

The origin of vertebrate limbs

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SUMMARY

The earliest tetrapod limbs are polydactylous, morphologically varied and do not conform to an archetypal pattern. These discoveries, combined with the unravelling of limb developmental morphogenetic and regulatory mechanisms, have prompted a re-examination of vertebrate limb evolution. The rich fossil record of vertebrate fins/limbs, although restricted to skeletal tissues, exceeds the morphological diversity of the extant biota, and a systematic approach to limb evolution produces an informative picture of evolutionary change. A composite framework of several phylogenetic hypotheses is presented incorporating living and fossil taxa, including the first report of an acanthodian metapterygium and a new reconstruction of the axial skeleton and caudal fin of *Acanthostega gunnari*. Although significant nodes in vertebrate phylogeny remain poorly resolved, clear patterns of morphogenetic evolution emerge: median fin origination and elaboration initially precedes that of paired fins; pectoral fins initially precede pelvic fin development; evolving patterns of fin distribu-

tion, skeletal tissue diversity and structural complexity become decoupled with increased taxonomic divergence. Transformational sequences apparent from the fish-tetrapod transition are reiterated among extant lungfishes, indicating further directions for comparative experimental research. The evolutionary diversification of vertebrate fin and limb patterns challenges a simple linkage between Hox gene conservation, expression and morphology. A phylogenetic framework is necessary in order to distinguish shared from derived characters in experimental model regulatory systems. Hox and related genomic evolution may include convergent patterns underlying functional and morphological diversification. *Brachydanio* is suggested as an example where tail-driven patterning demands may have converged with the regulation of highly differentiated limbs in tetrapods.

Key words: vertebrate, limb, fin, evolution, phylogeny, Hox gene, digits

INTRODUCTION

The history of vertebrate limbs has long been a popular subject for comparative anatomical research, combining fossil and recent morphologies with speculations about developmental evolution. More recently, advances in the investigation of developmental regulation have prompted experimental researchers to speculate about evolutionary morphology (cf. Coates, 1993a; Tabin and Laufer, 1993). This article continues in the tradition of morphology and speculation, but is also intended to provide an informative database emphasising the diversity of fin/limb patterns within an explicit phylogenetic framework. And an attempt has been made to include testable developmental-evolutionary speculations.

A glossary at the end of the text includes short explanations of selected phylogenetic and anatomical jargon (first use of included terms marked).*

FIN ARCHETYPES AND HYPOTHETICAL ANCESTORS

The striking similarities of tetrapod limb skeletons, or those of actinopterygian pectoral fins and girdles, have had a sustained influence upon the development of theoretical biology. Explanations of the apparent shared, underlying patterns include Geoffroy's special analogies and (attempted) unified theory of form, Owen's formulation of homology*, and Darwin's recognition of evolutionary descent from remote, common ancestry (Russell, 1916; Appel, 1987). Owen's archetype was subsequently reified as an actual ancestor (discussed in Goodwin and Trainor, 1983), and pre-Darwinian typological baggage was thereby incorporated into the new evolutionary paradigm. Gegenbaur (1878: translation and summary), probably the first evolutionist to consider tetrapod limbs in detail, promptly abstracted a theoretical ground-plan of fin skeletons, which he derived in turn from an ancestral branchial arch (Fig. 1A; note resemblance to the endoskeletal lungfish fin, Fig. 1C). But this surprisingly resilient tree-like 'archipterygium' (eg. Horder, 1989) was soon challenged by the lateral fin-fold theory (Thacher, 1877; Mivart, 1879; Balfour, 1881), in which paired appendages evolved from an ancestral, continuous lateral fin (Fig. 1B), resembling the embryonic fold precursing median (fish) fins. Corroborative evidence from the lateral inter-fin ridge of *Torpedo* embryos, plus support from Haeckel's influential biogenetic law (Gould, 1977), soon established this as the preferred, evolutionary scenario. Instead of Gegenbaur's archipterygium (1878), paired fin skeletons were thought to have evolved from parallel radials*. After an unspecified evolutionary period, pectorals then differentiated from pelvic fins,

and basal constriction produced a metapterygium* (Fig. 1D). Corresponding anterior and central sets of apparently fused radials were called the pro*- and mesopterygium* (as in the tri-basal lateral fin pattern characterising recent batoids* and sharks). No gill arch contribution was ever observed and, with increasing evidence for the exclusively mesodermal origin of endoskeletal pectoral girdles (Burke, 1991), little support remains for Gegenbaur's original theory (but see Tabin, 1992, noting the expression of otherwise gill patterning genes in the anteroventral corner of an amniote* pectoral girdle).

Although the continuous lateral fin-fold theory remains widely accepted (eg. Jarvik, 1980; Tabin and Laufer, 1993), it, too, has long been criticised for its assumption of an idealised, hypothetical ancestor (eg. Westoll, 1958; Romer, 1962) (Fig. 1B), which, as an *average*, vitiates the interpretation of the fossil record (Ghiselin, 1988). The embryological support is

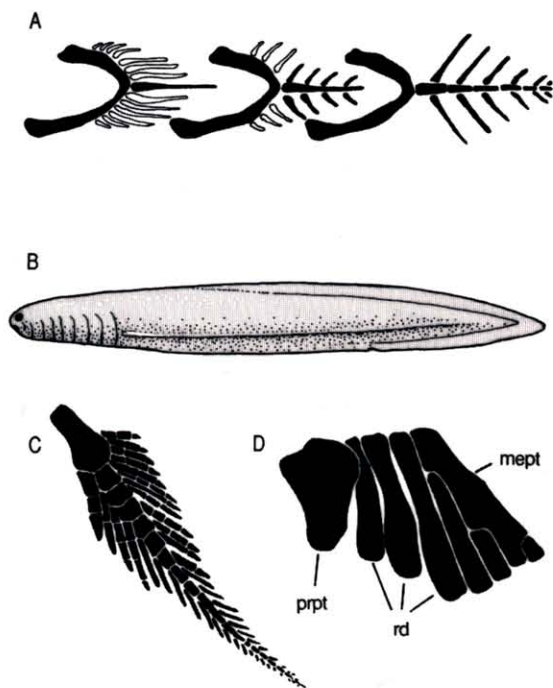


Fig. 1. Vertebrate fin archetypes. (A) An idealised gill arch, at left of figure, transformed into an archipterygial fin and girdle endoskeleton at right of figure (after Gegenbaur, in Jarvik, 1980). Conserved structures shown in black: the gill arch becomes a pectoral girdle resembling a large chondrichthyan scapulocoracoid; the most prominent gill-ray extends and trifurcates serially to produce a fin endoskeleton; and outlined gill-rays are those supposed to have been lost during evolution. Anterior to right of figure. (B) Balfour and other's (see text for refs) continuous lateral fin fold manifest in Jarvik's (1980) hypothetical ancestral vertebrate. (C) The archipterygium-like, but in fact exclusively metapterygial pectoral endoskeleton of an Australian lungfish (*Neoceratodus*). Each axial segment articulates with a single preaxial radial (left side); there is no simple, equivalent relation with the number of postaxial radials (after Haswell, 1882; includes figures of other fins showing significant variation in endoskeletal patterns). (D) The pectoral endoskeleton of a sturgeon *Acipenser sturio*, including a metapterygium (mept) supporting one postaxial and two preaxial radials, three median proximal radials (rd) and an anterior propterygium (prpt) (only proximal radials illustrated: after Grande and Bemis, 1991). Anterior of all structures to left of figure.

similarly questionable: Gegenbaur regarded the inter-fin ridge as recapitulating the pelvic fin's posterior, evolutionary migration (suggesting that pelvic fins predated pectorals, cf. Tabin, 1992), although Kerr (1899; deriving limbs from external gills) interpreted it as a specialisation of batoid fins. Goodrich's (1906) study of fin development in '*Scyllium*' (= the shark *Scyliorhinus*) remains probably the most authoritative embryological support for the fin fold theory, wherein abortive inter-fin muscle buds were interpreted as vestiges of ancestral, continuous folds. If these embryonic morphologies are interpreted within a phylogenetic framework (eg. Fig. 2A), then their significance is less convincing. Although these abortive muscle buds resemble the continuous, inter-limb bud amniote Wolffian ridges, in anamniotes* and teleosts such mesodermal out-growths are clearly disconnected (Balinsky, 1975). Furthermore, Ekman (1941) actually illustrates their discontinuity during the development of '*Acanthius*' (= the shark *Squalus*). These patchy, phylogenetic distributions of ontogenetic data are inconclusive as indicators of evolutionary polarity (Mabee, 1993). Phylogenetic trees are therefore fundamentally important to any further discussion of evolutionary patterns and processes. A detailed discussion of phylogenetic reconstruction methods is beyond the scope of this article, but the following references are suggested as clear, concise accounts of the application of phylogenetic systematics and the logic of evolutionary theory: Harvey and Pagel (1991) and Panchen (1992).

PHYLOGENETIC AND DEVELOPMENTAL HYPOTHESES

Theories of vertebrate phylogeny have not reached a stable consensus; certain nodes are relatively well resolved, but the origins of other major radiations remain contentious (eg. agnathan* interrelationships surrounding the base of the lampreys; the origin of gnathostomes*: Fig. 2A). This uncertainty affects directly theories of morphogenetic change, because altered phylogenetic topologies transform the way in which taxonomic ground-plans disintegrate (as all summaries of essential characters must, within an evolutionary paradigm: Simpson, 1961; Ghiselin, 1988).

The vertebrate phylogeny (considered in this work to be a monophyletic* subgroup of the Chordata) shown in Fig. 2, is a composite of several analyses incorporating morphological and molecular data: Forey and Janvier (1993) on agnathans and stem*-gnathostomes; Maisey on gnathostomes (1984) and chondrichthyans (1986); Young (1986) on placoderms; Long (1986) on acanthodians; and Meyer and Dolven (1992), Hedges et al., (1993) and Ahlberg (1989) on osteichthyans. The combined results do not constitute a highly corroborated set of interrelationships, and neither does the apparently high degree of resolution signify that all of the nodes are equally robust (Lanyon, 1993). For example, thelodonts and anaspids, although included within the agnathans (generally agreed to be paraphyletic*) are regarded by Wilson and Caldwell (1991) as stem-gnathostomes.

Morphological character distribution among stem-taxa is critically important for the detection of primitive conditions and convergent evolution (Panchen and Smithson, 1987; Gauthier et al., 1988). Although molecular phylogenies, constructed independently of morphological data, can supply

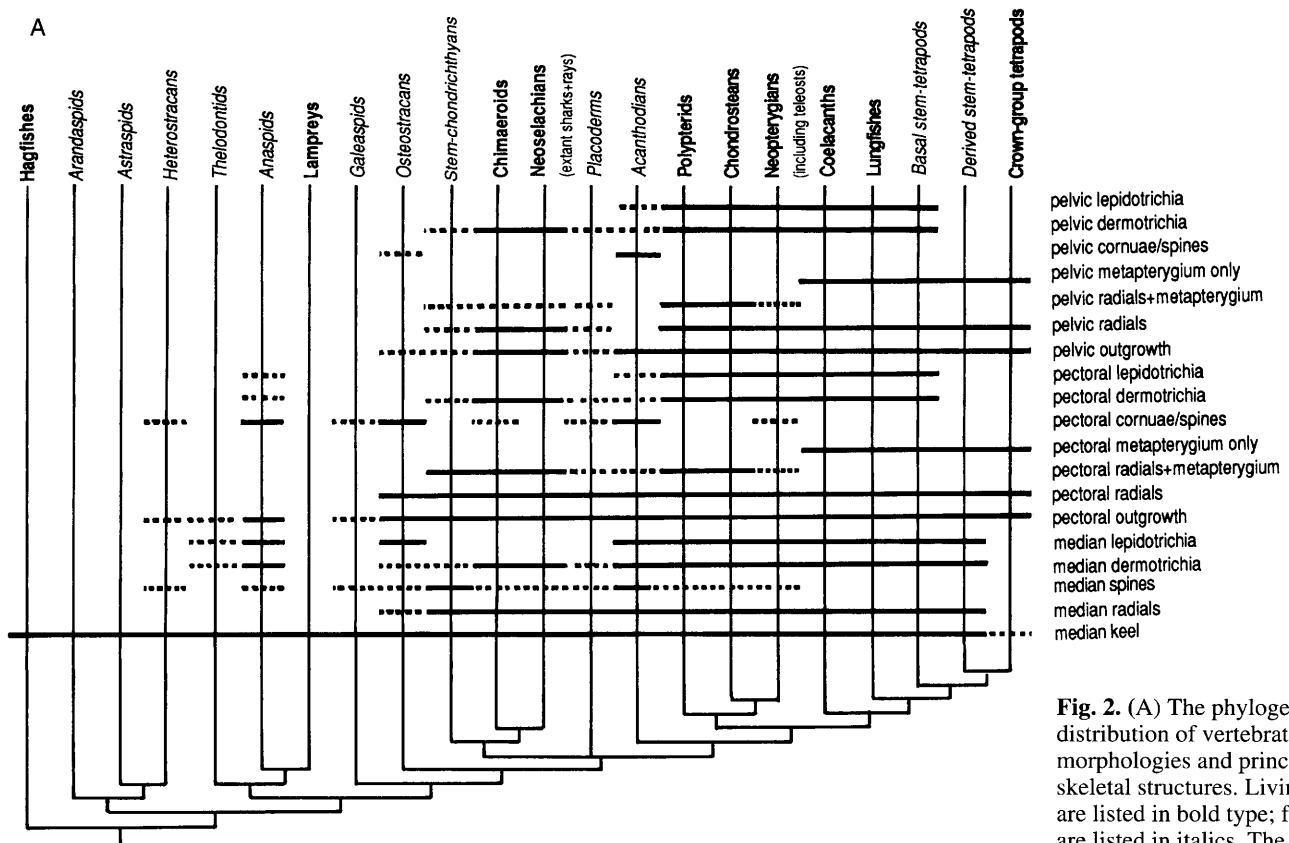
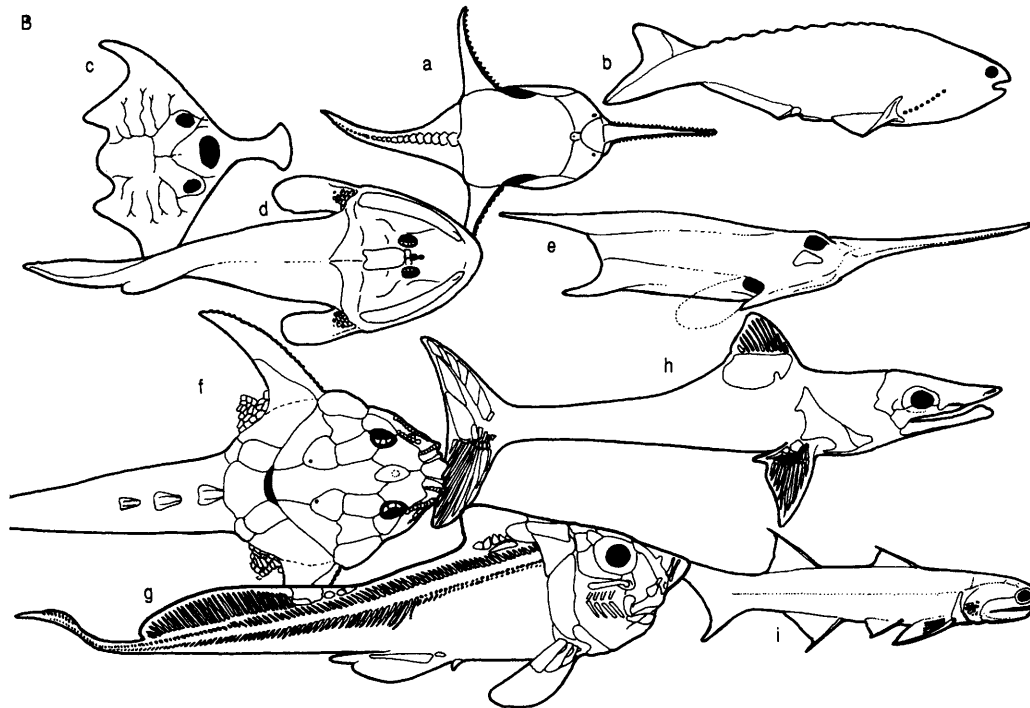


Fig. 2. (A) The phylogenetic distribution of vertebrate fin morphologies and principal skeletal structures. Living taxa are listed in bold type; fossil taxa are listed in *italics*. The branching sequence of vertebrate interrelationships is presented at the base (sources for the phylogeny are given in the text). Stem-taxa refer to an extinct taxon's closest relationships to a monophyletic group of living taxa (the crown-group). Thus polypterids, chondrosteans, neopterygians, coelacanth, lungfish and tetrapods constitute crown-group osteichthyans (bony fishes). Acanthodians in this scheme emerged after the chondrichthyan: osteichthyan evolutionary split, and are therefore stem-osteichthyans; similarly, galeaspids and osteostracans are stem-gnathostomes. Such stem-groups often supply unique data on the primitive conditions of living taxa. Horizontal bars crossing vertical branches indicate distribution of fin characteristics listed on vertical axis: solid bars = general or primitive condition; broken bars = uncertain data or significantly



incomplete character distribution in particular taxon. (B) Assorted extinct vertebrates, selected to exemplify morphological diversity lost from the extant biota (compare these with hypothetical ancestors such as that in Fig. 1B): (a) *Doryaspis*, dorsal view, a heterostracan (Carroll, 1988); (b) *Rhyncholepis*, lateral view, an anaspid (Ritchie, 1980); (c) *Sanchaspis*, head shield, dorsal view, a galeaspid (Janvier, 1984); (d) *Hemiclaspis*, dorsal view, an osteostracan (Janvier, 1984); (e) *Pituriaspis*, head shield, lateral view, an osteostracan (Young, 1991); (f) *Lunaspis*, dorsal view, a petalichthyid placoderm (Denison, 1978); (g) *Ctenurella*, lateral view, a ptyctodontid placoderm (Denison, 1978); (h) *Caseodus*, lateral view, a stem-group chondrichthyan (Zangerl, 1981); (i) *Ischnacanthus*, lateral view, an acanthodian (Denison, 1979).

equally important corroborative results (eg. Meyer and Dolven, 1992; Hedges et al., 1993), trees including recent and fossil taxa have a much greater information content, especially along internodal branches. Fossils may reveal unanticipated primitive morphologies (Coates, 1991), refute conjectured homologies, challenge recapitulatory inferences derived from ontogenetic sequences, overturn tenuous phylogenetic hypotheses (eg. Fig. 2A), and record minimum dates of taxonomic divergence (Patterson, 1981). Fossils therefore supply a unique source of data lost from the extant biota, and record the earliest examples of morphologies resulting from developmental processes known in living taxa.

The relationship between developmental research and phylogenetic reconstruction is reciprocal. Developmental research underpins a large body of work on the ontogeny of phylogenetically early, dermal skeletogenic and odontogenic tissues (eg. Smith and Hall, 1993, and references therein). Homologies based upon ontogenetic criteria are clearly dependent upon developmental research, which may therefore challenge phylogenetic hypotheses. The value of the amniote astragalus as a key character of established tetrapod phylogenies has been questioned recently in precisely this way (Rieppel, 1993a,b). Conversely, phylogenetic hypotheses frequently underpin interpretations of experimental research (eg. Tabin's, 1992, developmental-genetic explanation of the prevalence of pentadactyly assumes tetrapod monophyly). And comparative developmental theories are highly sensitive to phylogenetic changes. In Fig. 2A, the independent origins of paired fins suggest that whereas the lobate pectorals of stem-gnathostomes are scaled paddles, those of stem-lampreys have differentiated dermal tissues, implying earlier deployment of ectodermal derivatives. Furthermore, if a fin-related morphogenetic or regulatory system was identified in lampreys, it could imply retention from their finned ancestry, consistent with a gradualistic model of developmental evolution. Alternatively, if early finned taxa are unrelated to lampreys (cf. Wilson and Caldwell, 1993), then the resultant model may be saltatory (ie. acquisition of complete regulatory systems before functional diversification). These kinds of scenarios need to be assessed relative to the robustness of the underlying phylogeny.

VERTEBRATE LIMB STRUCTURES: PATTERNS, COMPOSITIONS AND RECONSTRUCTED EVOLUTIONARY PATHWAYS

The assumed absence of paired fins in most agnathans (including lampreys, hagfish, arandaspids, astraspids, heterostracans and galeaspids) may be an oversimplification (Fig. 2). Lateral fin-like processes, such as dermal branchial plates or postbranchial spines or cornuae* (Moy-Thomas and Miles, 1971; Janvier, 1993) (Fig. 2Ba,c,e,f) are widespread. These structures precede (complex) fins as they are usually recognised, perhaps recording the accumulation of basic fin components.

The first differentiated fin-ray like structures are found in median fins. Fork-tailed thelodonts (Wilson and Caldwell, 1991) and all anaspids (Fig. 2Bb) (Moy-Thomas and Miles, 1971; Ritchie, 1980) bear rows of lepidotrichia*-like, aligned dermal denticles. Certain thelodonts, like heterostracans, have suprabranchial lateral fins, while others, and all anaspids, have

pectoral fin-folds immediately behind the branchial openings. All thelodont paired fins are short-based (restricted to the pectoral region), whereas anaspids have both short and long ventrolateral fins. Long-based anaspid lateral fins are specialised and not primitive continuous folds. Thelodont pectoral fin scales resemble those covering the flank, whereas paired anaspid fins, supported anteriorly by spines, when long, may have lepidotrichia. None of these forms preserve direct evidence of dermatotrichia*, which may be necessary precursors for lepidotrichial outgrowth (Schaeffer, 1987; Thorogood, 1991). Fossil endoskeletons are similarly absent, but in living cyclostomes (hagfish and lampreys: a paraphyletic* group) the cartilagenous fins supports are neural and haemal arch prolongations, with no dermal contribution (Goodrich, 1904, 1930). Lampreys sometimes have branching, unsegmented radials intercalating between the neural spines (personal observation).

Stem-group gnathostomes repeat the sequence of median preceding paired fin elaboration. Some galeaspid (Fig. 2Bc) head shields bear near-pectoral spines/cornuae (cf. heterostracans) above the branchial openings, but median fin details are uncertain. In contrast, osteostracan (sister-group* to the crown*- gnathostome radiation: Fig. 2Bd) head shields have canalised pectoral fin insertions on the rear of the cornuae, and median fins with lepidotrichia and radials (Moy-Thomas and Miles, 1971). Pectoral insertions similarly extend to a point above the second or third gill openings (Westoll, 1958). Ventrolateral ridges extending from the head shield have been interpreted as further fossil evidence for ancestral continuous lateral fin-folds, but their overlapping conjunction (Patterson, 1981) with pectoral fins challenges an ancestor-descendent relationship (Forey, 1984). Alternatively, pituriaspids have pelvic fin-like flanges (Young, 1991: 'subanal laminae'; Fig. 2e) extending from the rear of a craniothoracic shield, but their phylogenetic affinities are unclear.

The major living lineages of crown-group gnathostomes, chondrichthyans and osteichthyans, are accompanied by two major extinct groups, placoderms and acanthodians, the relationships of which are uncertain (Fig. 2). Young (1986) inserts placoderms in a trichotomy between osteichthyans and chondrichthyans, whereas Forey and Gardiner (1986) interpret placoderms as stem-osteichthyans. Acanthodians may be stem-gnathostomes (Rosen et al., 1981), or stem-osteichthyans (Maisey, 1986; alternative hypotheses of basal gnathostome interrelationships are reviewed in these four references).

Placoderms (Fig. 2Bf,g) are relative late-comers to the gnathostome fossil record, appearing to have radiated, diversified and become extinct mostly within the Devonian period; their subgroup interrelationships are uncertain. Most placoderms have pectoral and pelvic fins (absence of pelvic fins does not appear to be primitive in current phylogenies, summarised in Carroll, 1988). Radials are rarely well preserved; certain taxa have metapterygia, some have dermatotrichia, while others' fins are near-plesodic* (Denison, 1978; Jarvik, 1980).

Stem-chondrichthyans (Fig. 2Bh) may be the earliest crown-gnathostomes (Lower Silurian: Karatajute-Talimaa, 1992); their fins may also be plesodic primitively. Some of the earliest (Devonian) articulated specimens, eg. *Cladoselache* (Zangerl, 1981), have branched, unsegmented radials interspersed distally with intercalaries, resembling lamprey (median) fin supports, and experimentally induced interdigitals, (cf. Hurlle et al., 1991). Dermatotrichia (ceratotrichia) may have been

present primitively (Zangerl, 1981) as in living taxa where their growth is persistent and extensive. If edestids and cladoselachians represent the primitive chondrichthyan condition (Maisey, 1984), then pectoral fin growth and elaboration greatly exceeded that of the pelvis (when present). In taxa with two dorsal fins, anterior fin development similarly exceeds that of the posterior. Chondrichthyan pelvic fins may not have been primitively metapterygial (Zangerl, 1981). Sexual dimorphism obscures the issue, because males have branched, metapterygium-like claspers*, while corresponding female pelvis are anaxial.

Acanthodians (Fig. 2Bi) are considered to be the sister-group of crown-group osteichthyans (actinopterygians and sarcopterygians) (cf. Maisey, 1986). Fins preceded by spines (the inter-fin spines of certain taxa are probably not primitive, Long, 1986), bear the first evidence of gnathostome lepidotrichially aligned scales, sometimes underlain with proximally mineralised dermatrichia (Fig. 3A). Perichondrally ossified pectoral girdles are present occasionally (Denison, 1979). Endoskeletal pectoral fin supports, thought to consist of "a few small nodules arranged irregularly" (Rosen et al., 1981; Miles, 1973), are metapterygial (refuting a principal argument used to exclude acanthodians from the gnathostome crown-group: Rosen et al., 1981; sustained in Forey, 1984; Forey and Gardiner, 1986). Furthermore, acanthodian-like fin spines are

found in the earliest actinopterygian-like osteichthyan remains (Gross, 1969), although they are absent from the earliest specimens of complete fish (Pearson and Westoll, 1979; Gardiner, 1984). It may also be significant that the pelvic fins of acanthodians and primitive actinopterygians tend to be less constricted proximally than pectorals. Actinopterygian pelvic fins usually enclose a series of simple radials, although pelvic metapterygia are present in certain chondrosteans (sturgeons and paddlefishes; Fig. 3B, Sewertzoff, 1924; Grande and Bemis, 1991). Pectoral radials primitively include a propterygium and a metapterygium (Fig. 1D) but the latter is secondarily absent in living (Goodrich, 1930) and many stem-teleosts. Adult actinopterygian dermatrichia are restricted to an apical fringe (cf. acanthodians), with the exception of certain teleosts' adipose fins which are supported exclusively by elongate dermatrichia.

Sarcopterygians (living groups include tetrapods, lungfish,

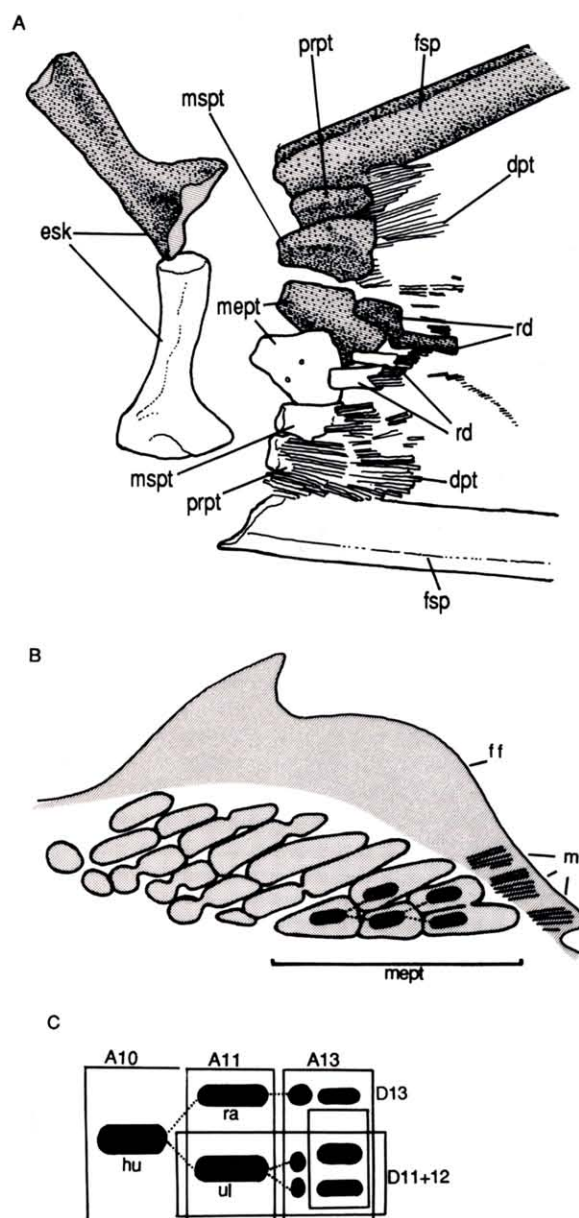


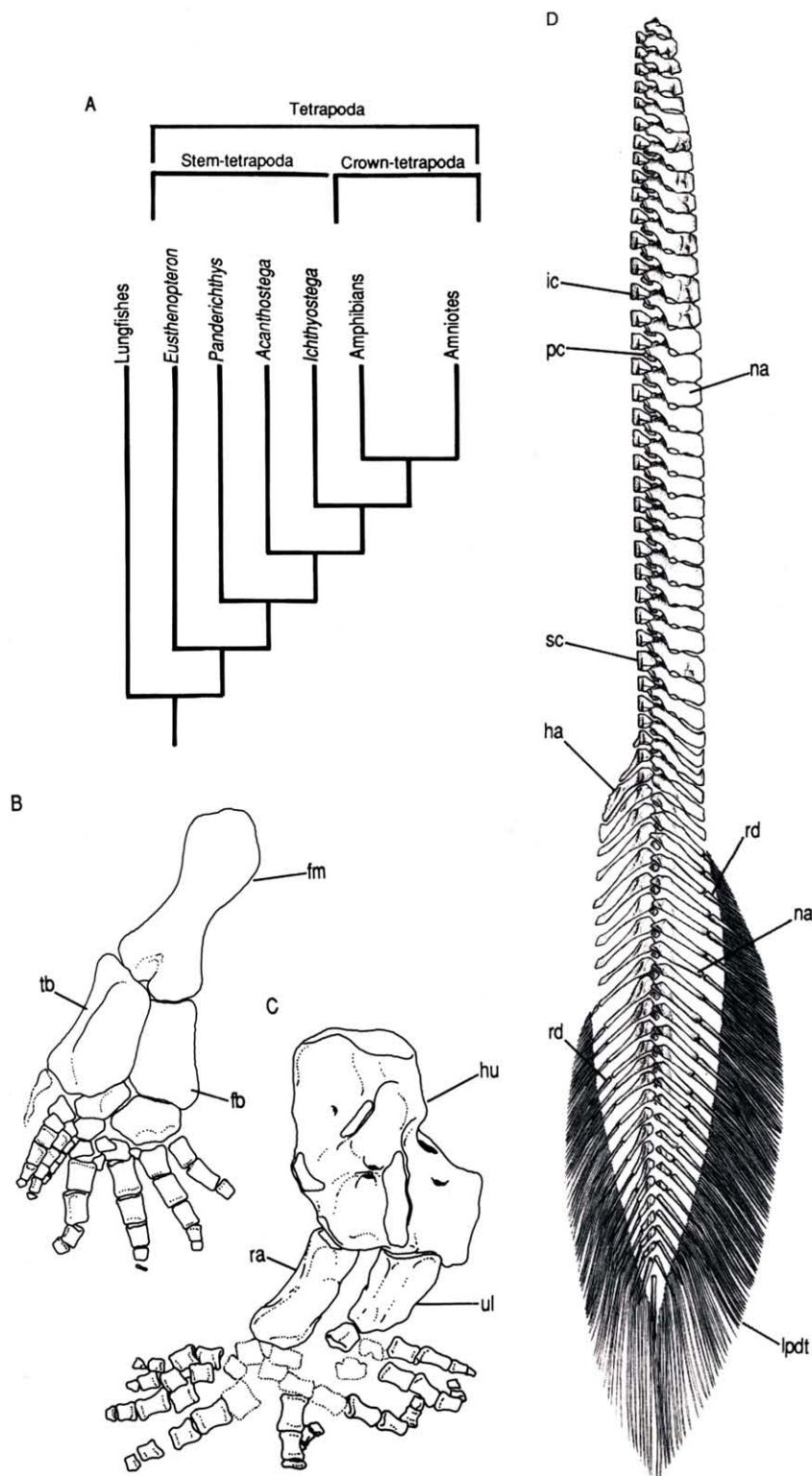
Fig. 3. (A) New data on the pectoral fin skeleton of *Acanthodes bronni*, (Permian: Lebach, Germany) specimen UMZC (University Museum of Zoology, Cambridge) GN15. Abbreviations: *dpt*, dermatrichia; *esk*, endoskeletal pectoral girdle; *fsp*, fin spine; *mept*, metapterygium; *mspt*, mesopterygium; *prpt*, propterygium; *rd*, radials; stippled structures = left fin; all viewed from ventral aspect. Acanthodian pectoral fin endoskeletons are known only from the perichondrally ossified radials of *Acanthodes*. The metapterygium is perforated by 2+ foramina and supports two radials (displaying a characteristic 1:2 ratio of proximal to distal elements), and the propterygium, unlike those of actinopterygians, is imperforate. The proximally mineralised dermatrichia conform to Miles' (1973) description. The accepted reconstruction of an acanthodian pectoral fin endoskeleton consists of three cylindrical rods, as reinterpreted by Miles (1973) after Watson's (1937) earlier attempt (also based upon UMZC GN15), including extensive proximal and distal radial series. But Miles based his reconstruction on casts of lost, original German specimens, which now appear to be incomplete; UMZC GN15 was not re-examined. The new data presented here was obtained from high definition silicone rubber peels of the original material after further, detailed, negative preparation. (B) Pelvic fin development in *Acipenser ruthens*, after Sewertzoff (1924: Figs 1 and 3), showing prechondrogenic cell clusters (stippled) segmenting to form radials distally and basals proximally (secondarily fused basals form the rudimentary pelvic girdle). Posterior-most condensations form 1:2 ratio branching pattern characteristic of metapterygium, here superimposed with a segmentation and bifurcation diagram, resembling those devised by Shubin and Alberch (1986). Differentiation and chondrification proceeds from posterior to anterior of fin base (right to left across page). Abbreviations: *ff*, fin fold (linear shading); *m*, muscular bundles associated with developing radials, not dermatrichia; *mept*, metapterygium. (C) Schematic diagram of endoskeletal pattern development in a st. 28 chick forelimb (after Yokouchi et al., 1991, Fig. 4f). Shubin and Alberch-style branching diagram shows 1:2 proximodistal ratio inferred as conserved from metapterygial fin axis; boxes outline Hox expression domains, with boundaries correlating with skeletal pattern branching events. Abbreviations: *hu*, humerus; *r*, radius; *ul*, ulna.

and coelacanth) have exclusively metapterygial paired fin endoskeletons. Although biserial fins (eg. Fig. 1C) resemble Gegenbaur's archipterygium, out-group analysis suggests that short uniserial metapterygia are primitive (Ahlberg, 1989). Pelvic metapterygia usually consist of fewer segments than pectoral metapterygia. Dermotrichial distribution is uncertain: they occur in the second dorsal fin of the extant coelacanth, *Latimeria* (Geraudie and Meunier, 1980), but are reported as absent from late juvenile and adult lungfish (Goodrich, 1904; Geraudie and Meunier, 1984). However, an untraced paper by Geraudie (1985, perhaps recorded incorrectly in Musick et al., 1991), entitled "...actinotrichia...in developing teleost and Dipnoi fish fins" implies their transient ontogenetic appearance. Lungfish lepidotrichial equivalents, camptotrichia (Goodrich, 1904; Geraudie and Meunier, 1984) are primitively well ossified, segmented and branched distally. In *Neoceratodus* and *Protopterus* the camptotrichia remain branched and segmented although demineralised distally but, in *Lepidosiren*, the median (caudal) camptotrichia are shorter, very soft, unbranched and scarcely jointed, and paired fin camptotrichia are entirely absent.

Differences between the fins of *Lepidosiren* and those of other lungfish resemble the evolutionary transformations between finned and increasingly finless, digitated stem-tetrapods (Fig. 4A). Basal stem-tetrapods (eg. *Eusthenopteron*)

have several median fins and paired fins with short, uniserial metapterygia (Jarvik, 1980). The lepidotrichia are ossified, segmented and branched distally, but dermotrichia are unknown. A more derived, finned (rather than digitated) stem-tetrapod, *Panderichthys*, retains only a single, median, caudal fin, but still has the primitive pattern of paired fins with short, uniserial metapterygia and ossified, segmented and branched lepidotrichia (Vorobyeva and Schultze, 1991). In comparison

Fig. 4. (A) Cladogram illustrating an Adams consensus tree of early crown- and stem-group tetrapods, and other selected sarcopterygian fish (work in progress; summarised in Coates, 1994). Note that *Acanthostega* and *Ichthyostega* fall outside of the tetrapod crown-group, and, using a node-based definition (Gauthier et al., 1988; Rowe and Gauthier, 1992), must be considered stem-tetrapods along with other extinct taxa such as *Eusthenopteron* and *Panderichthys*, which are usually described as fish (a taxonomically imprecise grade-group). Taxonomic definitions based upon the presence of key characters/ evolutionary novelties (eg. digits) are fraught with typological difficulties and post hoc explanatory scenarios of evolutionary success (see Cracraft, 1990, and previous refs). (B) *Ichthyostega*, hind limb, specimen MGUH 1349 (Geological Museum of University Copenhagen). Abbreviations: fb, fibula; fm, femur; tb, tibia. (C) *Acanthostega* pectoral limb, specimen MGUH 1227. Abbreviations: hu, humerus; ra, radius; ul, ulna. (D) *Acanthostega*, new reconstruction of the axial skeleton showing tail fin structure, based upon specimens UMCZ T1300, MGUH 1227, 1258 and 1324. Vertebrae bipartite with small pleurocentra and large intercentra; notochordal canal unstricted; weakly developed regionalization: cervical neural arch height gradually reduced anteriorly, anterior caudal vertebrae with specialised neural and haemal arches, presacral count = 30. Abbreviations: ha, haemal arch; ic, intercentrum; lpdt, lepidotrichia; na, neural arch; pc, pleurocentrum; rd, radial; sc, sacral intercentrum.



with these, *Acanthostega* (a digitated stem-tetrapod), like *Lepidosiren*, has lost paired fin lepidotrichia, but retains a well-developed caudal fin with unsegmented and unbranched lepidotrichia supported by radials (Fig. 4D). Furthermore, like *Lepidosiren*, the paired fin metapterygia are extended distally, although these are uniserial (preaxial radials proximally and postaxials, ie. digits, distally: Fig. 4C) and the entire axis appears to have been twisted anteriorly within the limb-bud (Shubin and Alberch, 1986).

Digitated limbs originated after tetrapods diverged from their shared ancestry with lungfish (tetrapod's living sister-group: Panchen and Smithson, 1987; Meyer and Dolven, 1992), but before the evolutionary radiation of living forms. Digitated limbs are therefore neither coincident with tetrapods in the restricted (exclusively crown-group) or the broad/total (crown- plus stem-group) definitions of the group (Fig. 4A). In effect, digitated limbs initially constitute another derivation of a plesiodic fin pattern. The general points which emerged from a previous review of early limb morphologies (Coates, 1991), are supported by a recently completed analysis of early tetrapod interrelationships. Early reptiliomorph (eg. *Tulerpeton*, Lebedev, 1984; Coates, 1994), crown-group tetrapods, and digitated stem-tetrapods, are polydactylous (Coates and Clack, 1990). Furthermore, polydactylous limbs accompany retained, lungfish-like tails in which unsegmented and unbranched lepidotrichia are supported by radials articulating with neural and haemal spines (Fig. 4D). Thus pentadactyly in batrachomorph (anamniote) hindlimbs, and reptiliomorph fore- and hindlimbs, probably originated and stabilised independently. Digits (segmented postaxial radials, supporting no lepidotrichia or dermotrichia) appear before the elaboration of ossified wrist and ankle joints; carpal remains tend to be rarer than tarsal, perhaps reflecting a trend of delayed ossification. Early tarsal patterns (eg. Fig. 4C) include relatively few large elements which cannot be related simply to those of more recent examples, and early carpal patterns appear to be similarly abbreviated. In fact, a striking feature of these early digitated limbs is their failure to exhibit fixed primitive patterns or canonical formulae.

DISCUSSION

Morphological change

A fairly robust series of parallel or convergent morphogenetic trends emerges from this overview of vertebrate limb evolution (Fig. 2A). The phylogenetic development and elaboration of median fins precedes that of paired fins, and pectoral fins initially precede pelvic fin development. The first fin-like outgrowths are usually associated with dermal cornuae, spines, and/or specialised scales, but these are impersistent; their phylogenetic distribution is patchy. Dermotrichial and lepidotrichial development is consistently secondary (assuming, as earlier, that lepidotrichial growth is dependent upon dermotrichial precursors), although these are the most widely distributed dermal components of fin skeletons. Early fin endoskeletons are much rarer, perhaps reflecting the apparent independence of dermal from endoskeletal skeletogenic systems (Patterson, 1977). Alternatively, the absence of early radials may be an artifact of the poor preservational potential of cartilage (chondrichthyan prismatic cartilage being a notable

exception). The occurrence of these dermal and endoskeletal features in median before paired fins is a striking feature of the earlier taxa in this phylogeny, although with further branching events the sequence is obscured by changes in tissue diversity and structural repatterning.

Endoskeletal changes preceding tetrapod limb evolution mostly concern metapterygial transformations, ie. evolutionarily conserved, specialised posterior basal radials and their associated distal structures (Figs 1D, 3). Metapterygia are unique to crown-group gnathostomes, and their characteristic asymmetry may record the evolutionary imposition of a regulatory mechanism, such as a ZPA, upon the phylogenetically more primitive branching properties of limb/fin bud mesenchyme (Pautou, 1973; Hinchliffe, 1989). Only sarcopterygian osteichthyans (including tetrapods) have consistently similar pectoral and pelvic fin patterns. Actinopterygian pectorals and pelvics differ: clear pelvic metapterygia are restricted to chondrosteans. Such strongly divergent osteichthyan fin evolution has been explained in part by the suggestion that most actinopterygian pelvic metapterygia are incorporated into the pelvic girdle (Sewertzoff, 1924; Rosen et al., 1981). Most actinopterygians emphasise the anterior of the fin skeleton; pectoral metapterygia are lost in the vast majority (teleosts), whereas propterygia are enlarged and elaborated. Sarcopterygians, in contrast, emphasise the posterior of the fin skeleton, losing all proximal radials anterior to the metapterygia (contrast Fig. 1C,D). Thus the simple pectoral endoskeleton of *Brachydanio rerio* has a complex evolutionary history of secondary reduction.

There appear to be similarly significant differences between non-sarcopterygian and sarcopterygian patterns of metapterygial development. Shubin and Alberch (1986) described phylogenetically conserved, dynamic sequences of prechondrogenic focal condensation, segmentation and bifurcation producing the branching endoskeletal patterns of tetrapod limbs. These patterns include a single continuous path of bifurcation and segmentation which they inferred to be a synapomorphy* of tetrapod limbs and sarcopterygian fins, conserving the developmental pattern of a metapterygial axis. In limbs these bifurcation nodes have been correlated closely with Hox gene expression boundaries (Yokouchi et al., 1991; Blanco et al., 1994; Fig. 3C) associated with pattern regulation. However, chondrosteans pelvic metapterygia also include secondarily fused, parallel prechondrogenic cell-clusters; branching events are restricted to a small region next to the posterior fin-bud boundary (Fig. 3B, Sewertzoff, 1924). Chondrichthyan metapterygia appear to be formed similarly. Thus primitive metapterygia probably also included these numerous, segmenting proximal focal condensations, characteristically absent in sarcopterygians (including tetrapods). The transformation to a sarcopterygian pattern could have resulted from changed tissue domain dimensions (ie. fin-base constriction as invoked by Goodrich, 1930, or Jarvik, 1980), and segmentation versus branching events may be related to structural packing properties (Shubin and Alberch, 1986; Oster et al., 1988) rather than direct genetic regulation (cf. Yokouchi et al., 1991). However, these kinds of explanations appear to be uninformative about the maintenance of limb- or fin-bud dimensions, or the regulation of meta- versus meso- or propterygial domains.

Dermal skeletal loss is an equally significant event in tetrapod limb evolution. Fin-bud apical ectodermal folds

enclosing lepidotrichial development must have been transformed into the short, apical ectodermal ridges of tetrapod limb buds (Thorogood, 1991). Fin-ray* loss also suggests changes affecting neural crest cellular migration, although there is no direct evidence of skeletogenic neural crest tissue in any paired fin bud (Smith and Hall, 1993; neural crest now confirmed in median fins, Smith et al., 1994). Thorogood and Ferretti (1993), however, have already suggested that paired limb buds with exclusively mesodermal mesenchyme may be a tetrapod specialisation (contra Thomson, 1987), as corroborated by the entry of melanophores into the mesenchyme of teleost pectoral fins (Trinkaus, 1988a,b). Devonian tetrapods illustrate the phylogenetic sequence of fin loss, with ray-less (ie. digitized) limbs accompanying tails retaining radials and unbranched, unsegmented lepidotrichia (Jarvik, 1980; Coates, 1991; Fig. 4D). As the living sister-group of tetrapods (Hedges et al., 1991; Meyer and Dolven, 1992), the parallel patterns of lungfish fin reduction (described earlier; Fig. 2) probably provide the best subjects for investigating these developmental changes which affected our own fin-limb transition. This "last hired, first fired" (Gould, 1991) pattern of fin loss (assuming that pelvics are novel relative to pectorals, Fig. 2) suggests that pelvic fins may have lost their rays before pectorals. Perhaps the more fish-like pectoral than pelvic skeletons in *Acanthostega* record this evolutionary sequence (Coates, 1991; Ahlberg, 1991). Paired fin origins, probably pectoral-led, may therefore have been superimposed by limb patterning, perhaps pelvic-led.

Developmental regulation, phylogeny and convergence

The use of tetrapod limbs as model systems within which to explore the developmental-regulatory role of homeobox genes has stimulated much of the renewed interest in vertebrate limb evolution. Homeobox genes are distributed and apparently conserved across a spectacularly diverse taxonomic range (Slack et al., 1993). In particular, expression patterns of members of the HoxA (Yokouchi et al., 1991) and HoxD clusters (Dolle et al., 1989) have been mapped during amniote limb bud development (Fig. 3C), and targeted misexpression of the HoxD complement appears to transform digit identities (Morgan et al., 1992). Consequently, the nested, pentate HoxD expression domains in limb buds have been interpreted as specifying five identities (via combinatorial codes) underlying tetrapod pentadactyly (Tabin, 1992). These five are even considered present within the Devonian (360+ million years BP) octodactylous array of *Acanthostega* (Tabin, 1992; Fig. 4C), and therefore retained from an unspecified pre-tetrapod, and perhaps pre-gnathostome condition. Influential biological theoreticians such as Goodwin (1993) have already used Tabin's interpretation of *Acanthostega*'s forelimb as evidence for an historically invariant genetic constraint.

This inference appears to be consistent with the theory that amniote Hox clusters are conserved from an episode of amplification and four-fold duplication early in vertebrate evolution (relative to the homologous *Antennapedia*-class genes of *Drosophila melanogaster*, and a hypothetical common ancestral complement: Krumlauf, 1992; Holland, 1992; Fig. 5A). Functionally, gene duplication and differentiation is thought to have provided regulatory systems for morphological differentiation (Lewis, 1978; Akam et al., 1988) in response to the increased demands of vertebrate embryogenesis

(Holland, 1992; Holland et al., 1994). So the relation of morphological evolution to gene duplication, differentiation and functional diversification may be represented as a correlation between the phylogenetic distribution of morphological characters and the spatiotemporal distribution of regulatory gene expression. Similarities between cognate genes' (ie. putative homologues) expression domains should be associated with symplesiomorphies*, while differences may be associated with autapomorphies*. This suggests that more attention should be paid to the structural and expression diversity of vertebrate Hox networks, such as those of *Xenopus* and *Brachydanio* which have yet to be published in detail equivalent to those of mice and humans (eg. Scott, 1992) instead of focusing upon their conserved features. Such an approach would test Tabin's model, or at least provide information about the evolution and/or phylogenetic insertion of the proposed genetic constraint.

In fact, the results of *HoxD11*(=*HoxD4.6*, Scott, 1992) overexpression (Morgan et al., 1992) are ambiguous, and may alternatively suggest a scenario of evolutionary change rather than invariance. The apparently reduced digit diversity (digit I transformed to resemble digit II) in an avian limb bud appears to result from a less diverse combination of overlapping Hox domains. And if applied to the less highly differentiated digits of *Acanthostega* (Fig. 4C), then, contra Tabin (1992), it may imply regulation by a similarly less elaborate Hox cluster (Coates, 1993b). Shubin and Alberch's (1986) analysis of limb development demonstrates clearly the serial, iterative generation of digits. If acanthostegid digits therefore represent a primitively undifferentiated sequence of serial homologues, then anatomical distinctions such as digit length and number could result simply from structural properties (eg. breadth of enclosing limb bud tissue domain: Oster et al., 1988). And the distinctive identities of first and last digits could result from the properties of 'endedness' (Bateson, 1913, discussed in Roth, 1984) superimposed upon an array preceding digit 'individualization' (Wagner, 1989) as exemplified by the nested genetic identities proposed for amniote limbs. Therefore, when attempting to draw homologies between our own five digits and those of *Acanthostega*, the biological content of such decisions covers a variety of inferences. The dynamic sequence of digit production (cf. Shubin and Alberch, 1986), indicates that the five furthest from the leading edge of the limb are topographic equivalents to those of pentadactyl amniotes. But if statements about taxic homology are conjectural inferences of conserved ontogenetic potential (discussed further in Coates, 1993b), then these early digits, like fin radials, may not share with us a nested sequence of elaborate, combinatorial Hox codes supplying an address for each of five digit-types: radials and early digits are evolutionarily indistinct. Simpler, more iteratively patterned, endoskeletal paired fin or limb morphologies (cf. *Neoceratodus* and *Acanthostega*, Figs 1C, 4D) may be regulated by either less elaborately expressed or differentiated Hox clusters. Furthermore, correspondingly simpler morphologies may be found in other structures linked pleiotropically by the same regulatory genes.

Phylogenetic hypotheses of morphological change can also suggest potential examples of evolutionary convergence. The HoxA and HoxD genes expressed in amniote limbs are members of the 5'-located and caudally expressed Abd-B subfamily (Fig. 5A) (Yokouchi et al., 1991; Dolle et al., 1989).

This subfamily includes members of all four clusters aligned as five subgroups related to the single Abd-B gene in *Drosophila* (Krumlauf, 1992). While this resemblance suggests a period of evolutionary 5'-cluster expansion, it is not clear how this relates to cluster duplication. Insufficient current evidence supports the inference of a single HoxB Abd-B gene as primitive relative to the multiple members of A, C, and D clusters (Izpisua Belmonte et al., 1989), although there is some suggestion that four-fold Hox clusters may have appeared within the gnathostome stem-group (lampreys appearing to have three clusters and cephalochordates two: Pendleton et al., 1993). The equivalent Hox complements of *Brachydanio* (a cypriniform teleost) will therefore provide a valuable comparison with those of tetrapods. If Hox elaboration is linked closely to the regulatory demands of morphological complexity, then perhaps the teleost equivalents of groups 11-13 (Scott, 1992) should be correspondingly less diverse, given the simplicity of the pectoral endoskeleton.

However, without out-group data distinctions of conserved from convergent features in Hox networks may be difficult to support and, in *Brachydanio*, the situation is probably confounded by the derived morphological complexity of the caudal skeleton. Teleost tails are highly specialised, asymmetric and taxon specific (Fig. 5B; Patterson and Rosen, 1977). The primary expression domains of the Abd-B subfamily are caudal (mapped in mice: Kessel and Gruss, 1991). This suggests that the phylogenetically accumulated complexities of teleost tails may well have required similar, but independent, instances of Hox gene duplication or functional diversification. These could resemble those driven by the similar regulatory requirements of secondary expression in tetrapod limbs, especially if Hox elaboration is constrained structurally to the thirteen paralogous sites proposed by Scott (1992) and others. Therefore, the apparently simple teleost pectoral endoskeleton may be over-written by secondarily expressed, redundant but highly differentiated tail-driven Abd-B genes. This reverses the equivalent expression pattern in mice, where elaborated D

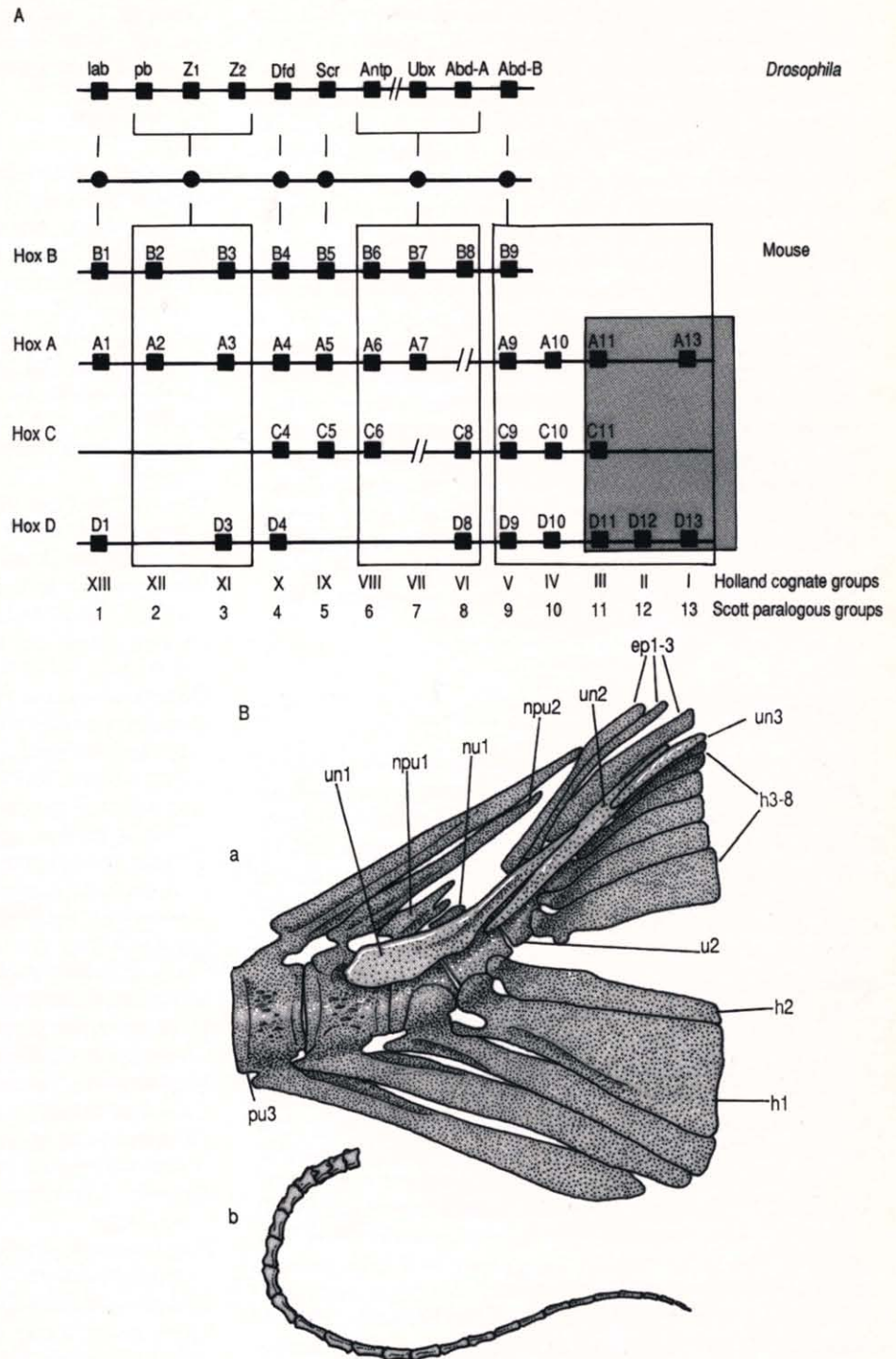


Fig. 5. (A) The four mammalian Hox clusters as found in a mouse; their inferred homologies with the *Drosophila* Hom-C complex, and a hypothetical most recent common ancestor of insects and vertebrates (Based on Krumlauf, 1992; Holland, 1992; Scott, 1992). The brackets/boxes define where homological relationships are established with greater confidence. Shaded box indicates paralogous groups associated with fin/limb patterning expected to differ most in non-tetrapod vertebrates. (B) A pair of vertebrate, osteichthyan, tail endoskeletons, illustrating the taxon specific complexity of (a) a teleost, *Anaethalion* (after Patterson and Rosen, 1977), contrasted with the simple, iterative pattern of (b) a rodent tail, *Paramys* (Carroll, 1988), both of which are assumed to be regulated by members of the Abd-B subfamily (Kessel and Gruss, 1991). Abbreviations: ep, epurals; h, hypurals; npu, neural arch/spine of numbered preural centrum; nu1, neural arch of first ural centrum; pu3, third preural centrum; u2, second ural centrum; un, uroneural bones.

Abd-B genes, apparently required for limb patterning (Morgan et al., 1992), are expressed primarily and redundantly in a simple, iteratively patterned rodent tail (Kessel and Gruss, 1991) (Fig. 5B). A phylogenetic framework is therefore needed to inform the selection of appropriate further out-group comparisons. In this example, a dipnoan, chondrosteian or chondrichthyan would provide more clearly informative results, because the phylogenetic history of each reveals none of the extreme caudal axial patterning of teleost evolution.

Finally, and somewhat speculatively, expression distributions with redundancy between primary, secondary and even tertiary fields suggest a plausible mechanism for Muller's (1990) 'side-effect' hypothesis for the evolution of morphological novelties. In this teleost example, redundant expression in the secondary (fin) field could deploy a sequence of pattern regulators available for co-option in an independently evolved suite of highly derived appendages. Antennariid teleosts, including several pseudo-limbed taxa with complex appendicular skeletons and musculature, may exhibit this phenomenon. Examples such as this and other mechanisms of functional diversification (Holland, 1992) are probably related to the failure to obtain a close correlation between genetic and morphological evolution (John and Miklos, 1988).

CONCLUSION

The early evolution of vertebrate appendages consists of parallel trends of increasing morphological complexity spreading from the median to anterior paired fins. But as phylogeny diversified, this simple pattern of fin elaboration became complicated by tissue loss and repatterning of the remaining structures. Pelvic fins may have originated as a reiteration of pectorals, but as with the discussion about digit evolution, pectoral and pelvic individualisation diverged within the different gnathostome lineages. Thus, in agreement with Hall (1991), elements of several past theories fit the morphological, ontogenetic and phylogenetic data, but none is individually sufficient. Hox gene expression and manipulation in limb development is beginning to provide new ways of thinking about morphological conservation, change and perhaps individualisation or homology. But this approach requires caution. It has long been argued that homology cannot be defined in terms of invariant gene action (de Beer, 1971; Goodwin, 1993), but perhaps more success will be achieved with reference to hypotheses of gene evolution. The relation of Hox genes to morphology may well have become obscured by functional diversification and convergence in experimental subjects' individual evolutionary backgrounds. This re-emphasises the importance of a phylogenetic framework within which to identify such convergent events. Subsequent comparisons between carefully selected out-groups' regulatory systems, and induced misexpressions in the primary experimental subjects, should enable the dissection of developmental regulation networks into individually specialised and shared general characteristics. I think that this kind of approach will become increasingly necessary in order to assess the relevance of choices such as "the fish as a simple model for our own development" (Kimmel, 1989).

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GLOSSARY

- Agnathan*: paraphyletic group of jawless vertebrates.
Amniote: a monophyletic group including turtles, lizards, crocodiles, birds, mammals, and their fossil relatives.
Anamniotes: used here to define a monophyletic group including anurans, urodeles, apodans, and their fossil relatives.
Autapomorphy: a character unique to a monophyletic group.
Batoid: skates and rays.
Claspers: male intromittent organ extending from rear of pelvic fin, supported by metapterygium-like endoskeleton.
Cornuæ: horn-like projections from the craniothoracic dermal armour.
Crown-group: a monophyletic group defined by living taxa and their most recent common ancestor, including collateral fossil descendents.
Dermotrichia: protein fin rays produced within developing apical ectodermal fold of fin bud.
Fin ray: dermal fin supports: includes dermotrichia and lepidotrichia; not to be confused with radials.
Gnathostomes: the jawed vertebrates, a monophyletic group.
Homology: in this article used in the sense of 'taxic homology' (Patterson, 1982), equating in practise with synapomorphy (see below), ie. a conjectural inference of shared derived ontogenetic potential relative to a phylogenetic hypothesis. This definition applies equally to hypotheses of genomic evolution (paralogy) and the developmental concept of identity; for current debates about the meaning and utility of homology see Hall, 1994.
Lepidotrichia: specialised scales forming dermal fin rays: aligned ontogenetically with subjacent dermotrichia.
Mesopterygium: middle compound radial.
Metapterygium: posterior compound radial, usually branching to support distal radials.
Monophyletic: a group including a common ancestor and all of its descendents.
Paraphyletic: a group descended from a common ancestor but with incomplete membership.
Plesodic: a fin endoskeleton where the radials extend to the fin perimeter.
Propterygium: anterior compound radial, usually penetrated by appendicular nerve and blood supply.
Radials: rod-like endoskeletal fin supports; not dermal.
Sister-group: a pair of most closely related terminal taxa in a dichotomously branching phylogeny.
Stem-group: a series of fossil taxa most closely related to, but not included within, a crown group.
Symplesiomorphy: characters defining a group at a higher rank than that under consideration.
Synapomorphy: uniquely shared derived characters, uniting a group with another to which it is most closely related.

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