly complex systems.

Internal developmental co-ordination

The developmental system of an organism contains mechanisms that are potentially able to maintain the structural and functional integration of parts, even after perturbation of one of them by mutation or direct environmental effect. One such mechanism is a form of developmental feedback. For example (e.g. Wolpert et al. 2002), the development of the chick limb involves mesenchymal cells forming the cartilaginous precursors of the bones and the connective tissue framework. The muscle cells are derived from somatic cells that migrate into the limb bud and acquire an appropriate pattern by attaching to the connective tissue tendons already present. Another mechanism is a form of internal selection, which can also be illustrated by vertebrate limb development. The innervation of the limb is by the axons of neurones in the nerve cord, which grow outwards and into the developing limb bud. Many more neurones do this than eventually become functional, but only those whose axons fortuitously reach and make a synaptic connection with a muscle cell survive. The rest die. These two processes can ensure that a functionally integrated osteology, musculature and innervation is retained after a genetic perturbation has altered the size, proportions, or position of the limb bones, without requiring additional mutations. However, important though these processes are for maintaining functional integration, they will be limited to the relationships between the different tissues that form parts of structurally contiguous organs, such as limbs, hearts, etc.

Higher order co-ordination of developmental mechanisms ensuring appropriate co-variation in different, non-contiguous characters also exists, in the form of heterochrony and allometry (Klingenberg 1998). Heterochrony is a change in the rates and timings of development of different dimensions and shapes of the organism, and many evolutionary changes can be described in terms of heterochronic change (e.g. McNamara 1995). In a few cases there is evidence that a simple genetic change may underlie the relationships, for example modification in the pattern of activity of a growth hormone. This implies that there is an integrated response among the variously affected parts, which maintains overall integration. In most inferred cases of heterochrony, however, virtually nothing is yet understood about the underlying genetic cause. In any given case of heterochronic evolution, it may be that rather than one or a few mutations with an integrated action, a large number of successive, dissociated mutations was required and that the phenotypic integration was maintained over time by natural selection. Indeed, it is not clear whether heterochronic change actually differs in principle from other patterns of adaptive morphological evolution, as far as the underlying mechanism is concerned (Zelditch and Moscarella 2004).

Allometry is another higher level organizational principle in phenotypes for which there may be developmental mechanisms ensuring maintenance of integration. Here, rates of evolutionary change of parts or processes of the phenotype differ from the rate of change in size of the body as a whole, and therefore often from each other (e.g. Klingenberg 1998; Gayon 2000). As with heterochrony, there may be a relatively simple pre-existing genetic basis for maintaining the allometric relationships during phylogenetic change. But again, it may alternatively be the case that evolution involving allometric change of parts in relation to reduced or enlarged body size, requires a range of independent mutations to ensure maintenance of the integration that the very existence of the allometric relationships imply (Preston and Ackerly 2004).

Modularity

The most widely held current view about evolvability is that it is a consequence of modular organization, although there are problems in applying this concept to long-term evolution. Organisms are self-evidently built from modules, which are parts having a high degree of internal integration, but a significant degree of structural and functional independence from other parts. The concept has been discussed by many authors concerned with the principles underlying the phenotypic structure of organisms, for example Riedl (1978), who described morphological architecture as a hierarchy of interconnected standard parts, and Raff (1996) who explicitly referred to such parts as modules. Cells, the segments of a metameric animal, individual limbs, and internal organs are all examples of such structural modules.

In recent years, a more carefully formulated concept of modularity has been developed as a way of understanding the nature of the control of gene expression during ontogeny (e.g. Wagner and Altenberg 1996; Bolker 2000; Schlosser 2002, 2004; Hansen 2003; Klingenberg 2004; Schlosser and Wagner 2004; Griswald 2006). As it became clearer that there were remarkably highly conserved mechanisms for regulating developmental processes, both at different sites and tissues within the same organism, and among phylogenetically remotely related taxa, the idea grew that such mechanisms were fundamentally modular in character. Exact definitions differ among authors (Bolker 2000), but in general a developmental module can be envisaged as a set of genes and gene products, interacting as a unit, that regulates the transcription activity of other genes directly responsible for causing developmental processes to occur. There is little input from outside the module, which is therefore relatively autonomous, and within the module the individual molecules and their interactions tend to be conserved. The role of the homologous *Hox* genes in determining the position of a developing structure along the body axis, conserved throughout the animal kingdom, was the first such module-like gene regulatory system to be identified. Other regulatory gene families are known that control such aspects of development as cell movements and induction patterns, as well as position. Cell signalling systems form another class of developmental modules, for example Hedgehog (Borycki 2004). Identified in *Drosophila*, Hedgehog is involved in segment formation, leg development and wing development; in vertebrates, the homologue of Hedgehog is called Sonic Hedgehog, and it is involved in the development of the somites, the neural tube and the limbs. An embryonic tissue might also be regarded as a developmental module, such as the vertebrate neural crest. Cells derived from neural crest develop into several different types of cell and are associated with several very disparate morphological structures such as sensory and autonomic nerves, branchial arches and their derivatives, and the pigmented layer of the skin (e.g. Wolpert *et al.* 2002).

The empirical evidence that the developmental regulatory system is modular in architecture, and that modules are capable of adopting new functions, of replicating or being lost, and of remaining conserved throughout major evolutionary change leads to the proposition that modularity offers a resolution of the conflict between integration and evolvability (Kirschner and Gerhart 1998). While there has to be a high level of integration of the parts within a module for it to remain functional as a unit, the low level of integration between modules allows them to evolve new functions and sites of activity, and therefore the phenotype to evolve.

Given this modularity of the developmental system, and how in principle it might facilitate evolutionary change, the question arises of whether it maps directly onto the resultant phenotype (Fig. 2A). If so, the parts and processes of the organism would be expected to consist of an array of phenotypic modules associated with specific developmental modules, each phenotypic module strongly integrated internally but only weakly integrated externally with other phenotypic modules: they would be ‘semi-independent’ to use Lewontin’s term (Lewontin 1978). Such an organization would be a way of resolving the conflict between integration and evolvability at the phenotypic level. However, there is actually very little evidence of direct mapping of developmental modules onto the phenotype (Weiss 2005). For example, the variety of different tissues and structures whose development includes the Sonic Hedgehog signalling system is too great for them all to be regarded as constituting a single phenotypic module in any functional sense. The same may be said of the range of organs that include neural crest-derived cells. The *Hox* gene complex as a module controls the position of structures along an axis of the animal, but a position as such does not fall under any reasonable definition of a module of an organism. Even more problematic, those parts of an organism that can reasonably be regarded as phenotypic modules, such as body segments or limbs, are not the result of anything corresponding to single developmental modules, but of contributions from several different ones.

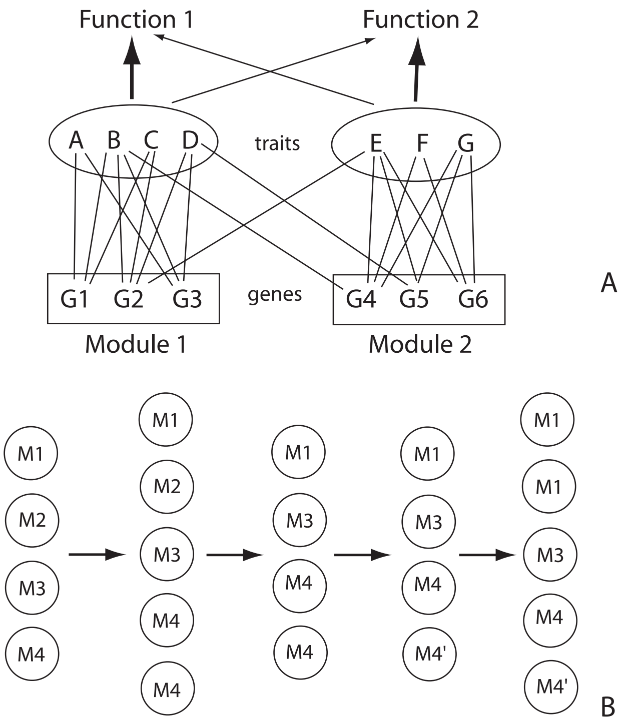


Fig. 2—Modularity in development, structure and evolution. —**A**. Each developmental module consists of a set of genes acting pleiotropically on the development of a set of traits, which in turn constitutes a phenotypic module. Each phenotypic module has one primary function. There is only a relatively small degree of interaction between modules, illustrated by a few of the genes also having a pleiotropic effect on the alternative phenotypic module, and each phenotypic module also having a small influence on the alternative function. Modified from Wagner and Altenberg (1996). —**B**. Modular evolution of a phenotype, showing the replication and loss of complete modules, but only very limited modification of individual modules, indicated as M4 to M4′.

An alternative, looser argument relating developmental and putative phenotypic modularity is that the modular architecture of the developmental system is an instance of the way in which any complex, integrated system can be evolvable, and therefore by analogy a comparable modular architecture should be expected in the phenotype. An individual phenotypic module would not readily evolve because of the strong integration between its parts: any mutation causing a change in one part is likely to reduce the effective functioning of the module as a whole. However, weak integration between modules would permit evolutionary change in the numbers and spatial dispositions of the modules, without disturbing the integration of the organism as a whole (Fig. 2B). For example, evolutionary change of the structure of a module, such as a limb or a body segment, might be difficult, but loss of a limb or addition of an extra segment would be relatively easy to achieve.

To repeat and stress a point already made, there is no doubting the role that modularity, in the sense of repeated parts, plays in the structure of an organism. The issue is whether this of itself is the resolution of the integration versus evolvability conflict, to which the answer appears to be negative. Genetically determined co-variation among the characters of an identifiable part of an organism has been taken as evidence for integrated modular structure. The best known detailed case is the rodent mandible, where Cheverud *et al.* (1997) and Cheverud (2004) demonstrated co-variation between the parameters of the anterior alveolar region on the one hand, and between those of the posterior, ascending ramus region on the other, but much less co-variation between the two respective sets This presumably reflects a pattern of pleiotropic activity of the genes responsible. Subsequently, more detailed studies have revealed a more complicated picture, with a greater number of modular-like units constituting the mandible, and some genes identified as having pleiotropic effects across module boundaries (Cheverud 2004; Klingenberg 2004). Even more significantly in the present context, a recent comparative study of genera and species of echimyid spiny rats showed that the pattern of correlation of mandible characters differs in different taxa, indicating that the specific modular organization is phylogenetically transient (Monteiro *et al.* 2005), and not maintained across macroevolutionary transitions.

A few examples at an even higher phylogenetic level have recently been discussed in support of the thesis that phenotypic modularity is responsible for evolvability. Yang (2001) suggested that the evolution of holometaboly in insects represented an increase in modularity, in the sense that life-history stages are modules. He then attributed the greater disparity of holometabolous compared to hemimetabolous insects to a consequent increase in evolvability. However, a more plausible explanation is that a greater range of potential niches is available for holometabolous taxa because of the possibility of highly distinct larval and adult adaptations. In this light, their radiation is interpreted as an adaptive response to an increase in ecological opportunities, rather than being the result of an increase in the potential to evolve. Shubin and Davis (2004) proposed that the paired fin of the sarcopterygians consists of two separate modules, an endochondral one supplying the internal bony skeleton, and a dermal one supplying the fin rays. They argued that this made possible the evolution of appendages with different proportions of the two respective modules, including the tetrapod limb in which the dermal module was completely lost, leaving only the endochondral module. However, this postulated modular mechanism appears to differ in no other way than terminology from a conventionally described mechanism, consisting of a reduction of one part of the appendage with a correlated increase in another part. Indeed, the very fact that these two changes are evidently correlated with one another is at variance with the concept of modularity invoked.

Thus the empirical evidence for the hypothesis that phenotypic evolvability results from modularity is weak: quantitative genetic studies do not reveal clear-cut and stable phenotypic modules, and morphological studies are open to more plausible explanations. There are also serious conceptual problems for the hypothesis of evolutionary phenotypic modules. The crucial issue is the degree of integration between the parts of an organism. The modular concept implies that there are essentially only two categories of integration, high level within modules and low level between modules. However, proponents have always found it necessary in practice to recognize grades of integration between these two extremes. For example (present author's emphases), Lewontin (1978) felt it necessary to coin the expression '*semi-independence*'; Raff (1996) described modules as '*dynamic* entities, *not stable* anatomical structures'; Schlosser (2002) writes of modules having '*relative* autonomy' and of the parts of a module states: 'Any perturbation of constituents is likely to affect *mainly* those other constituents with which they are strongly connected,' (page 56); Weiss (2005) refers to sequestration, his equivalent term for the evolution of modularity, as '*only partial*'.

The strength of functional linkage between two traits of a phenotype may be anywhere between zero, in which case the one is free to evolve without any affect on the other, and total, in which case neither trait can evolve at all without compensatory co-evolutionary change in the other. To take a vertebrate limb as an example of a putative evolutionary module, undoubtedly it does indeed have, to some degree, the modular property of co-variation between its parts. However, limbs can perfectly well evolve large changes in some but not all the parts, as witness the classic disparity of the pentadactyl limb. Furthermore, limb structure is also functionally correlated to a greater or lesser extent with some decidedly non-limb parts of the organism, including the central nervous organization controlling its movements, the metabolic rate controlling contraction rates of its muscles, and even the dentition dictating the animal's food source and therefore the locomotory function required of the limb. Where is the boundary of the limb as a phenotypic module meaningfully to be drawn? Moreover, the pattern of functional integration between the limb and other parts of the organism will alter over time, consequent upon evolutionary changes. At certain times during phylogenetic transitions, functional correlation between feeding structures and locomotory structures may be high, so that evolutionary changes in one but not the other may be difficult; at other times it may be low, and therefore a modification of the feeding strategy may evolve while the locomotory function remains unchanged.

To conclude, in the context of the phenotype, the expression 'module' should be restricted to mean only 'repeated part' in a descriptive sense, with no particular implications bearing upon evolvability or evolutionary units.

Correlated progression

An alternative concept to the modular construction of a phenotype is reticulate construction, where in principle all the parts are integrated with one another, as a multidimensional network. The level of integration between respective parts can be of any value from very high to very low and, unlike modularity, a value can readily alter as a consequence of evolutionary change. This interpretation stresses the view that the organism is an integrated entity that depends on the interrelationship and activities of all its structures and functions in the course of its existence. No one structure or function is properly regarded as independent of, or paramount over, others.

By assuming that a phenotype has a reticulate architecture of this nature, the conflict between integration and evolvability can more realistically be resolved, by means of the mode of evolution referred to as correlated progression (Thomson 1966; Kemp 1982, 1985, 1999; Lee 1996; Budd 1998). Under the conditions of correlated progression, all the characters, or traits, of the phenotype are regarded as integrated with one another, but each such functional link between traits has a small degree of flexibility. Therefore, an evolutionary change of any trait is possible, but only to a small enough extent at any one time that it does not disrupt the functional integration of the organism as a whole (Fig. 3). A larger change of a trait in isolation is constrained by reduction in the effectiveness of the functional interactions of that trait with other traits of the organism, thereby reducing the fitness of the phenotype as a whole. The correlated progression model avoids the problems associated with the modularity model. The organism does not have to be interpreted as consisting of evolutionary modules, for which there is no consistent empirical evidence. At any one instant, certain groups of relatively tightly integrated, contiguous traits might appear to be modules, but they are transient, and membership of such groups changes through evolutionary time. Thus, on this model all the traits of the phenotype can potentially evolve, but each one only by a small increment at a time, loosely in association with complementary small changes occurring in all the others over evolutionary time. Conversely, no one character can lag far behind changes in others, without becoming too great a constraint on their evolution.

The correlated progression model entails several corollaries about the course of evolution of new higher taxa.

- The pattern of acquisition of new traits and character-states is an incremental progression of small changes in many characters in parallel, rather than evolution of a single, or small number of characters. Thus correlated progression is incompatible with the familiar concept of the key innovation, which has figured prominently in discussions of major evolutionary change (e.g. Simpson 1944; Hunter 1998; Schluter 2000). A key innovation may be defined as a trait that is both necessary and sufficient for a taxon to enter a new habitat or adaptive zone and

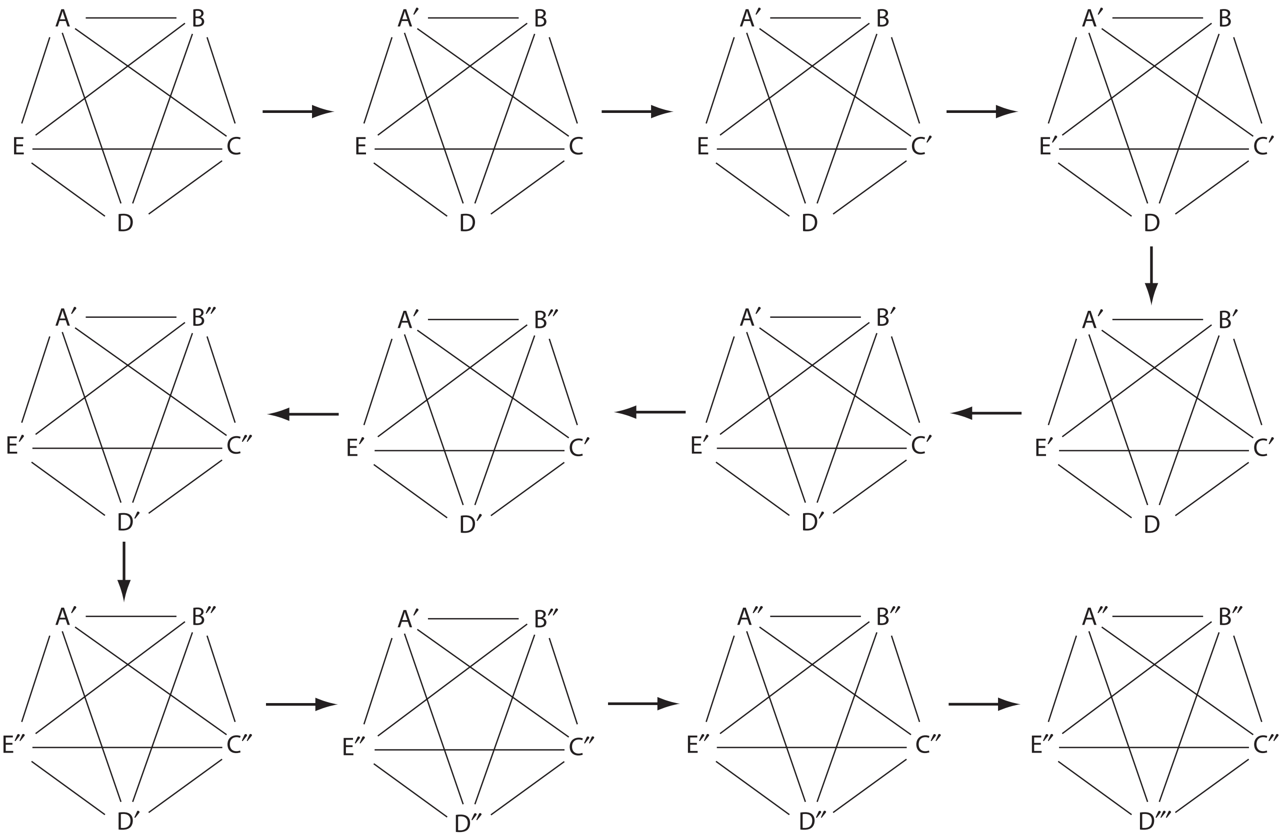


Fig. 3—Schematic illustration of correlated progression. Five hypothetical traits are integrated with each other, as indicated by the lines. Each trait can only evolve by a single increment at a time, and can never be more than one increment ahead of any other trait.

commence an adaptive radiation. Cases in which a key innovation has been at all convincingly identified are associated with radiation at a relatively low taxonomic level, such as the pharyngeal apparatus of cichlid fish (Liem 1974; but see Turner 1999 for a sceptical view), and the hypocone of the molar tooth of herbivorous mammals (Hunter and Jernvall 1995). However, in the case of higher taxonomic level evolutionary transitions, the large number and wide range of characters that all evolved in functional association with each other implies that no single one of them can be viewed in isolation as more important than the others in enabling the transition to a new higher taxon. A herbivorous molar is of little use to a mammal lacking the biological equipment to find, ingest and digest suitable vegetation while simultaneously avoiding predation, attracting mates and rearing offspring.

- No single selection force causing change in one character of the organism will act for more than a very brief period of evolutionary time; at different times different characters will be undergoing selection. Averaged over the period of the transition, the focus of selection cannot be reduced to anything less than the overall fitness of the whole organism and therefore of the integrated effect of all its characters.
- Rate of change will be slow compared to the theoretically possible rate of evolution where a single trait at a time is under selection, unconstrained by the need to maintain integration with all the other traits. Wagner (1988) analysed the reduced rate of evolution of a trait whose fitness value depends on the variation in other traits, a situation he referred to as a 'malignant' fitness landscape. Schwenk and Wagner (2001) discussed the role played by the anatomical and functional relationships of a trait to other traits in determining its potential for evolution, referring to the phenomenon by Whyte's term 'internal selection' (Whyte 1965), and to the consequent results as 'functional tradeoffs'. Hansen and Houle (2004) similarly suggested that selection of one particular trait may be slowed down by the need for selection to ensure that other traits remain tuned to it. Merilä and Björklund (2004) discussed the principle of phenotypic integration as a constraint on evolution through the need for tradeoffs among the fitnesses of different traits. This control on the overall rate of evolution by correlated progression may be termed 'correlated drag', and the greater the number of traits functionally correlated, the greater the effect will be. Indeed, there may be a potentially testable inverse

relationship between the number of characters involved in a phylogenetic transition and the average rate of change of a character.

Williams (1992) reprised the issue known as Haldane's dilemma, concerning the cost of selection. This is the conceptual difficulty in explaining how a large number of traits can all be subjected to selection at the same time, when each one, by the very definition of selection, requires a number of selective deaths of individuals carrying the less fit variants (Haldane 1957). Above a certain number of traits, either the population is reduced below a viable size, or the surviving individuals have a reduced average overall fitness. The problem has been extremely widely discussed in the context of molecular evolution, ever since it became part of the argument for the neutral theory of molecular evolution (e.g. Kimura 1983). The dilemma also applies in principle to phenotypic characters, where genetic variation in virtually all the characters can be observed in living populations, and inferred for major evolutionary transitions. Williams (1992) discussed several proposed solutions. In the present context, it could be the case that selection favours the appearance of patterns of genetic co-variance among characters, a process termed parcellation (Wagner and Altenberg 1996), and which would effectively reduce the number of phenotypic elements subject to selection. However, it has already been argued that such modularity provides an unrealistic view of the integration and evolvability of phenotypes as a whole. The particular combinations of traits genetically so linked would have to include very disparate characters, and would need to be forever breaking and new ones forming, which in turn would only add to the number of phenotypic elements required to be under selection. An alternative resolution of the dilemma follows from the correlated progression model. At any given time, only a small number of the phenotypic traits are under directional selection pressure for change, namely those that are less well integrated because they have lagged behind the evolutionary progression of the majority of traits. Under standard selection theory, all the remainder of the traits ought to be undergoing stabilizing selection, and therefore still contributing to Haldane's selective deaths. However, if these traits are sufficiently flexibly integrated into the organism that small variation does not significantly affect the overall fitness of the organism, then they will be more or less selectively neutral. Slight changes in them can be fixed by drift. At subsequent times, certain of these neutral traits will in their turn start to constrain evolutionary change in linked characters, and therefore become subject to directional selection. What this means in descriptive terms, is that phenotypes consisting of a wide variety of different combinations of variants of most of the traits do not actually differ much in overall fitness from one another. Indeed, slight deleteriousness of a trait can be accepted if it is part of a phenotype whose overall fitness is high. When considering the long-term, multi-trait trends associated with the origin of higher taxa, this possibility that a significant proportion of the changes in many of the characters is the result of neutral drift rather than selection becomes an important consideration.

To conclude, support for the correlated progression model of major evolutionary transition derives primarily from (a) the evidence that at this level the structural and functional integration of the phenotype is a result of reticular rather than modular architecture and (b) the logical inference that the degree of evolvability seen in major evolutionary change requires such a reticular architecture. It does need stressing at this point that, to a large extent, the phenotype can be *described* as being built from modules at various structural levels, such as cells, segments and appendages. What is argued here is that phenotypic modularity of itself cannot be the *cause* of the more extensive degree of evolvability that involves many characters, and is manifested by major evolutionary transitions and the origin of new higher taxa.

The correlated progression model can also be tested directly by the various methods for reconstructing the combinations of characters at hypothetical nodes of a cladogram, to recreate the pattern of acquisition of new characters during an evolutionary transition. In the case of the origin of new higher taxa, the fossil record is the source of most of this information, as will be discussed later in the particular case of the mammals.

Driving the trend

Given the existence of evolvability, the next question is what causes the large magnitude changes, in a multitude of characters that lead to the eventual emergence of a new higher taxon. Analyses of phenotypic fitness and natural selection, based on modelling or field studies, generally assume that at a given time there is a single, simple selection force acting on one identifiable focal trait, perhaps constrained by simultaneous selection for a second trait. However, the fossil record indicates that the length of time it takes to complete the assembly of all the new characters associated with the origin of a new higher taxon such as a tetrapod, a bird, or a mammal from the common ancestor shared with its living sister group is counted in tens of millions of years, and it is usually assumed that the same is true, though less readily demonstrated, of the major invertebrate taxa. This is a timescale far in excess of the conceivable persistence of a single, simple selective pressure, and neither would such a force be expected to affect so many different characters. Yet if, over such time spans, the selection pressure varied and so affected different characters at different times, it is not obvious why an apparently consistent trend towards the new descendent phenotype should nevertheless occur. Having argued earlier that these trends towards new higher taxa are not simply artefacts of the way a phylogenetic tree is presented, but do in fact constitute cases of long-term directional change, an explanation for what drives them needs to be sought. Matters become even more complicated on recalling that a very large number of speciation events must have occurred along the lineage, with all that this might entail in the way of interrupting a smooth journey through morphospace.

Possible causes of long-term trends have been proposed ever since their existence became apparent from the fossil record. These include a range of versions of a vitalistic force, whereby the trend is attributed to some sort of intrinsic property of organisms directing evolutionary change in a predetermined direction. The innate perfecting principle of Lamarck, orthogenesis of Theodor Eimer, nomogenesis of L.S. Berg and aristogenesis of H.F. Osborn are all variations on this theme that are familiar to historians of biology (e.g. Mayr 1982). All pre-date the development of the mid-20th century evolutionary synthesis and accompanying abandonment of any thoughts of vitalism, an exclusion which Darwin himself had, of course, insisted upon.

A modern, and somewhat more respectable, non-Darwinian hypothesis of the cause of long-term trends is drawn from the second law of thermodynamics, and an analogy with the behaviour of complex energy systems over time. As reviewed by McShea (1998), there are two versions, one that stresses increase in information entropy with complexity, and the other that proposes the spontaneous origin of energy dissipative structures in the form of increasingly complex molecular systems. At any event, the types of evolutionary trends to which such physical processes might conceivably be relevant are likely to be very general in nature, such as increases in level of complexity, or intensity of energetic levels. From what is currently believed about the mechanism of evolution, such processes as these are assumed to be overridden by the process of selection acting under local conditions.

Leaving aside thoughts of vitalism and of thermodynamics, there are two candidates for the driving force behind evolutionary trends, natural selection and species selection, which are not necessarily exclusive of one another.

Natural selection

For most authors, the default explanation for trends is Darwinian natural selection. Until the advent of cladistic analysis for its own sake caused a near-cessation in thinking about such matters, the literature on the origin of specified new higher taxa frequently attempted to identify a simple selection pressure that drove the evolutionary trend. To take one recent example, Carroll *et al.* (2005) argued that the selective force behind the origin of tetrapods was the advantage of gaining heat by basking. However, as already argued earlier in the context of maintaining integration, such a simplified view of the relationship between an evolving lineage and its environment is unrealistic, and it can clearly be traced to an inappropriate extrapolation from microevolutionary studies to macroevolutionary events. Most of what is currently understood about natural selection is derived from quantitative genetic studies of the behaviour of a small number of genes or phenotypic characters with assumed or measured selective values, and variances and co-variances (G-matrices or P-matrices). The process is modelled on the basis of a Simpsonian adaptive landscape, in which the horizontal axes represent phenotypic values for the characters, and the contours represent the phenotypic fitness values of different combinations of these (e.g. Lande 1979; Schluter 2000; Arnold *et al.* 2001). Revealing as these types of studies are for cases of short-term adaptive radiation at low taxonomic levels, such as beak size in finches (Schluter 1989) or body size in mammalian orders (Kingsolver and Pfennig 2004), there are fundamental problems to simply extrapolating the insights so gained to the long-term trends associated with the origin of major new taxa. Here, a far greater number of functionally integrated traits contributing to the overall phenotypic fitness have to be taken into account, and the time period over which the evolutionary trend runs is vastly longer.

The first problem concerns the kind of consistent gradient of successive, overlapping ecological niches necessary if Darwinian evolution is to drive the trend, that could persist for the tens of millions of years duration of the trend, and which would affect a large number of phenotypic traits. Over that order of time period, environments change frequently and extensively in climate, physical geography and biotic composition. An ecological gradient that persists through this wide range of transitorily varying conditions must be of a very general nature, undisturbed by immediate local conditions and the necessary short-term adaptations for them. A series of niches associated with increasing body size is an obvious candidate. Others are increasing metabolic rate and energy usage, and increasing homeostatic regulatory ability. Whichever of these broad attributes of the organism is being selected, the evolving lineage will behave as if it is moving along a ridge on the adaptive landscape (Schluter 2000; Arnold *et al.* 2001) (Fig. 4). Successive combinations of characters do not represent climbing an adaptive peak, which would be equivalent to increasing phenotypic fitness for the existing niche, but shifting to new niches further along the ecological gradient. It may be asked why, if the model is a ridge, the lineage does not track backwards as well as forwards. The answer is presumably that the ridge immediately behind the current point reached by the evolving lineage is still occupied by the less progressive members of the taxon, or perhaps by new taxa that entered the ecosystem as a consequence of the new conditions created by the passage of the focal lineage.

The second problem concerns the relationship between the large number of traits involved, the process of natural selection, and the exact trajectory of the evolving lineage. It relates to Haldane's dilemma, which has already been addressed in the context of correlated progression. The solution proposed, that variation in many of the characters has so small an effect on overall phenotypic fitness that they

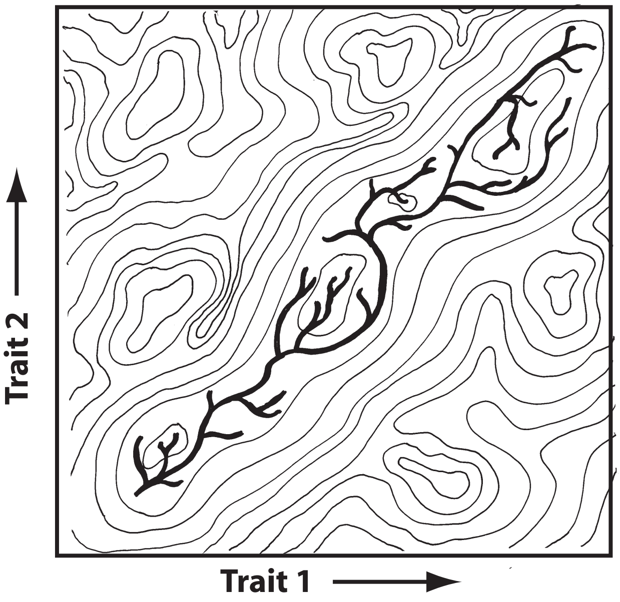


Fig. 4—A ridge in a Simpsonian adaptive landscape. The axes represent the values of phenotypic traits and the contours represent overall fitness value of the phenotype. The major axis of the ridge represents a sequence of overlapping niches leading in the direction of the trend from the ancestral niche to that of the new higher taxon. The lineage tracks this but there is also a degree of near-random drifting around the major axis, and occasional low adaptive hillocks offer the ecological opportunity for brief adaptive radiations.

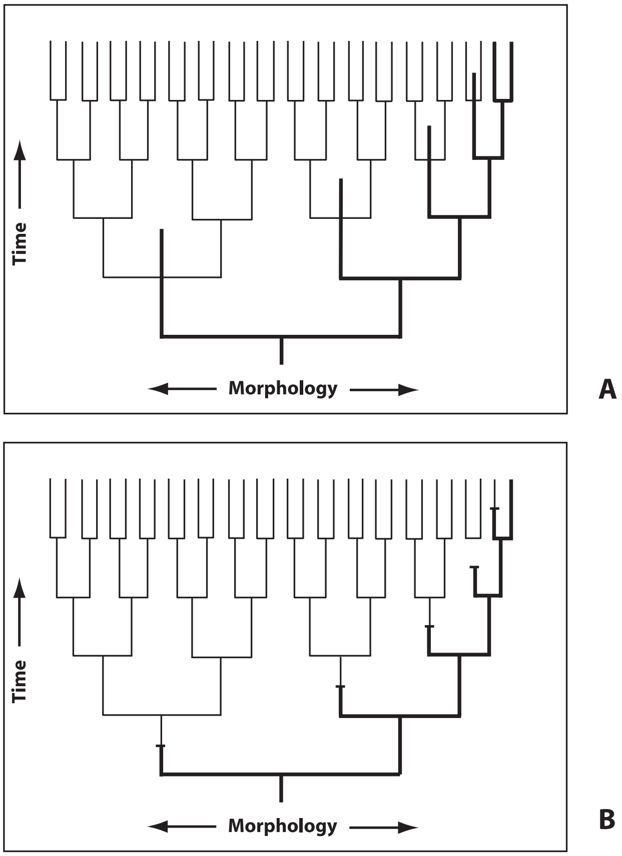


Fig. 5—Species selection. —**A**. The effect of differential probability of speciation between species consisting of organisms with the alternative variants of a phenotype. —**B**. The effect of differential probability of extinction between species consisting of organisms with the alternative variants of a phenotype. In both cases, the heavy line indicates the driven trend over time towards one extreme of the morphology, superimposed on what would have been an unbiased pattern of speciation.

evolve by drift rather than by natural selection, has an interesting implication for the nature of the trend. It suggests that the adaptive ridge is better represented as an elongated adaptive plateau (Fig. 4). The major axis is the direction of the general ecological gradient, but a degree of random wandering around the major axis will occur. Phenotypes having different combinations of the variant states of many of the traits do not actually differ much in overall fitness from one another. However, if occasional low adaptive 'hillocks' occur on the plateau, and one of these is approached by a random branch of the main lineage, it may be climbed by that branch. In real terms, this would represent local environmental conditions offering an occasional ecological opportunity for an adaptive radiation to occur along the general trend, a phenomenon that may indeed be inferred from the fossil record.

Species selection

A long-term trend is manifested by a phylogenetic lineage that must be assumed to have undergone numerous speciation events, in each of which one species survived to continue the trend and the other was a short-lived side branch. On some occasions a side branch formed an adaptive radiation of its own that is known from fossil or living taxa; on an unknown number of others it disappeared without trace, with or without first radiating. The possibility exists that the phylogenetic trend resulted from differential patterns of speciation and/or species extinction (Fig. 5), a process referred to as 'among-lineage' as distinct from 'within-lineage' selection (examples of the very many discussions include Vrba 1989; Gould 1990, 2002; McNamara 1990; McShea 1994; Grantham 1995; Kemp 1999; Alroy 2000). In principle, the underlying process may be one of two categories (Vrba 1989). Species sorting, or clade selection, is caused by the differential probability of a species or higher clade surviving or going extinct as the result of characteristics of the organisms that constitute it. Species selection is caused by the differential probability of survival or extinction as the result of species-level characters such as population size, pattern of geographical distribution, dispersal pattern, or sex ratio.

Williams (1992) pointed out that the two categories are actually closely interrelated and may be hard to distinguish, because the species-level characters usually emerge from the interactions of the organisms, which are in turn caused by their organism-level characters. For example, a non-continuous distribution of a species is an emergent species-level character that may result from organism-level adaptations for utilizing a disjunct rather than a continuously distributed food resource. The potential overlap between an organism-level trait that causes organism-level selection, and an organism-level trait that causes species-level selection via an emergent trait was recognized by Lloyd and Gould (Lloyd and Gould 1993; Gould and Lloyd 1999). They proposed that the significant property responsible for differential species survival is better termed 'emergent fitness' of the species, with regard not to its origin but only to its effect on the probability of speciation or extinction. Thus they accept that, in addition to strictly emergent characters, aggregated organism-level characters can also drive species selection. With this more liberal interpretation of the concept of species selection, several authors freely accept that it is not only possible, but virtually certain to be a significant component of macroevolution (e.g. Alroy 2000; Erwin 2000; Coyne and Orr 2004).

However, establishing cases where species selection has driven an evolutionary trend is difficult. With a fossil record of high enough resolution, the direction of evolution of a trend might be shown to differ from the direction of evolutionary change within separate species constituting the trend, but this is only likely to be applicable to short trends in taxa with very dense fossil records (Cheetham 1986, 1987). For longer trends, preserved in the fossil record at a lower taxonomic resolution, it may be possible to infer consistent characteristics of the hypothetical sequence of ancestor–descendant stages that are not consistently present in the members of the known side branches. If, furthermore, it can plausibly be proposed that such characteristics would be expected to cause differential probabilities of speciation or extinction, then species selection must be considered a possible cause of the trend. A simple, though disputed, illustration is size increase, as discussed for example by Alroy (1998) and Kingsolver and Pfennig (2004). Cope's Law is the commonly observed trend of body size increase in a lineage. It has been argued that, for various possible reasons, a species consisting of larger organisms is more likely to speciate than a related species consisting of smaller organisms. If so, then species selection may at least partially drive the trend. A more complex and potentially more interesting case is discussed later.

The expected frequency of phenotypic changes as a result of the process of species selection would be of the same order as the frequency of speciation along the lineage. From the relatively little that is actually known about real rates of speciation (as distinct from rates of change of diversity, which also embraces rates of extinction) this would be expected to be of the order of one every 1–10 million years. If species selection were indeed a major cause of a trend, then the relative rarity of this event would help to account for the relatively slow pace of evolutionary change during the origin of a new higher taxon.

The case of the origin of mammals

Arguments have been presented above that at the phylogenetic level of the origin of new higher taxa, the primary mechanism for maintaining the structural and functional integration between the many, separately evolving traits of the organisms that constituted the evolving lineage is correlated progression rather than modularity. The long-lasting trend follows some version of a general ecological gradient of successive, overlapping niches, which can be modelled as the major axis of a narrow plateau on an adaptive landscape. Species selection may also play a significant role in controlling the direction and pace of the trend. This set of hypotheses, or model, can be tested for compatibility with those few actual cases where there is a fossil record adequate enough to reveal aspects of the pattern of acquisition of new character states.

Of all the usually acknowledged higher taxa, the mammals have by far the most extensively preserved fossil stem group, and therefore constitute the best available case for assessing how well the model performs when faced with a real long-term evolutionary trend. The record of the stem mammals ('non-mammalian synapsids', or 'mammal-like reptiles') has been reviewed in some detail by Kemp (2005) and only a brief resumé is presented here (Fig. 6). The earliest known synapsids occur in the Upper Carboniferous (Pennsylvanian), approximately contemporaneous with the earliest stem sauropsids (reptiles plus birds); this gives a latest possible date for the divergence of the two taxa of about 310 million years ago (Ma). There are up to about a dozen grades of pre-mammalian synapsid fossils known, with increasing numbers of mammalian characters. The relationships of some of these taxa are only supported by a few, minor characters, and their exact places on the cladogram are in doubt (Kemp 2006a). The positions of the remaining eight are relatively well supported, and they allow reconstruction of a set of successive hypothetical ancestor-descendants at this number of nodes on the phylogenetic tree (Fig. 8), during the ensuing 100 Ma that led to the earliest mammaliaforms of Late Triassic age. Traditionally three paraphyletic supergrades have been distinguished phenetically, which therefore include three arbitrarily defined segments of the evolving lineage (Fig. 6). The most basal are the pelycosaurs of Late Carboniferous and Early Permian age, which retained a generally ancestral amniote form, with homodont dentition, heavily built sprawling gait, and by inference ectothermic temperature physiology. The next supergrade consists of the basal therapsids, which first appeared in the Mid-Permian and dominated the Late Permian terrestrial vertebrate biota.

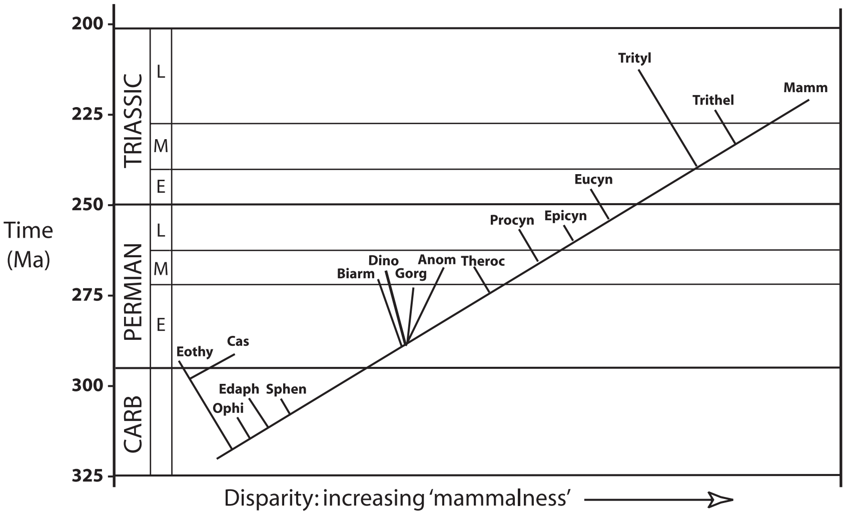


Fig. 6—Chart of the phylogeny of synapsids showing approximate times of first occurrence in the fossil record and a subjective assessment of degrees of 'mammalness'. Anom, Anomodontia; Biarm, Biarmosuchidae; Cas, Caseidae; Dino, Dinocephalia; Edaph, Edaphosauridae; Eothy, Eothyrididae; Epicyn, Epicynodontia; Eucyn, Eucynodontia; Gorg, Gorgonopsia; Mamm, Mammaliaformes; Ophi, Ophiacodontidae; Procyn, Procynosuchidae; Sphen, Sphenacodontidae; Theroc, Therocephalia; Trithel, Tritheledontidae; Trityl, Tritylodontidae; Ma, million years ago.

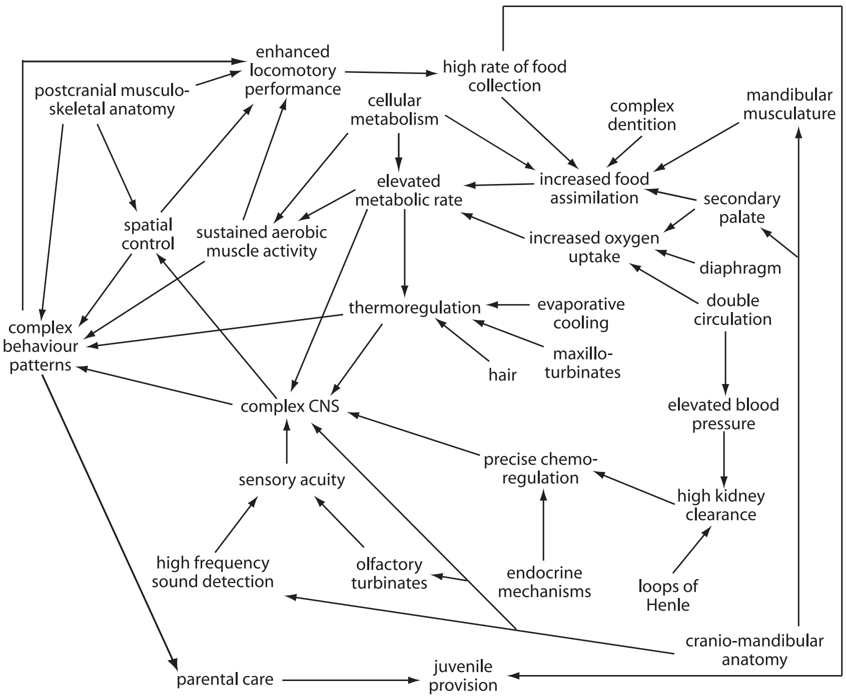


Fig. 7—Diagrammatic representation of the integration of the structures and functions of a mammal.

They had evolved incipiently mammalian characters of the dentition, jaw musculature, gait and, presumably, physiology. One of these therapsid groups, the cynodonts, constitutes the third conventional supergrade. They survived the end-Permian mass extinction and radiated throughout the ensuing Triassic, although increasingly in the company of new archosaurian groups. Several grades included within the cynodont supergrade illustrate the continual acquisition of mammalian traits, and by the end of the Triassic mammaliaforms, such as *Morganucodon*, had acquired almost all of the characteristics of the crown group Mammalia.

The nature of the integration of mammalian traits – reticular rather than modular

A revised version of a diagram first published by Kemp (1982), and frequently reproduced since, illustrates the functional interrelationship of many of the structures and processes of mammals (Fig. 7). Its purpose is as a reminder that virtually every part of the organism is ultimately both dependent upon, and necessary for, the effective functioning of almost every other part, whether directly or indirectly. For simplicity's sake many links are not shown, including the far greater permeation of the central nervous system and vascular system into all aspects of the animal's life. 'Cellular metabolism' too, stands for a vastly more complex set of relationships.

This reticular organization contrasts with the concept of modular construction, in which some parts are grouped together as modules largely independent of other such modules. At the anatomical level there are only a few repeated parts in adult mammals, although at the cellular and molecular levels there is, of course, an essentially modular architecture. More importantly, there is nothing resembling a division into functional modules that stands up to scrutiny. To consider one possibility, the function of endothermy might seem to be a candidate functional module. However, once all the structures and processes necessary for the maintenance of mammalian endothermy are listed, it becomes clear that this function involves virtually the whole organism (Kemp 2006b). Most immediately, it includes such disparate traits as the number of mitochondria in the cells, the rate of circulation of the blood, the conductance properties of the integument, and all manner of behavioural responses. Then there is the endocrine control of water conservation necessary in an organism with an elevated body temperature, the evaporative cooling mechanism, and the entire neural, musculature and mechanical design of the phenotype for collecting the 10 times as much food per day needed for such an extravagant mode of temperature physiology. Conversely, there is little about the biology of a mammal that does not depend upon the existence of endothermy. Another possible module might be the limbs, but again it is clear that the functioning of the limbs is so embedded within the entire biological organization of the organism that there are no functional boundaries allowing them to be recognized as having even a semi-independent existence.

In so far as this is a realistic picture of the nature of mammalian phenotypic integration, it corroborates the correlated progression model. The degree of flexibility of the functional linkage between a particular trait and other traits can be thought of as a measure of the variation possible in that trait, without compromising the functional integration of the system as a whole to the point of significant reduction in the fitness of the organism. A trait might be relatively flexibly integrated and therefore capable of an incremental evolutionary change. However, the change itself may then stiffen the linkage, such that no further change in that trait at that time would be possible, because now the effect would be to reduce the trait's integration into the system.

It is inherent to this view of mammalian phenotypic organization that it is not possible to predict the actual sequence by which small changes in a great many traits led through morphospace to the fully expressed mammalian condition. It can, however, be predicted that no one trait ever evolved a large change in isolation of changes in many others.

The sequence of acquisition of characters – correlated progression rather than modular shuffling

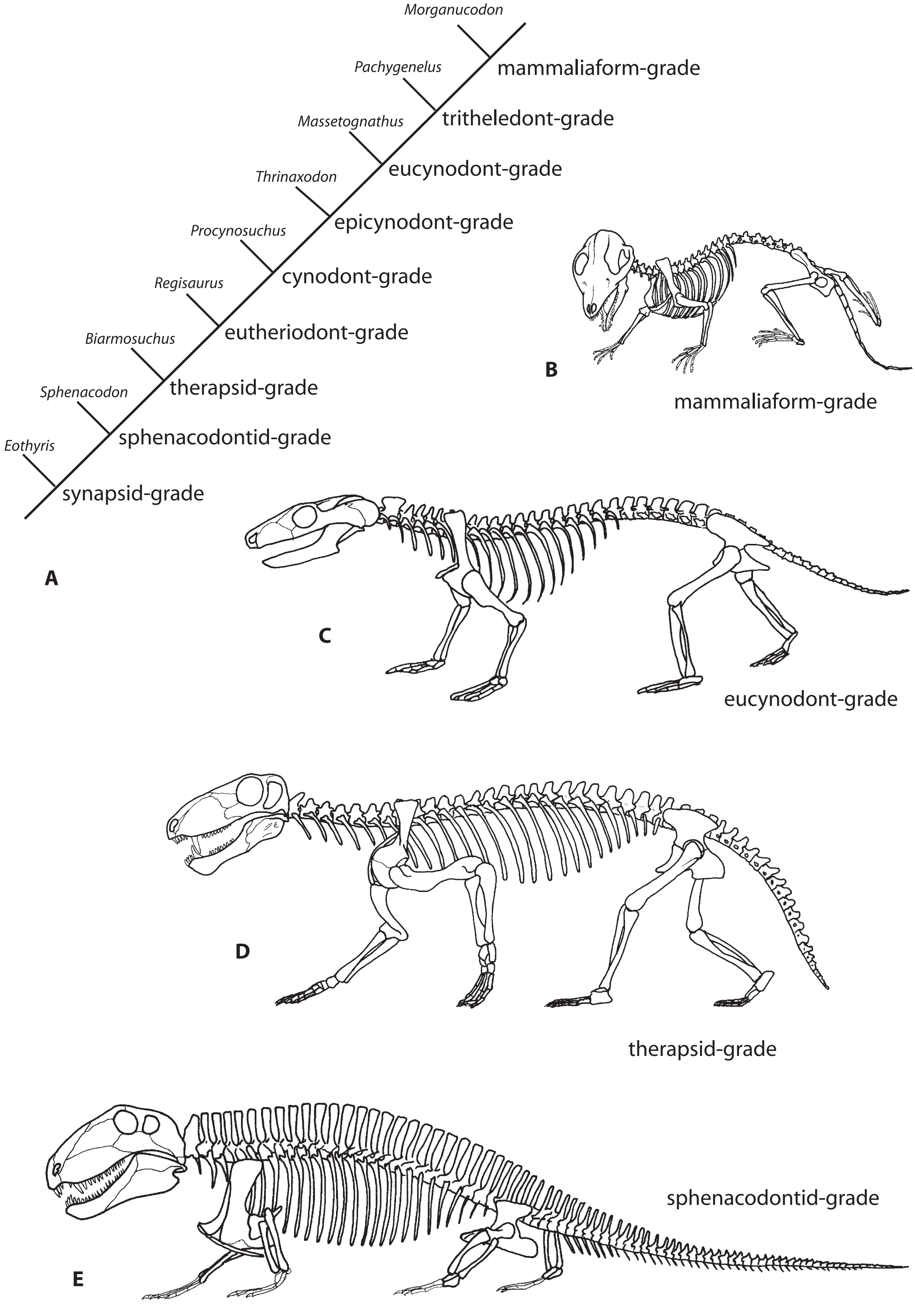
Osteological characters associated with the nodes of the cladogram (Fig. 8) are listed in Sidor and Hopson (1998) for all taxa; Kemp (2006a) for Therapsida; Hopson and Kitching (2001) for Cynodontia onwards; Abdala (in press) for Eutheriodontia onwards; and Kielan-Jaworowska *et al.* (2004) for Mammaliaformes. To establish that the pattern of acquisition of mammalian traits as inferred from the cladogram is consistent with the correlated progression model, a general description of the main features that evolved will suffice.

Synapsid node. The only prominent new traits compared to the ancestral amniote were the slight enlargement of teeth in the canine region, and the small temporal fenestra, indicating a more powerful bite. The structure of the occiput was modified to increase its strength. The vertebral zygapophyses were inclined rather than horizontal and there were other minor modifications to the postcranial skeleton.

Sphenacodontid node (Fig. 8E). The teeth in the canine region were distinctly enlarged, and the anterior, incisiform teeth were differentiated from the blade-like post-canine teeth. The temporal fenestra was enlarged and a small reflected lamina of the angular had appeared, indicating a reorganization of the adductor musculature. There was an additional sacral rib and a more slender, curved femur, indicating a more versatile hindlimb.

Therapsid node (Fig. 8D). This is the most pronounced node of all in terms of the evolution of the incipiently mammalian condition. Kemp (2006a) noted 29 cranial, four dental, one vertebral, nine forelimb and 12 hindlimb characters. The outcome was a substantially more powerful and accurate bite force, with greatly enlarged canines and incisors, and far larger adductor musculature. The limbs were longer and more gracile, giving more agile, versatile locomotory abilities, while the brain was enlarged and there was an increase in sensitivity of the middle ear to airborne sound. The nasal cavity was enlarged and there is evidence of an increase in the extent of turbinates carrying olfactory epithelium. By inference, the basal metabolic rate was increased, with consequences for thermoregulatory ability and the maximum level of aerobic activity. The bone histology had become fibro-lamellar, indicating increased growth rates, itself possibly correlated with evolving endothermy.

Eutheriodont node. There was a further substantial modification to the adductor jaw musculature by narrowing of the roof to create a sagittal crest, and some of the muscle fibres started to invade the outer surface of the jaw as an incipient masseter muscle. There is some suggestion of the presence of maxillo-turbinates, which would correlate with endothermy.


Morganucodon
mammaliaform-grade
Pachygenelus
tritheledont-grade
Massetognathus
eucynodont-grade
Thrinaxodon
epicynodont-grade
Procynosuchus
cynodont-grade
Regisaurus
eutheriodont-grade
Biarmosuchus
therapsid-grade
Sphenacodon
sphenacodontid-grade
Eothyris
synapsid-grade
A
B
mammaliaform-grade
C
eucynodont-grade
D
therapsid-grade
sphenacodontid-grade
E

The tail was reduced and the limbs were slender, indicating enhanced mobility.

Cynodont node. This was another important shift, with differentiation between pre-molariform and molariform post-canine teeth. The dentary bone had started to enlarge relative to the post-dentary bones. A definitive masseter muscle had evolved, originating on the bowed zygomatic arch and inserting on the external surface of the mandible, and the deepened sagittal crest accommodated a large temporalis muscle. There was a secondary palate, and the form of the rib cage indicates the presence of a diaphragm. The brain was further enlarged, and hearing by means of the reduced post-dentary bones and stapes was improved. The occipital condyle and atlas–axis vertebrae created increased mobility of the head. Greater mobility of the forelimb had evolved, and in the pelvis, the ilium had started to expand forwards and the pubis had started to reduce in size.

Epicynodont node. The jaw musculature had continued to enlarge and reorganize, leading to a reduced hinge reaction and increased force and accuracy of bite. In the postcranial skeleton, evolution of costal plates on the ribs indicated a permanently parasagittal hindlimb and highly active gait.

Eucynodont node (Fig. 8C). The dentary dominated the lower jaw and the reorganization of the adductor musculature was complete, so that the hinge reaction force was very small, and both the force and accuracy of the bite were close to mammalian levels. The upper and lower teeth actively worked together, and tooth replacement was reduced towards the mammalian pattern. The costal ribs were replaced by direct muscular support of the vertebral column, increasing its flexibility, and it was fully differentiated into cervical, thoracic and lumbar regions. The shoulder girdle was narrow and the forelimbs were yet more versatile. The ilium was further expanded and the pubis was small and reflected backwards. Sound reception was improved by the reduction of the post-dentary bones. The brain was more enlarged.

Tritheledont node. The body was very reduced in size and the post-orbital bar was lost. The dentary contacted the squamosal, forming the new, mammalian jaw articulation. The enamel of the teeth was prismatic, indicating greater resistance to wear during occlusion. The post-cranial skeleton was close to fully mammalian, including reduction of the coracoid, bulbous humeral head, and elongated ilium bearing a longitudinal ridge.

Mammaliaform node (Fig. 8B). There were complex, molariform teeth capable of a very precise shearing action. The dentary–squamosal jaw articulation was a condyle and glenoid system, which permitted the teeth on one side to be activated by the adductor jaw musculature of both sides. The brain was enlarged about four times, and high frequency hearing was now possible. Locomotion was highly agile, and capable of arboreality. Tooth replacement was diphyodont, suggesting the occurrence of lactation.

The pattern. At every stage, evolutionary changes in both the feeding mechanism and the locomotory function occurred, never in just one of them alone. Furthermore, the osteology indicates that other structures, such as brain size, nasal cavity elaboration, hearing ability, secondary palate and evolution of a diaphragm occurred by increments spread over more than one grade. Taken together, the pattern of acquisition of mammalian traits points to a pattern of relatively small changes in several functional systems having occurred by each new stage. To this direct evidence may be added the inferences to be drawn from those osteological characters related to unpreservable features such as increasing metabolic rates, elevated levels of food intake, raised ventilation rates, enhanced locomotory energetics and increasingly sophisticated neural control mechanisms. Mapping all these onto the scheme of integrated mammalian function indicates beyond question that the characters that are unpreserved in fossil specimens must also have been undergoing this pattern of incremental, correlated evolution.

The sequence of acquisition of mammalian characters strongly corroborates the correlated progression model.

Ecological gradient

It was concluded above that a long-term trend of morphological change, leading eventually to a new higher taxon, implies the existence of a fairly general ecological gradient of overlapping potential niches. For a lineage to track it requires evolutionary change in many correlated traits. The relatively few authors who have discussed the adaptive force driving the evolution of mammals from their remote, pelycosaur-grade ancestors have all concluded that the evolution of endothermic temperature physiology played the central role, although with different opinions about what was the primary selective force for it (Kemp 2006b). Some attributed it to the thermoregulatory function, for either physiological reasons (Olson 1969, 1971; McNab 1978), or ecological reasons (Crompton *et al.* 1978; Taylor 1980); others to increased aerobic activity (Bennett *et al.* 1986; Ruben 1995); and a

Fig. 8—Cladogram of synapsids indicating hypothetical ancestor–descendant stages on the lineage from basal synapsid to mammals, with illustrations of the skeletons of four of them. Redrawn from Romer and Price (1940), Kemp (2006a), Jenkins (1970) and Jenkins and Parrington (1976).

third group to the function of parental provision (Farmer 2000; Koteja 2000).

However, in the light of the correlated progression model, an even broader view of the adaptive significance of the trend from pelycosaur-grade to mammal must be taken, which accounts not just narrowly for the origin of mammalian endothermy but also for all the other characteristic attributes of mammals. Kemp (1982, 1985) proposed that the overarching attribute manifested by the origin of the mammals is increasing homeostatic ability: the maintenance of a constant internal environment in the face of a fluctuating external environment, by means of high-energy regulatory processes. Therefore, in terms of the adaptive landscape discussed earlier, the ecological gradient along which the lineage leading to mammals evolved can be represented as a series of overlapping niches that required, for their successive occupation, an ever-increasing internal regulatory ability. To an ever-increasing extent as the lineage evolved, this allowed the organisms to remain active in a range of ambient temperatures, diurnally and seasonally, and fluctuating water availability such as seasonal aridity. At the start of the trend was a niche for some particular basal amniote with low metabolic rate, incapable of maintaining its activity beyond a narrow range of ambient temperatures, low resistance to desiccation, poor spatial manoeuvrability in food collection, and a low level of central nervous control. By the end there was a niche occupied by an organism whose metabolic rate was elevated several-fold, which allowed it to remain at full activity level over a wide range of ambient temperatures, and to control precisely its internal water, solute and osmotic levels even within a desiccating environment. It was capable of collecting the more or less 10-fold increase in food required to provide the very high energetic cost of regulatory mechanisms, and had a large, complex brain to precisely control the physiology, and to endow the flexibility of behaviour needed to ensure such things as adequate foraging ability. There was also the necessity for parental provision for the neonate, which on its own would be too undeveloped to regulate adequately for itself. Such, in essence, is a mammal (Fig. 7). The ridge on the adaptive landscape, connecting these two idealized niches at either end, consisted of a series of overlapping niches spanning the intervening ecospace. The transitional phenotypes occupying them necessarily had to evolve modifications in many structures and functions by correlated progression.

It is difficult, but potentially very informative, to consider the rate of evolution of the lineage along the ecological gradient, and what might have controlled it. Overall it took about 100 Ma for all the characters to evolve from pelycosaurian to mammaliaform state. Sidor and Hopson (1998) attempted to show whether the rate of evolution observed over the whole lineage was relatively steady or unsteady, by comparing the number of synapomorphies at the nodes of their synapsid cladogram with the estimated length of the time intervals between nodes. They found a significant positive correlation, from which they inferred that there had been a roughly constant rate of acquisition of mammalian characters. Of course, their necessary assumption that the individual characters scored represent quantitatively equal units of evolutionary change, the very large number of non-osteological characters missing in fossils, the uncertainty of dating nodes by using the dates of known fossils, and the unknown number of nodes for which there is no fossil evidence all conspire together to render their conclusion tentative. Nevertheless, if Sidor and Hopson (1998) are in fact correct in their belief that the rate of acquisition of mammalian characters was relatively constant, this would be compatible with the idea of correlated drag, discussed earlier. Under the conditions of the correlated progression model, it was noted that the effect of selection acting simultaneously on the variation of many characters will be to reduce the rate of evolution of any one of them. If all the characters were indeed similarly affected, then the rate of change of all them would be expected to fall to the same low value.

A second possible control on the rate of evolution is ecological opportunity, which is relevant when parts of the ecological gradient only become available to the evolving lineage at certain historic moments in time. In contrast to correlated drag, ecological opportunity may tend to cause periods of accelerated rate of evolution. Within the trend to mammals, on at least one occasion a transition was evidently correlated with specific palaeogeographical circumstances that opened up hitherto unavailable climatic regions, offering conditions appropriate for continuing the development of mammalian biology (Kemp 2006a). This was the transition from the sphenacodontid pelycosaur-grade to the basal therapsid-grade, as represented by *Biarmosuchus* (Fig. 6). The pelycosaurs of the Early Permian were largely restricted to an equatorial, permanently humid biome analogous to the modern-day tropical rain forest. However, the evolving therapsids appear to have been able to enter the adjacent, seasonally dry tropical biome, within which they evolved many new mammalian characters, suggesting that the ecological opportunity offered by this new habitat did indeed promote an acceleration in the rate of evolution of the lineage. During the mid-Permian, another ecological opportunity opened up, when the Pangaea-wide deserts that had isolated the tropical from the temperate regions of the earth retreated along the eastern margin of Pangaea sufficiently for synapsids to reach the cooler, temperate biomes of both southern and northern hemispheres. It was in these cooler conditions that the main therapsid radiation took place, including, significantly, the earliest cynodonts, which was another point of the lineage marked by a substantial increase in mammalian characters.

A third possible ecological opportunity may be indicated by the final stages in the transition to mammals, which consisted of a lineage of eucynodonts that underwent miniaturization (Bonaparte and Crompton 1994; Kielan-Jaworowska *et al.* 2004; Kemp 2005; page 135). This is believed to have been associated with entry into a nocturnal, insectivorous habitat and, although the palaeoecology of this event has been little discussed, it may well represent another critical extension of the adaptive ridge, which permitted the final stage of the transition to mammals.

Species selection

There is a bias in the pattern of evolution of synapsids which points to the possibility of a role for species selection (Kemp 1982, 1985, 2005). The hypothetical ancestor reconstructed by cladistic methodology for every node along the lineage (Fig. 8), from ancestral amniote to mammal, was carnivorous to judge by the distribution of dental characters among the fossils. Evolution of an herbivorous dentition only occurred as a modification in certain side branches, such as caseid pelycosaurs, tapinocephalid dinocephalians, anomodont therapsids, traversodontid eucynodonts and tritylodontids. The cladistic analysis also suggests that each of the hypothetical ancestors was at the lower end of the respective size range of the carnivorous forms in the side branches they generated. This bias is inconsistent with natural selection being the sole explanation for the evolutionary trend. If selection of more mammal-like characters occurred in relatively small carnivores, it is difficult to see why it should not also have occurred in herbivores or large carnivores as well. Indeed, over time less mammal-like versions of these latter ecotypes were replaced in the biota by more mammal-like versions, but not by direct evolution. Instead, more mammal-like herbivores and large carnivores evolved anew each time, from a progressive, relatively small carnivorous ancestor.

This aspect of the evolutionary pattern is *prima facie* evidence for a species-selection cause of the trend, whereby relatively small, relatively more mammal-like carnivores have a higher probability of speciating compared to the other types. Under these circumstances, a trend of increasingly mammal-like, relatively small carnivores will occur over time. The cause of such differential speciation must be speculative, for extremely little is actually understood about the factors that affect probabilities of speciation in different kinds of organisms (e.g. Barraclough *et al.* 1999; Coyne and Orr 2004). In the light of the current acceptance, discussed earlier, that an aggregated organism-level character in principle can be the cause of species selection, the range of possibilities is quite wide. Carnivorous species, especially those whose members have relatively higher metabolic rates and therefore higher food requirements, may be expected to exist as smaller populations; those consisting of smaller organisms may have lower vagility. Both parameters taken together may create a greater tendency for isolation of small subpopulations, and hence, on a simple allopatric model of speciation, a greater probability of speciating. Alternatively the explanation may lie in differential extinction probabilities. If those kinds of species other than relatively small, relatively more mammal-like carnivores have a higher probability of extinction, the trend would also occur, but as with speciation, too little is known of the variables that affect extinction probabilities to say more than that the possibility exists.

Whatever its proximate cause might have been, this process of species selection may well have been a significant part of the explanation for why the trend ran for tens of millions of years in a consistent direction. Suppose, as is evidently typical for mammals, a speciation event in the lineage occurred on average every couple of million years, and that each such event was indeed differential and so triggered an incremental step along the trend. There would have been 50 such trend-driving speciation events, spread over the course of the 100 million years from the start of the trend to the appearance of the first mammaliaform. This inferred species-selection process was presumably superimposed upon the natural selection of small changes in many traits by correlated progression, occurring within each evolving species. Certainly the two processes are potentially complimentary, not mutually exclusive.

Conclusions

A descriptive model for the origin of mammals

By combining general ideas about the causes of macroevolutionary change, the nature of mammals, and the fossil record of the stem-group, a model of the origin of mammals can be proposed.

- From an ancestral basal amniote, an evolutionary trend tracking a sequence of overlapping niches occurred, lasting about 100 million years. It followed a ridge or narrow, elongated plateau in a Simsonian adaptive landscape, in a direction of increasing adaptation for fully active, terrestrial life under fluctuating environmental conditions. Selection was based on the overall phenotypic fitness resulting from the simultaneous interaction of the many characters associated, directly or indirectly, with internal regulatory mechanisms, neuromuscular control, and adaptability of behaviour. Virtually all the traits underwent evolutionary changes, and functional integration between them was maintained by correlated progression of small, incremental changes in all of them.
- The pace of the trend was slow because of the process of correlated progression, in part because at any one time many of the traits were constrained from evolving by tight functional integration with other traits, and in part because many traits were evolving by close to neutral drift, rather than by selection.
- Species selection in the form of a higher probability of speciation of relatively small, relatively more mammal-like carnivores was a significant part of the mechanism driving the trend in a consistent direction.
- On at least two occasions, specific environmental opportunities occurred that allowed the trend to proceed. One was when the lineage entered a seasonally dry, tropical biome, and another when it invaded temperate climatic

regions. These promoted periods of adaptive radiation at intervals along the adaptive ridge.

Are the mammals a typical case?

It has to be asked whether the origin of the mammals is a unique and atypical case, and therefore that a comparable model does not apply to other examples of the origin of new higher taxa. It is not the purpose of the present paper to explore in depth other such cases, but simply to suggest that the mammal case does in fact highlight certain possibly general features of the evolutionary processes involved at this phylogenetic level. To start with, a very general ecological gradient, modelled as a lengthy adaptive ridge, can certainly be postulated for other vertebrate groups. In the case of the birds, it would have been similar to the one proposed for mammals, involving increasing independence of environmental fluctuations, and requiring the same kinds of physiological processes for internal regulation and associated structural, functional, and behavioural correlates. For the tetrapods, it is easy to visualize an adaptive ridge, consisting of an ecological gradient starting from a mid-freshwater habitat, via shallow water and wet mudflats, to dry land. Tracking it would have required correlated changes in many functionally integrated traits concerned with water and temperature physiology, food collection, substrate locomotion, sensory modalities, central nervous control, and reproductive habits, rather than selection for but few characters. For the various higher invertebrate taxa, it is less clear what such a general gradient might have been. Perhaps the increasing oxygen levels of the Cambrian created an adaptive ridge, leading to selection for increased body size, and the necessarily associated complexity of structure and function.

The theoretical arguments presented in favour of correlated progression apply equally to these other cases, although much less is known about the actual pattern of acquisition of derived traits, for want of more complete fossil records. In the case of both the tetrapods (Clack 2002; Daeschler *et al.* 2006; Shubin *et al.* 2006) and the birds, what is known certainly seems to be compatible with this aspect of the model.

The role of species selection in driving long-term trends is perhaps the most challenging aspect. In the case of the mammals, there is empirical evidence for it, in the form of the bias among the successive ancestor–descendant stages towards one particular kind of phenotype. It would be interesting to search other examples for comparable evidence of differential speciation along the trend.

Does the origin of a new higher taxon differ from normal evolution?

The question posed at the start of this paper was whether the origin of a new higher taxon is the result of normal micro-evolutionary processes continuing for long enough, or whether there are special genetic or environmental circumstances associated with it. The answer offered here is that there are indeed special circumstances.

The first is that a long ridge in the adaptive landscape must exist, the tracking of which demands changes in the general biological nature of the phenotype, and therefore accounts for the large number of traits involved. This contrasts with the view that normal evolutionary transitions are initiated by a key adaptation in a single character, and that selection for a single, or at most a very few, traits drives the ensuing adaptive evolution.

The second is that maintenance of phenotypic integration is by the correlated progression of functionally linked characters, and that many characters for much of the time may behave as close to selectively neutral. This is in contrast to the view that integration is normally maintained by changes in the external relationships between phenotypic modules that are relatively invariant internally.

The third is that species selection, based on differential probability of speciation or of extinction can be a significant part of the process driving the lineage along the adaptive ridge. This is in contrast to the view that selection at a higher hierarchical level than that of the organism is not significant in evolution.

References

Abdala, F. in press. Redescription of *Platycraniellus elegans* (Therapsida, Cynodontia) from the Early Triassic of South Africa, and the cladistic relationships of eutheriodonts. – *Palaeontology*.

Alroy, J. 1998. Cope's rule and the dynamics of body mass evolution in North American fossil mammals. – *Science* **280**: 731–734.

Alroy, J. 2000. Understanding the dynamics of trends within evolving lineages. – *Paleobiology* **26**: 319–329.

Arnold, S. J., Pfrender, M. E. and Jones, A. G. 2001. The adaptive landscape as a conceptual bridge between micro and macrevolution. – *Genetica* **112–113**: 9–32.

Barraclough, T. G., Vogler, A. P. and Harvey, P. H. 1999. Revealing the factors that promote speciation. In Magurran, A. E. and May, R. M. (Eds): *Evolution of Biology Diversity*, pp. 202–219. Oxford University Press, Oxford.

Bennett, A. F. and Ruben, J. A. 1986. *The Metabolic and Thermoregulatory Status of Therapsids*. In Hotton, N. III, MacLean, P. D., Roth, J. J. and Roth, E. C. (Eds): *The Ecology and Biology of Mammal-like Reptiles*. Smithsonian Institution, Washington DC.

Bolker, J. A. 2000. Modularity in development and why it matters. – *American Zoologist* **40**: 770–776.

Bonaparte, J. F. and Crompton, A. W. 1994. A juvenile probainognathid cynodont skull from the Ischigualasto Formation and the origin of mammals. – *Revista Museo Argentino de Ciencias Naturales, Paleontología* **5**: 1–12.

Borycki, A.-G. 2004. Sonic hedgehog and Wnt signalling pathways during development and evolution. In Schlosser, G. and Wagner, G. P. (Eds): *Modularity in Development and Evolution*, pp. 101–131. Chicago University Press, Chicago.

Budd, G. E. 1998. Arthropod body-plan evolution in the Cambrian with an example from anomalocaridid muscle. – *Lethaia* **31**: 197–210.

Carroll, R. L., Irwin, J. and Green, D. M. 2005. Thermal physiology and the origin of terrestriality in vertebrates. – *Zoological Journal of the Linnean Society* **143**: 345–358.

Cheetham, A. H. 1986. Tempo of evolution in a Neogene bryozoan: rates of morphologic change within and across species boundaries. – *Paleobiology* **12**: 190–202.

Cheetham, A. H. 1987. Tempo of evolution in a Neogene bryozoan: are trends in single morphological characters misleading? *Paleobiology* **13**: 286–296.

Cheverud, J. M. 2004. Modular pleiotropic effects of quantitative trait loci on morphological traits. In Schlosser, G. and Wagner, G. P. (Eds): *Modularity in Development and Evolution*, pp. 132–153. Chicago University Press, Chicago.

Cheverud, J. M., Routman, E. J. and Irschick, D. J. 1997. Pleiotropic effects of individual gene loci on mandibular morphology. – *Evolution* **51**: 2006–2016.

Clack, J. A. 2002. *Gaining Ground: the Origin and Evolution of Tetrapods*. Indiana University Press, Bloomington.

Coyne, J. A. and Orr, H. A. 2004. *Speciation*. Sinauer Associates, Sunderlamd, MA.

Crompton, A. W., Taylor, C. R. and Jagger, J. A. 1978. Evolution of homeothermy in mammals. – *Nature* **272**: 333–336.

Daeschler, E. B., Shubin, N. H. and Jenkins, F. A. Jr. 2006. A Devonian tetrapod-like fish and the evolution of the tetrapod body plan. – *Nature* **440**: 757–763.

Depew, D. J. and Weber, B. H. 1995. *Darwinism Evolving: Systems Dynamics and the Genealogy of Natural Selection*. Massachusetts Institute of Technology, Cambridge, MA.

Erwin, D. H. 2000. Macroevolution is more than repeated rounds of microevolution. – *Evolution and Development* **2**: 78–84.

Farmer, C. G. 2000. Parental care: the key to understanding endothermy and other convergent features in birds and mammals. – *American Naturalist* **155**: 326–334.

Foote, M. 1997. The evolution of morphological diversity. – *Annual Review of Ecology and Systematics* **28**: 129–152.

Gayon, J. 2000. History of the concept of allometry. – *American Zoologist* **40**: 748–758.

Gould, S. J. 1990. Speciation and sorting as the source of evolutionary trends, or 'things are seldom what they seem'. In McNamara, K. J. (Ed.): *Evolutionary Trends*, pp. 3–27. Belhaven Press, London.

Gould, S. J. 1991. The disparity of the Burgess Shale arthropod fauna and the limits of cladistic analysis: why we must strive to quantify morphospace. – *Paleobiology* **17**: 411–423.

Gould, S. J. 2002. *The Structure of Evolutionary Theory*. Belknap Press, Harvard.

Gould, S. J. and Lloyd, E. A. 1999. Individuality and adaptation across levels of selection: how shall we name and generalise the unit of Darwinism? – *Proceedings of the National Academy of Sciences of the USA* **96**: 11904–11909.

Grantham, T. A. 1995. Hierarchical approaches to macroevolution: recent work on species selection and the 'effect hypothesis'. – *Annual Review of Ecology and Systematics* **26**: 301–321.

Griswald, C. K. 2006. Pleiotropic mutation, modularity and evolvability. – *Evolution and Development* **8**: 81–93.

Haldane, J. B. S. 1957. The cost of natural selection. – *Journal of Genetics* **55**: 511–524.

Hansen, T. F. 2003. Is modularity necessary for evolvability? Remarks on the relationship between pleiotropy and evolvability. – *Biosystem* **69**: 83–94.

Hansen, T. F. and Houle, D. 2004. Evolvability, stabilising selection, and the problem of stasis. In Pigliucci, M. and Preston, K. (Eds): *Phenotypic Integration: Studying the Ecology and Evolution of Complex Phenotypes*, pp. 130–150. Oxford University Press, Oxford.

Hopson, J. A. and Kitching, J. W. 2001. A probainognathan cynodont from South Africa and the phylogeny of nonmammalian cynodonts. – *Bulletin of the Museum of Comparative Zoology* **156**: 5–35.

Hunter, J. P. 1998. Key innovations and the ecology of macroevolution. – *Trends in Ecology and Evolution* **13**: 31–36.

Hunter, J. P. and Jernvall, J. 1995. The hypocone as a key innovation in mammalian evolution. – *Proceedings of the National Academy of Sciences of the USA* **92**: 10718–10722.

Jenkins, F. A. 1970. The Chañares (Argentina) Triassic reptile fauna VII. The postcranial skeleton of the traversodontid *Massetognathus pascuali* (Therapsida, Cynodontia). – *Breviora* **352**: 1–28.

Jenkins, F. A. and Parrington, F. R. 1976. The postcranial skeleton of the Triassic mammals *Eozostrodon*, *Megazostrodon*, and *Erythrotherium*. – *Philosophical Transactions of the Royal Society B* **273**: 387–431.

Kauffman, S. A. 1993. *The Origins of Order: Self-Organisation and Selection in Evolution*. Oxford University Press, Oxford.

Kemp, T. S. 1982. *Mammal-like Reptiles and the Origin of Mammals*. Academic Press, London.

Kemp, T. S. 1985. Synapsid reptiles and the origin of higher taxa. – *Special Papers in Palaeontology* **33**: 175–184.

Kemp, T. S. 1999. *Fossils and Evolution*. Oxford University Press, Oxford.

Kemp, T. S. 2005. *The Origin and Evolution of Mammals*. Oxford University Press, Oxford.

Kemp, T. S. 2006a. The origin and evolution of the therapsid mammal-like reptiles: a palaeobiological hypothesis. – *Journal of Evolutionary Biology* **19**: 1231–1248.

Kemp, T. S. 2006b. The origin of mammalian endothermy: a paradigm for the evolution of complex biological structure. – *Zoological Journal of the Linnean Society* **147**: 473–488.

Kielan-Jaworowska, Z., Cifelli, R. L. and Luo, Z.-X. 2004. *Mammals from the Age of Dinosaurs: Origins, Evolution, and Structure*. Columbia University Press, New York.

Kimura, M. 1983. *The Neutral Theory of Molecular Evolution*. Cambridge University Press, Cambridge.

Kingsolver, J. G. and Pfennig, D. W. 2004. Individual-level selection as a cause of Cope's rule of phyletic size increase. – *Evolution* **58**: 1608–1612.

Kirschner, M. and Gerhart, J. 1998. Evolvability. – *Proceedings of the National Academy of Sciences of the USA* **95**: 8420–8427.

Klingenberg, C. P. 1998. Heterochrony and allometry: the analysis of evolutionary change in ontogeny. – *Biology Reviews* **73**: 79–123.

Klingenberg, C. P. 2004. Integration, modules, and development: molecules to morphology to evolution. In Pigliucci, M. and Preston, K. (Eds): *Phenotypic Integration: Studying the Ecology and Evolution of Complex Phenotypes*, pp. 213–230. Oxford University Press, Oxford.

Koteja, P. 2000. Energy assimilation, parental care and the evolution of endothermy. – *Proceedings of the Royal Society of London B* **267**: 479–484.

Lande, R. 1979. Quantitative genetic analysis of multivariate evolution, applied to brain : body size allometry. – *Evolution* **33**: 402–416.

Lee, M. S. Y. 1996. Correlated progression and the origin of turtles. – *Nature* **379**: 812–815.

Lewontin, R. C. 1978. Adaptation. – *Scientific American* **239**: 156–169.

Liem, K. F. 1974. Evolutionary strategies and morphological innovation: cichlid pharyngeal jaws. – *Systematic Zoology* **22**: 425–441.

Lloyd, E. A. and Gould, S. J. 1993. Species selection on variability. – *Proceedings of the National Academy of Sciences of the USA* **90**: 595–599.

Mayr, E. 1982. *The Growth of Biological Thought: Diversity, Evolution, and Inheritance*. Belknap Press, Cambridge, MA.

McNab, B. K. 1978. The evolution of endothermy in the phylogeny of mammals. – *American Naturalist* **112**: 1–21.

McNamara, K. J., Ed. 1995. *Evolutionary Change and Heterochrony*. John Wiley and Sons, Chichester.

McNamara, K. J. 1990. *Evolutionary Trends*. – Belhaven Press, London.

McShea, D. W. 1994. Mechanisms of large-scale evolutionary trends. – *Evolution* **48**: 1747–1763.

McShea, D. W. 1998. Possible largest-scale trends in organismal evolution. – *Annual Review of Ecology and Systematics* **29**: 293–318.

Merilä, J. and Björklund, M. 2004. Phenotypic integration as a constraint and adaptation. In Pigliucci, M. and Preston, K. (Eds): *Phenotypic Integration: Studying the Ecology and Evolution of Complex Phenotypes*, pp. 107–129. Oxford University Press, Oxford.

Monteiro, L. R., Bonato, V. and Reis, S. F., dos. 2005. Evolutionary integration and morphological diversification in complex morphological structures: mandible shape divergence in spiny rats (Rodentia, Echimyidae). – *Evolution and Development* **7**: 429–439.

Olson, E. C. 1969. The evolution of mammalian characters. – *Evolution* **13**: 344–353.

Olson, E. C. 1971. *Vertebrate Paleozoology*. John Wiley and Sons, New York.

Preston, K. and Ackerly, D. D. 2004. The evolution of allometry in modular organisms. In Pigliucci, M. and Preston, K. (Eds): *Phenotypic Integration: Studying the Ecology and Evolution of Complex Phenotypes*, pp. 80–106. Oxford University Press, Oxford.

Raff, R. A. 1996. *The Shape of Life*. University of Chicago Press, Chicago.

Riedl, R. 1978. *Order in Living Organisms: a Systems Analysis of Evolution*. John Wiley and Sons, Chichester.

Romer, A. S. and Price, L. W. 1940. Review of the Pelycosauria. – *Geological Society of America Special Papers* **28**: 1–538.

Ruben, J. 1995. The evolution of endothermy in mammals: from physiology to fossils. – *Annual Review of Physiology* **57**: 69–95.

Schindewolf, O. W. 1993. *Basic Questions in Paleontology: Geologic Time, Organic Evolution, and Biological Systematics* (translated by Judith Schaefer). Chicago University Press, Chicago.

Schlosser, G. 2002. Modularity and the units of selection. – *Theory in Biosciences* **121**: 1–80.

Schlosser, G. 2004. The role of modules in development and evolution. In Schlosser, G. and Wagner, G. P. (Eds): *Modularity in Development and Evolution*, pp. 519–582. University of Chicago Press, Chicago.

Schlosser, G. and Wagner, G. P. 2004. Introduction: the modularity concept in developmental and evolutionary biology. In Schlosser, G. and Wagner, G. P. (Eds): *Modularity in Development and Evolution*, pp. 1–11. Chicago University Press, Chicago.

Schluter, D. 1989. Bridging populations and phylogenetic approaches to the evolution of complex traits. In Wake, D. B. and Roth, G. (Eds): *Complex Organismal Functions: Integration and Evolution in Vertebrates*, pp. 79–95. John Wiley and Sons, Chichester.

Schluter, D. 2000. *The Ecology of Adaptive Radiation*. Oxford University Press, Oxford.

Schwenk, K. and Wagner, G. P. 2001. Function and evolution of phenotypic stability: connecting pattern and process. – *American Zoologist* **41**: 552–563.

Schwenk, K. and Wagner, G. P. 2004. The relativism of constraints on phenotypic evolution. In Pigliucci, M. and Preston, K. (Eds): *Phenotypic Integration: Studying the Ecology and Evolution of Complex Phenotypes*, pp. 390–408. Oxford University Press, Oxford.

Shubin, N. H., Daeschler, E. B. and Jenkins, F. A. Jr. 2006. The pectoral fin of *Tiktaalik roseae* and the origin of the tetrapod limb. – *Nature* **440**: 764–771.

Shubin, N. H. and Davis, M. D. 2004. Modularity in the evolution of vertebrate appendages. In Schlosser, G. and Wagner, G. P. (Eds): *Modularity in Evolution and Development*, pp. 429–440. Chicago University Press, Chicago.

Sidor, C. A. and Hopson, J. A. 1998. Ghost lineages and 'mammalness': assessing the temporal pattern of character acquisition in the Synapsida. – *Paleobiology* **24**: 254–273.

Simpson, G. G. 1944. *Tempo and Mode in Evolution*. Columbia University Press, New York.

Taylor, C. R. 1980. Evolution of mammalian homeothermy: a two-step process? In Schmidt-Nielsen, K., Bolis, L. and Taylor, C. R. (Eds): *Comparative Physiology: Primitive Mammals*, pp. 100–111. Cambridge University Press, Cambridge.

Thomson, K. S. 1966. The evolution of the tetrapod middle ear in the rhipidistian–amphibian transition. – *American Zoologist* **6**: 379–397.

Turner, G. F. 1999. Explosive evolution in African cichlid fish. In Magurran, A. E. and May, R. M. (Eds): *Evolution of Biology Diversity*, pp. 113–129. Oxford University Press, Oxford.

Vrba, E. 1989. Levels of selection and sorting with special reference to the species level. – *Oxford Surveys in Evolutionary Biology* **6**: 111–168.

Wagner, G. P. 1988. The influence of variation and of developmental constraints on the rate of multivariate phenotypic evolution. – *Journal of Evolutionary Biology* **1**: 45–66.

Wagner, G. P. and Altenberg, L. 1996. Complex adaptations and the evolution of evolvability. – *Evolution* **50**: 967–976.

Weiss, K. M. 2005. The phenogenetic logic of life. – *Nature Reviews Genetics* **6**: 36–45.

Whyte, L. L. 1965. *Internal Factors in Evolution*. George Braziller, New York.

Williams, C. G. 1992. *Natural Selection: Domains, Levels, and Challenges*. Oxford University Press, Oxford.

Wolpert, L., Beddington, R., Jessell, T., Lawrence, P., Meyerowitz, E. and Smith, J. 2002. *Principles of Development*. Oxford University Press, Oxford.

Yang, A. S. 2001. Modularity, evolvability, and adaptive radiations: a comparison of the hemi- and holometabolous insects. – *Evolution and Development* **3**: 59–72.

Zelditch, M. L. and Moscarella, R. A. 2004. Form, function, and life history. In Pigliucci, M. and Preston, K. (Eds): *Phenotypic Integration: Studying the Ecology and Evolution of Complex Phenotypes*, pp. 274–301. Oxford University Press, Oxford.