African Coelacanth (Latimeria chalumnae), 2016-2024

Bibliography

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Background & Scope

The goal of this bibliography is to provide a comprehensive review of the scientific literature published between 2016 and 2024 on the African coelacanth (Latimeria chalumnae), with special emphasis on the Tanzanian Distinct Population Segment (DPS). The articles provided here will support NOAA Fisheries' 5-year review of this DPS of the coelacanth.

Sources Reviewed

Along with a web search for relevant grey literature materials the following databases were used to identify sources: ProQuest's Aquatic Science and Fisheries Abstracts Database and Earth-Atmospheric & Aquatic Science Database, Dimensions, Lens.org, Clarivate Analytics' Web of Science: Science Citation Index Expanded, Wiley Online Library, ProQuest's Science Direct, BioOne Complete, Google Scholar, and JSTOR. Only English language materials were considered.

Bibliography

Behrens, M., Di Pizio, A., Redel, U., Meyerhof, W., & Korsching, S. I. (2021). At the Root of T2R Gene Evolution: Recognition Profiles of Coelacanth and Zebrafish Bitter Receptors. *Genome Biology and Evolution,* 13(1). https://doi.org/10.1093/gbe/evaa264

The careful evaluation of food is important for survival throughout the animal kingdom, and specialized chemoreceptors have evolved to recognize nutrients, minerals, acids, andmany toxins. Vertebrate bitter taste, mediated by the taste receptor type 2 (T2R) family, warns against potentially toxic compounds. During evolution T2R receptors appear first in bony fish, but the functional properties of bony fish T2R receptors are mostly unknown. We performed a phylogenetic analysis showing the "living fossil" coelacanth (Latimeria chalumnae) and zebrafish (Danio rerio) to possess T2R repertoires typical for early-diverged species in the lobe-finned and the ray-finned clade, respectively. Receptors from these two species were selected for heterologous expression assays using a diverse panel of bitter substances. Remarkably, the ligand profile of the most basal coelacanth receptor, T2R01, is identical to that of its ortholog in zebrafish, consistent with functional conservation across >400 Myr of separate evolution. The second coelacanth receptor deorphaned, T2R02, is activated by steroid hormones and bile acids, evolutionary oldmolecules that are potentially endogenously synthesized agonists for extraoral T2Rs. For zebrafish, we report the presence of both specialized and promiscuous T2R receptors. Moreover, we identified an antagonist for one of the zebrafish receptors suggesting that bitter antagonism contributed to shape this receptor family throughout evolution.

Braulik, G. T., Rubens, J. R., & Macaulay, J. (2020). *Acoustic Monitoring of Blast Fishing in Tanzania in 2018 and 2019: Final Report.* Downstream Research & Conservation, Retrieved from https://hdl.handle.net/10023/21119

Since the 1960s fishing with home-made and, later, industrial explosives has been widespread throughout the coastal zone of Tanzania with large negative environmental and social consequences. Land-based monitoring estimated that in 2016 there were approximately 42,000 blasts at 24 hotspot locations along the Tanzania mainland coast. Government enforcement resulted in a substantial drop in blast fishing during the period 2016-2018, and since mid-2018 blast fishing levels in Tanzania have been at their lowest for decades. Gathering data on the location, timing and number of explosions over time is essential to be able to understand exactly when and where blasting occurs, to be able to guide enforcement into the right time and location, and to be able to monitor whether interventions have been effective. The overall goal of this current work was to use underwater acoustic monitoring stations to document the occurrence, and triangulate the exact location, of blast fishing explosions at key blasting hotspots in Tanzania. The acoustic monitoring was focused at four sites in two Tanzanian regions, Dar es Salaam and Tanga, both areas that have been subject to very high levels of blast fishing activity over many years. A total of 54 blasts (on a 50% duty cycle) were detected during 695 acoustic recording days between June 2018 and May 2019, giving an estimate of 108 blasts in total during that time period. A total of 49 blasts were recorded, and 98 blasts estimated to have occurred, in Tanga during the 279 days of acoustic recordings. By contrast off the coast of Dar es Salaam only 5 blasts were recorded, corresponding to an estimate of 10 blasts during 416 days of recordings over the same period. The recording location with by far the largest number of blasts detected was the area to the north of Pangani, towards Tanga Coelacanth Marine Park, where 80 blasts, representing 74% of the total were estimated. The majority of blast fishing activity occurred during the morning hours between 7am and

2pm and there was no preference for specific days of the week. Blast fishing occurred predominantly during low and falling tides (65% of detected blasts, n=35), and more than half (53.5%, n=29) of all blasts detected occurred during spring low tides. During extreme low tides it is easier to retrieve blasted fish (which generally sink) in the shallow, calm, low tide conditions, and also fishers are able to access deeper, less impacted and heavily fished habitats, thereby maximising their yields. When human land-based recorders and underwater acoustic recorders were deployed simultaneously, land-based recorders did not document a single blast, while the acoustic recorders continued to pick up small numbers of explosions. This suggests that in the face of increased enforcement blast fishers stopped blasting in coastal areas, but continued in more remote locations, such as the seaward side of offshore reefs, out of ear shot of enforcement officials on land, where only acoustic recorders were able to detect them. Based on this study, it is concluded that the dramatic reduction in blast-fishing seen during 2016-2018 along the Tanzanian coast continued into at least the middle of 2019. However, blast fishing had not been completely eliminated and persisted at very low levels, particularly in offshore waters off the coast of Tanga Region. The frequency and pattern of blasts detected during this study suggests that only a very small number of fishing vessels (perhaps as low as one or two) are responsible for the residual blast-fishing effort in Tanga. The remnant blasting activity is in two areas: mainly off the outer reefs of Tanga Coelacanth Marine Park, and in offshore waters in the northern half of Mkinga District. It is recommended that for maximum effectiveness, enforcement agencies could focus effort on identifying and intercepting the vessels that continue to practice blast fishing by monitoring around the offshore reefs in the above-mentioned areas, during morning hours, especially during spring low tides.

Brownstein, C. D., & Bissell, I. C. (2022). Species delimitation and coexistence in an ancient, depauperate vertebrate clade. *BMC Ecology and Evolution,* 22(1), 90. https://doi.org/10.1186/s12862-022-02043-4

BACKGROUND: A major challenge to understanding how biodiversity has changed over time comes from depauperons, which are long-lived lineages with presently low species diversity. The most famous of these are the coelacanths. This clade of lobe-finned fishes occupies a pivotal position on the vertebrate tree between other fishes and tetrapods. Yet only two extant species and fewer than 100 extinct forms are known from the coelacanth fossil record, which spans over 400 million years of time. Although there is evidence for the existence of additional genetically isolated extant populations, a poor understanding of morphological disparity in this clade has made quantifying coelacanth species richness difficult. RESULTS: Here, we quantify variation in a sample of skulls and skeletons of the Triassic eastern North American coelacanth daggerDiplurus that represents the largest assemblage of coelacanth individuals known. Based on the results of these quantitative comparisons, we identify a diminutive new species and show that multiple lacustrine ecosystems in the Triassic rift lakes of the Atlantic coastline harbored at least three species of coelacanths spanning two orders of magnitude in size. CONCLUSIONS: Conceptions about the distribution of species diversity on the tree of life may be fundamentally misguided when extant diversity is used to gauge signals of extinct diversity. Our results demonstrate how specimen-based assessments can be used to illuminate hidden biodiversity and show the utility of the fossil record for answering questions about the hidden richness of currently species-poor lineages.

Bruton, M. (2018). *The Annotated Old Fourlegs: The Updated Story of the Coelacanth*: University Press of Florida. Retrieved from https://upf.com/book.asp?id=9780813064642

When scientist JLB Smith published Old Fourlegs: The Story of the Coelacanth in 1956, he created an international sensation. A dramatic account of the discovery of a creature thought to have been extinct for 65 million years, the book brought science into the living rooms of thousands. It was published in six English editions and translated into ten foreign languages. The Annotated Old Fourlegs brings this incredible story back to life for today's readers.

Smith's famous account begins with the finding of a strange fish off the coast of South Africa by a local fisherman. As large as a person, the fish had fins like arms and vicious snapping jaws. Smith became certain that what had been caught was the legendary coelacanth, previously known only through fossils. The book follows Smith's obsessive drive to track down other specimens and to learn more about this extraordinary fish that has lived on Earth from the era of the dinosaurs to modern times.

The Annotated Old Fourlegs features a facsimile reprint of the original book with extensive margin notes, providing insights on JLB Smith, updates on coelacanth research, and comments on the coelacanth's influence on contemporary culture. Mike Bruton, an ichthyologist who has dedicated his life to continuing the pioneering studies begun by Smith, provides a new introduction and concluding chapters that bring the coelacanth story up to date.

Buonocore, F., & Gerdol, M. (2016). Alternative adaptive immunity strategies: coelacanth, cod and shark immunity. *Molecular Immunology,* 69, 157-169. https://doi.org/10.1016/j.molimm.2015.09.003

The advent of high throughput sequencing has permitted to investigate the genome and the transcriptome of novel non-model species with unprecedented depth. This technological advance provided a better understanding of the evolution of adaptive immune genes in gnathostomes, revealing several unexpected features in different fish species which are of particular interest. In the present paper, we review the current understanding of the adaptive immune system of the coelacanth, the elephant shark and the Atlantic cod.

The study of coelacanth, the only living extant of the long thought to be extinct Sarcopterygian lineage, is fundamental to bring new insights on the evolution of the immune system in higher vertebrates. Surprisingly, coelacanths are the only known jawed vertebrates to lack IgM, whereas two IgD/W loci are present. Cartilaginous fish are of great interest due to their basal position in the vertebrate tree of life; the genome of the elephant shark revealed the lack of several important immune genes related to T cell functions, which suggest the existence of a primordial set of TH1-like cells. Finally, the Atlantic cod lacks a functional major histocompatibility II complex, but balances this evolutionary loss with the expansion of specific gene families, including MHC I, Toll-like receptors and antimicrobial peptides.
Overall, these data point out that several fish species present an unconventional adaptive immune system, but the loss of important immune genes is balanced by adaptive evolutionary strategies which still guarantee the establishment of an efficient immune response against the pathogens they have to fight during their life.

Camila, C., Gaël, C., François, J. M., Marc, H., Yoshitaka, Y., & Paulo, M. B. (2020). The long-time adaptation of coelacanths to moderate deep water: reviewing the evidences. *Bulletin of the Kitakyushu Museum of Natural History and Human History, Series A (Natural History),* 17, 29-35. https://doi.org/10.34522/kmnh.17.0_29

The evolutionary history of coelacanths is long and complex with indications of adaptations to different aquatic environments. Fossil coelacanths are registered in shallow brackish, fresh or marine waters, while extant coelacanths inhabit moderate deep marine environments. Here we review some evidences of this long-time adaptation to moderate deep waters, focusing mainly on the hypothesis of bimodal respiration (gas exchange through gills and lungs) in most fossil coelacanths and on the aquatic gas exchange and the presence of a non-functional lung in the extant coelacanth Latimeria chalumnae. Another morphological evidence is the high rate of lipid accumulation in the whole body of L. chalumnae.

Cardoso, J. C. R., Bergqvist, C. A., Félix, R. C., & Larhammar, D. (2016). Corticotropin-releasing hormone family evolution: five ancestral genes remain in some lineages. *Journal of Molecular Endocrinology,* 57(1), 73-86. https://doi.org/10.1530/jme-16-0051

The evolution of the peptide family consisting of corticotropin-releasing hormone (CRH) and the three urocortins (UCN1-3) has been puzzling due to uneven evolutionary rates. Distinct gene duplication scenarios have been proposed in relation to the two basal rounds of vertebrate genome doubling (2R) and the teleost fish-specific genome doubling (3R). By analyses of sequences and chromosomal regions, including many neighboring gene families, we show here that the vertebrate progenitor had two peptide genes that served as the founders of separate subfamilies. Then, 2R resulted in a total of five members: one subfamily consists of CRH1, CRH2, and UCN1. The other subfamily contains UCN2 and UCN3. All five peptide genes are present in the slowly evolving genomes of the coelacanth Latimeria chalumnae (a lobe-finned fish), the spotted gar Lepisosteus oculatus (a basal ray-finned fish), and the elephant shark Callorhinchus milii (a cartilaginous fish). The CRH2 gene has been lost independently in placental mammals and in teleost fish, but is present in birds (except chicken), anole lizard, and the nonplacental mammals platypus and opossum. Teleost 3R resulted in an additional surviving duplicate only for crh1 in some teleosts including zebrafish (crh1a and crh1b). We have previously reported that the two vertebrate CRH/UCN receptors arose in 2R and that CRHR1 was duplicated in 3R. Thus, we can now conclude that this peptide-receptor system was quite complex in the ancestor of the jawed vertebrates with five CRH/UCN peptides and two receptors, and that crh and crhr1 were duplicated in the teleost fish tetraploidization.

Cavin, L., & Alvarez, N. (2022). Why Coelacanths Are Almost “Living Fossils”? *Frontiers in Ecology and Evolution,* 10. https://doi.org/10.3389/fevo.2022.896111

Darwin pointed out that “species of different genera and classes have not changed at the same rate” (Darwin, 1859, chapter X). Besides, he coined the expression “living fossils” for lineages whose “new forms will have been more slowly formed, and old forms more slowly exterminated” (chapter IV), among other characteristics. This expression has become popular, but has sometimes been misunderstood as meaning that some organisms do not evolve. It has also been commonly used by paleontologists and evolutionary biologists to describe a general pattern of relative stasis in morphological evolution in some lineages. Darwin's definition of the concept was imprecise and he considered that “species and groups of species, which are called aberrant, and which may fancifully be called living fossils, will aid us in forming a picture of the ancient forms of life” (Darwin, 1859, Chapter XIV). For more than 200 years, nevertheless, debates have raged on the definition of the concept (e.g., Bennett et al., 2017, 2018; Lidgard and Love, 2018; Turner, 2019), and more generally on the merits of its use in the life sciences (e.g., Casane and Laurenti, 2013; Naville et al., 2015). Although Darwin (1859) cited several taxa of fish as examples of “living fossils,” he did not mention the coelacanths, or actinistians, which were only known as fossils at his time. Huxley, however, soon after (1866) noticed the low anatomical disparity of coelacanths throughout their history. Since that time, and especially after the discovery of the living Latimeria in 1938 (Smith, 1939), the coelacanth has become an iconic symbol of the “living fossil” due to the slow morphological evolution illustrated by the fossil record of the clade, and its supposed affinities with tetrapods. Only the question of evolutionary rate is addressed here, not the question of ancestral status or other “living fossil” characteristics attributed to coelacanths. The low rate of evolution based on a lasting generalist morphological Bauplan has been confirmed by most subsequent authors who have worked on the group (Schaeffer, 1952; Cloutier, 1991; Forey, 1998; Schultze, 2004; Zhu et al., 2012; Cavin and Guinot, 2014), knowing that there are also exceptions to this general Bauplan (e.g., Friedman and Coates, 2006; Wendruff and Wilson, 2012; Cavin et al., 2017). However, part of the community of researchers working on fossil and living coelacanths avoids using this expression.

Most twenty-first century genetic studies have confirmed that the substitution rate of the genome of Latimeria was found to be slower than that of other vertebrate lineages in the mitochondrial (Sudarto et al., 2010; Nikaido et al., 2011; Lampert et al., 2012; Kadarusman et al., 2020) as well as in the nuclear genome (Nikaido et al., 2013) at least for the genes encoding proteins (Amemiya et al., 2010, 2013), when measured in substitution per year, although alternative interpretations remain (Bockmann et al., 2013; Casane and Laurenti, 2013; Grandcolas et al., 2014; Minelli and Baedke, 2014; Naville et al., 2015). It should be noted that although there is evidence for active transposable dynamics in the Latimeria genome (Smith et al., 2012; Chalopin et al., 2014; Naville et al., 2015), these elements have found to be highly conserved (Smith et al., 2012). The fact that at the level of transposable element activity, the coelacanth genome does not reveal slow dynamics (Chalopin et al., 2014) is thus not related to the global substitution rate.

Cavin, L., Piuz, A., Ferrante, C., & Guinot, G. (2021). Giant Mesozoic coelacanths (Osteichthyes, Actinistia) reveal high body size disparity decoupled from taxic diversity. *Scientific Reports,* 11(1), 11812. https://doi.org/10.1038/s41598-021-90962-5

The positive correlation between speciation rates and morphological evolution expressed by body size is a macroevolutionary trait of vertebrates. Although taxic diversification and morphological evolution are slow in coelacanths, their fossil record indicates that large and small species coexisted, which calls into question the link between morphological and body size disparities. Here, we describe and reassess fossils of giant coelacanths. Two genera reached up to 5 m long, placing them among the ten largest bony fish that ever lived. The disparity in body size adjusted to taxic diversity is much greater in coelacanths than in ray-finned fishes. Previous studies have shown that rates of speciation and rates of morphological evolution are overall low in this group, and our results indicate that these parameters are decoupled from the disparity in body size in coelacanths. Genomic and physiological characteristics of the extant Latimeria may reflect how the extinct relatives grew to such a large size. These characteristics highlight new evolutionary traits specific to these "living fossils".

Cavin, L., Torino, P., Van Vranken, N., Carter, B., Polcyn, M. J., & Winkler, D. (2021). The first late cretaceous mawsoniid coelacanth (Sarcopterygii: Actinistia) from North America: Evidence of a lineage of extinct 'living fossils'. *Plos One,* 16(11), e0259292. https://doi.org/10.1371/journal.pone.0259292

Today, the only living genus of coelacanth, Latimeria is represented by two species along the eastern coast of Africa and in Indonesia. This sarcopterygian fish is nicknamed a "living fossil", in particular because of its slow evolution. The large geographical distribution of Latimeria may be a reason for the great resilience to extinction of this lineage, but the lack of fossil records for this genus prevents us from testing this hypothesis. Here we describe isolated bones (right angular, incomplete basisphenoid, fragments of parasphenoid and pterygoid) found in the Cenomanian Woodbine Formation in northeast Texas that are referred to the mawsoniid coelacanth Mawsonia sp. In order to assess the impact of this discovery on the alleged characteristic of "living fossils" in general and of coelacanths in particular: 1) we compared the average time duration of genera of ray-finned fish and coelacanth in the fossil record; 2) we compared the biogeographic signal from Mawsonia with the signal from the rest of the vertebrate assemblage of the Woodbine formation; and 3) we compared these life traits with those of Latimeria. The stratigraphical range of Mawsonia is at least 50 million years. Since Mawsonia was a fresh, brackish water fish with probably a low ability to cross large sea barriers and because most of the continental components of the Woodbine Fm vertebrate assemblage exhibit Laurasian affinities, it is proposed that the Mawsonia's occurrence in North America is more likely the result of a vicariant event linked to the break-up of Pangea rather than the result of a dispersal from Gondwana. The link between a wide geographic distribution and the resilience to extinction demonstrated here for Mawsonia is a clue that a similar situation existed for Latimeria, which allowed this genus to live for tens of millions of years.

Cavin, L., Valentin, X., & Garcia, G. (2016). A new mawsoniid coelacanth (Actinistia) from the Upper Cretaceous of Southern France. *Cretaceous Research,* 62, 65-73. https://doi.org/10.1016/j.cretres.2016.02.002

Axelrodichthys megadromos sp. nov. is a coelacanth described based on a single specimen collected in the lower Campanian site of Ventabren motorway, Southern France. The new species is referred to the mawsoniids because of the ornamentation of the skull roof and of the proportionally wide supraorbital series. The specimen belongs to the Mawsonia-Axelrodichthys complex based on features present on the lower jaw and on the basisphenoid. The new species is referred to the genus Axelrodichthys because of proportions of its parietonasal shield and because of the arrangement of the posterior parietals relative to the supraorbitals. Autapomorphic characters, in particular on the parasphenoid, justify the inclusion of the specimen in a new species. The occurrence of a mawsoniid in the Ibero-American Island that formed part of the European Archipelago in the terminal Cretaceous is an evidence of a dispersal event from the southern land masses. The occurrence of A. megadromos in the Campanian-Maastrichtian represents the last occurrence of mawsoniids worldwide, after a gap in the fossil record of about 30 million years. This belated occurrence of Axelrodichthys extends the time range of this genus to approximately 40myr and suggests that this genus, together with its sister genus Mawsonia, were organisms with a slow morphologic evolution.

Challands, T. J., Pardo, J. D., & Clement, A. M. (2020). Mandibular musculature constrains brain-endocast disparity between sarcopterygians. *Royal Society Open Science,* 7(9), 200933. https://doi.org/10.1098/rsos.200933

The transition from water to land by the earliest tetrapods in the Devonian Period is seen as one of the greatest steps in evolution. However, little is understood concerning changes in brain morphology over this transition. Here, we determine the brain-braincase relationship in fishes and basal lissamphibians as a proxy to elucidate the changes that occurred over the fish-tetrapod transition. We investigate six basal extant sarcopterygians spanning coelacanths to salamanders (Latimeria chalumnae, Neoceratodus, Protopterus aethiopicus, P. dolloi, Cynops, Ambystoma mexicanum) using micro-CT and MRI and quantify the brain-braincase relationship in these extant taxa. Our results show that regions of lowest brain-endocast disparity are associated with regions of bony reinforcement directly adjacent to masticatory musculature for the mandible except in Neoceratodus and Latimeria. In Latimeria this deviation from the trend can be accounted for by the possession of an intracranial joint and basicranial muscles, whereas in Neoceratodus difference is attributed to dermal bones contributing to the overall neurocranial reinforcement. Besides Neoceratodus and Latimeria, regions of low brain-endocast disparity occur where there is less reinforcement away from high mandibular muscle mass, where the trigeminal nerve complex exits the braincase and where endolymphatic sacs occupy space between the brain and braincase wall. Despite basal tetrapods possessing reduced adductor muscle mass and a different biting mechanism to piscine sarcopterygians, regions of the neurocranium lacking osteological reinforcement in the basal tetrapods Lethiscus and Brachydectes broadly correspond to regions of high brain-endocast disparity seen in extant taxa.

Chng, Y. R., Ong, J. L. Y., Ching, B., Chen, X. L., Hiong, K. C., Wong, W. P., . . . Ip, Y. K. (2016). Molecular Characterization of Aquaporin 1 and Aquaporin 3 from the Gills of the African Lungfish, Protopterus annectens, and Changes in Their Branchial mRNA Expression Levels and Protein Abundance during Three Phases of Aestivation. *Frontiers in Physiology,* 7, 532. https://doi.org/10.3389/fphys.2016.00532

African lungfishes can undergo long periods of aestivation on land during drought. During aestivation, lungfishes are confronted with desiccation and dehydration, and their gills become non-functional and covered with a thick layer of dried mucus. Aquaporins (Aqps) are a superfamily of integral membrane proteins which generally facilitate the permeation of water through plasma membranes. This study aimed to obtain the complete cDNA coding sequences of aqp1 and aqp3 from the gills of Protopterus annectens, and to determine their branchial mRNA and protein expression levels during the induction, maintenance and arousal phases of aestivation. Dendrogramic analyses of the deduced Aqp1 and Aqp3 amino acid sequences of P. annectens revealed their close relationships with those of Latimeria chalumnae and tetrapods. During the induction phase, there were significant decreases in the transcript levels of aqpi and aqp3 in the gills of P. annectens, but the branchial Aqp1 and Aqp3 protein abundance remained unchanged. As changes in transcription might precede changes in translation, this could be regarded as an adaptive response to decrease the protein abundance of Aqp1 and Aqp3 in the subsequent maintenance phase of aestivation. As expected, the branchial transcript levels and protein abundance of aqp//Aqp1 and aqp3/Aqp3 were significantly down regulated during the maintenance phase, probably attributable to the shutdown of branchial functions and the cessation of volume regulation of branchial epithelial cells. Additionally, these changes could reduce the loss of water through branchial epithelial surfaces, supplementing the anti desiccating property of the dried mucus. Upon arousal, it was essential for the lungfish to restore branchial functions. Indeed, the protein abundance of Aqp1 recovered partially, with complete recovery of mRNA expression level and protein abundance of Aqp3, in the gills of P annectens after 3 days of arousal. These results provide insights into how P annectens regulates branchial Aqp expression to cope with desiccation and rehydration during different phases of aestivation.

Choat, J. H. (2021). Marine biology: Ageing a 'living fossil'. *Current Biology,* 31(16), R998-R1000. https://doi.org/10.1016/j.cub.2021.06.092

A novel approach to determine the lifespan of an iconic fish, the coelacanth Latimeria chalumnae, reveals that they can live up to a hundred years. This re-focuses attention on the need to measure life-history traits that determine the demographics of fish populations.

Cooke, A., Bruton, M., & Ravololoharinjara, M. (2021). Coelacanth discoveries in Madagascar, with recommendations on research and conservation. *South African Journal of Science,* 117(3-4), 80-90. https://doi.org/10.17159/sajs.2021/8541

The presence of populations of the Western Indian Ocean coelacanth (Latimeria chalumnae) in Madagascar is not surprising considering the vast range of habitats which the ancient island offers. The discovery of a substantial population of coelacanths through handline fishing on the steep volcanic slopes of Comoros archipelago initially provided an important source of museum specimens and was the main focus of coelacanth research for almost 40 years. The advent of deep-set gillnets, or jarifa, for catching sharks, driven by the demand for shark fins and oil from China in the mid- to late 1980s, resulted in an explosion of coelacanth captures in Madagascar and other countries in the Western Indian Ocean. We review coelacanth catches in Madagascar and present evidence for the existence of one or more populations of L. chalumnae distributed along about 1000 km of the southern and western coasts of the island. We also hypothesise that coelacanths are likely to occur around the whole continental margin of Madagascar, making it the epicentre of coelacanth distribution in the Western Indian Ocean and the likely progenitor of the younger Comoros coelacanth population. Finally, we discuss the importance and vulnerability of the population of coelacanths inhabiting the submarine slopes of the Onilahy canyon in southwest Madagascar and make recommendations for further research and conservation. Significance: The paper contributes significantly to knowledge of the distribution and ecology of the Indian Ocean coelacanth, Latimeria chalumnae. The paper provides the first comprehensive account of Madagascar coelacanths and demonstrates the existence of a regionally important population and extensive suitable habitat, correcting an earlier hypothesis that coelacanths in southwest Madagascar were strays from the Comoros. The results have application in the study of the evolution, biology, ecology and conservation of the species. The significant threat posed by gillnet fishing to coelacanths and other species is highlighted as are the negative effects of the shark-fin trade. The paper emphasises the importance of the Onilahy marine canyon in southwest Madagascar as an especially important habitat and provides the basis for the development of a national programme of research and conservation.

Critical Ecosystem Partnership Fund. (2022). *Ecosystem Profile: Madagascar and the Indian Ocean Islands Biodiversity Hotspot.* Retrieved from https://www.cepf.net/sites/default/files/cepf_ecosystem_profile_madio_10nov22_en.pdf

Founded in 2000, the Critical Ecosystem Partnership Fund (CEPF) is a joint initiative of l'Agence Française de Developpement (AFD), Conservation International (CI), the European Union (EU), the Global Environment Facility (GEF), the Government of Japan and the World Bank that supports civil society actors in their efforts to conserve the world's most severely threatened ecosystems, known as biodiversity hotspots. Funding from the Green Climate Fund (GCF) has been made available to CEPF for Madagascar and the Indian Ocean Islands through AFD as an accredited entity to the GCF. The fundamental purpose of conserving ecosystems is to enable them to perform their various functions, called ecosystem services, for the benefit and needs of people, including: food security; water supply; energy supply; health security; material and economic comfort; and the maintenance of cultural values and social cohesion. In recent decades, however, in the face of massive and accelerated exploitation perpetrated by humans to satisfy these needs, ecosystems have undergone transformations tending towards forms of degradation that risk becoming irreversible, because the rate of exploitation largely exceeds the capacity for regeneration that these ecosystems have. This trend of irreversible degradation is exacerbated in a context where other factors have come into play: climate change, on the one hand; and COVID-19 and other possible unexpected health hazards, on the other. As a result, pressures on ecosystems are increasing, at the risk of losing their functions and at the expense of the development and wellbeing of local populations.

Criveanu, D., Bergqvist, C. A., Larhammar, D., & Walczewska-Szewc, K. (2023). Identification of a new Kir6 potassium channel and comparison of properties of Kir6 subtypes by structural modelling and molecular dynamics. *International Journal of Biological Macromolecules,* 247, 125771. https://doi.org/10.1016/j.ijbiomac.2023.125771

ATP-sensitive potassium ion channels (KATP) are transmembrane proteins that modulate insulin release and muscle contraction. KATP channels are composed of two types of subunit, Kir6 and SUR, which exist in two and three isoforms respectively with different tissue distribution. In this work, we identify a previously undescribed ancestral vertebrate gene encoding a Kir6-related protein that we have named Kir6.3, which may not have a SUR binding partner, unlike the other two Kir6 proteins. Whereas Kir6.3 was lost in amniotes including mammals, it is still present in several early-diverging vertebrate lineages such as frogs, coelacanth, and rayfinned fishes. Molecular dynamics (MD) simulations using homology models of Kir6.1, Kir6.2, and Kir6.3 from the coelacanth Latimeria chalumnae showed that the three proteins exhibit subtle differences in their dynamics. Steered MD simulations of Kir6-SUR pairs suggest that Kir6.3 has a lower binding affinity for the SUR proteins than either Kir6.1 or Kir6.2. As we found no additional SUR gene in the genomes of the species that have Kir6.3, it most likely forms a lone tetramer. These findings invite studies of the tissue distribution of Kir6.3 in relation to the other Kir6 as well as SUR proteins to determine the functional roles of Kir6.3.

Cupello, C., ClÉMent, G., Meunier, F. J., Herbin, M., Yabumoto, Y., & Brito, P. M. (2019). The long-time adaptation of coelacanths to moderate deep water: reviewing the evidences. *Bulletin of the Kitakyushu Museum of Natural History and Human History, Series A (Natural History),* 17, 29-35. https://doi.org/10.34522/kmnh.17.0_29

The evolutionary history of coelacanths is long and complex with indications of adaptations to different aquatic environments. Fossil coelacanths are registered in shallow brackish, fresh or marine waters, while extant coelacanths inhabit moderate deep marine environments. Here we review some evidences of this long-time adaptation to moderate deep waters, focusing mainly on the hypothesis of bimodal respiration (gas exchange through gills and lungs) in most fossil coelacanths and on the aquatic gas exchange and the presence of a non-functional lung in the extant coelacanth Latimeria chalumnae. Another morphological evidence is the high rate of lipid accumulation in the whole body of L. chalumnae.

Cupello, C., Meunier, F. J., Herbin, M., Clément, G., & Brito, P. M. (2017). Lung anatomy and histology of the extant coelacanth shed light on the loss of air-breathing during deep-water adaptation in actinistians. *Royal Society Open Science,* 4(3), 161030. https://doi.org/10.1098/rsos.161030

Lungs are specialized organs originated from the posterior pharyngeal cavity and considered as plesiomorphic for osteichthyans, as they are found in extant basal actinopterygians (i.e. Polypterus) and in all major groups of extant sarcopterygians. The presence of a vestigial lung in adult stages of the extant coelacanth Latimeria chalumnae is the result of allometric growth during ontogeny, in relation with long-time adaptation to deep water. Here, we present the first detailed histological and anatomical description of the lung of Latimeria chalumnae, providing new insights into its arrested differentiation in an air-breathing complex, mainly represented by the absence of pneumocytes and of compartmentalization in the latest ontogenetic stages.

Cupello, C., Meunier, F. J., Herbin, M., Janvier, P., Clément, G., & Brito, P. M. (2017). The homology and function of the lung plates in extant and fossil coelacanths. *Scientific Reports,* 7(1), 9244. https://doi.org/10.1038/s41598-017-09327-6

The presence of a pulmonary organ that is entirely covered by true bone tissue and fills most of the abdominal cavity is hitherto unique to fossil actinistians. Although small hard plates have been recently reported in the lung of the extant coelacanth Latimeria chalumnae, the homology between these hard structures in fossil and extant forms remained to be demonstrated. Here, we resolve this question by reporting the presence of a similar histological pattern-true cellular bone with star-shaped osteocytes, and a globular mineralisation with radiating arrangement-in the lung plates of two fossil coelacanths (Swenzia latimerae and Axelrodichthys araripensis) and the plates that surround the lung of the most extensively studied extant coelacanth species, L. chalumnae. The point-for-point structural similarity of the plates in extant and fossil coelacanths supports their probable homology and, consequently, that of the organ they surround. Thus, this evidence questions the previous interpretations of the fatty organ as a component of the pulmonary complex of Latimeria.

Daley, J. (2018). This Fish Outlived Dinosaurs But Oil and Gas Drilling May Threaten Its Survival. *Smithsonian Magazine*. Retrieved from https://www.smithsonianmag.com/smart-news/energy-development-could-threaten-south-africas-dino-fish-180970073/

Oil exploration is set to begin near the habitat of the critically endangered coelacanth, a type of fish that has survived over 400 million years

Décamps, T., Herrel, A., Ballesta, L., Holon, F., Rauby, T., Gentil, Y., . . . Herbin, M. (2017). The third dimension: a novel set-up for filming coelacanths in their natural environment. *Methods in Ecology and Evolution,* 8(3), 322-328. https://doi.org/10.1111/2041-210x.12671

Here, we describe a novel design to obtain three-dimensional data on the movements of aquatic organisms at depths of up to 140m. The set-up consists of two synchronized high-speed cameras fixed to two articulated arms. The set-up was successfully used to film and quantify the locomotion of coelacanths Latimeria chalumnae living at a depth of about 120m in Sodwana Bay, South Africa. As an example, the detailed motion of the dorsal fin is presented here. This set-up can be used for any underwater applications that require synchronized video recordings of medium- to large-sized animals.

deCastro, M., Semba, M., Lumpkin, R., Kimirei, I., Shaghude, Y., & Nyandwi, N. (2019). Seasonal and spatial variation of surface current in the Pemba Channel, Tanzania. *Plos One,* 14(1). https://doi.org/10.1371/journal.pone.0210303

The surface current speeds within the Pemba channel were examined using 24 years of drifter data received from the Global Drifter Program. This study aimed to uncover varying surface current in the Pemba Channel in different seasons. The results revealed the Pemba Channel experiences relatively higher median surface current speeds during the southeast (SE) monsoon season compared to the northeast (NE) and inter-monsoon (IN) periods. The strongest current speeds were confined in waters deeper than 200 meters between ~39.4°E and 39.7°E. These results prove that surface currents from the drifters can be used to uncover the patterns of surface circulation even in areas where in-situ measurements are scarce.

Dutel, H., Galland, M., Tafforeau, P., Long, J. A., Fagan, M. J., Janvier, P., . . . Herbin, M. (2019). Neurocranial development of the coelacanth and the evolution of the sarcopterygian head. *Nature,* 569(7757), 556-+. https://doi.org/10.1038/s41586-019-1117-3

The neurocranium of sarcopterygian fishes was originally divided into an anterior (ethmosphenoid) and posterior (otoccipital) portion by an intracranial joint, and underwent major changes in its overall geometry before fusing into a single unit in lungfishes and early tetrapods(1). Although the pattern of these changes is well-documented, the developmental mechanisms that underpin variation in the form of the neurocranium and its associated soft tissues during the evolution of sarcopterygian fishes remain poorly understood. The coelacanth Latimeria is the only known living vertebrate that retains an intracranial joint(2,3). Despite its importance for understanding neurocranial evolution, the development of the neurocranium of this ovoviviparous fish remains unknown. Here we investigate the ontogeny of the neurocranium and brain in Latimeria chalumnae using conventional and synchrotron X-ray micro-computed tomography as well as magnetic resonance imaging, performed on an extensive growth series for this species. We describe the neurocranium at the earliest developmental stage known for Latimeria, as well as the major changes that the neurocranium undergoes during ontogeny. Changes in the neurocranium are associated with an extreme reduction in the relative size of the brain along with an enlargement of the notochord. The development of the notochord appears to have a major effect on the surrounding cranial components, and might underpin the formation of the intracranial joint. Our results shed light on the interplay between the neurocranium and its adjacent soft tissues during development in Latimeria, and provide insights into the developmental mechanisms that are likely to have underpinned the evolution of neurocranial diversity in sarcopterygian fishes.

Edeye, K. O. (2022). *Shallow and Mesophotic Reef Communities of the Western Indian Ocean: Implications for Management and Conservation.* (Ph.D.), University of York, York, UK. Retrieved from https://etheses.whiterose.ac.uk/31223/1/Edeye_205050347_FinalThesis.pdf

Coral ecosystems in the Western Indian Ocean are considered highly threatened and therefore in need of improved knowledge to inform management and conservation policy measures. The reef habitats and fish communities in Pemba Island are under-researched despite experiencing human-related pressures. This study involved application of size-spectra analysis, deployment of marine robots comprising autonomous underwater vehicles (AUVs) and baited remote underwater videos (BRUVS) together with long swims (LS) underwater visual census. Results on size-spectra relationships indicated that highly and well-protected Marine Protected Areas (MPAs) are more productive and support high abundances of small fish. Use of marine robots highlighted the capability of using AUVs to fill the knowledge gap on mesophotic coral ecosystems (MCE), and their potential application for initial survey and subsequent monitoring of MPAs. BRUVS surveys revealed the importance of depth and healthy coral habitats in providing refuge for coral reef predatory fishes from fishing. Identical estimates of species richness, community structure and relative abundance of reef predatory fish species was found between BRUVS and LS. The study suggests: 1) restoration of fish community structure requires addressing fisher needs and supporting effective MPA management to secure ecosystem benefits for coastal communities, 2) presence of MCE composed of corals, algae and fishes on the western margins of Pemba Island, and steeply inclined substrate particularly in mesophotic depths (>30m) that support a highly bio-diverse community, 3) reef fish predator types are discordantly predicted by depth and habitat type, although high abundance and species richness occur in deeper waters and hard and soft coral habitat types, 4) BRUVS and LS are complementary, together providing a complete assessment of reef fish communities. Careful management through effective area and species protection measures, particularly on deeper reefs, are needed to conserve the biologically important area of Pemba Island and prevent further depletion of reef-associated communities.

Fennessy, S. T. (2016). Subtropical demersal fish communities on soft sediments in the KwaZulu-Natal Bight, South Africa. *African Journal of Marine Science,* 38(sup1), S169-S180. https://doi.org/10.2989/1814232x.2016.1140677

The project entitled Ecosystem Processes in the KwaZulu-Natal Bight, part of the African Coelacanth Ecosystem Programme (ACEP), enabled the description of demersal fish communities over soft sediments, including from some areas that have rarely been explored in the subtropical waters of the east coast of South Africa. A total of 165 fish taxa from 78 families were caught, and were dominated by the Sparidae (five species), Triglidae (four species), Acropomatidae (three species), Macrouridae (eight species), Chlorophthalmidae (one species), Paralichthyidae (three species) and Sciaenidae (six species), which together contributed 75% and almost 60% to numbers and weight, respectively. The most ubiquitous species were Chlorophthalmus punctatus and Pagellus natalensis. Species composition was structured mainly by depth, and proximity to the Thukela River, the latter being particularly influential on the adjacent Thukela Bank that harbours a unique community. There are close affinities between KZN Bight soft-sediment fish communities and those off Western Australia, and particularly with communities from East Africa. The unique nature of fish communities off the Thukela River is part-motivation towards the establishment of a large marine protected area in the northern part of the KZN Bight, which is increasingly the focus of disruptions such as impoundments and mining.

Fennessy, S. T., Roberts, M. J., & Paterson, A. W. (2016). A brief overview of the ACEP project: Ecosystem Processes in the KwaZulu-Natal Bight. *African Journal of Marine Science,* 38(sup1), S1-S6. https://doi.org/10.2989/1814232x.2016.1141116

This introductory paper lays the basis for this supplementary issue by briefly presenting the state of knowledge on the KwaZulu-Natal (KZN) Bight at the start of this multi-disciplinary, multi-institutional, ship-based research project that ran from 2009 to 2013. The rationale and aims of the project are also described. The project was a major component of the South African Department of Science and Technology's African Coelacanth Ecosystem Programme (ACEP), which has been prominent in supporting research on the east coast of South Africa and the wider South-West Indian Ocean. Pivotal to this was the RS Algoa, which was made available for two 30-day surveys (winter and summer) in the KZN Bight by the Department of Environmental Affairs. Although some aspects of the bight ecology are known, much of the research is dated and fragmented, and required refreshing and consolidation in order to produce a platform upon which the understanding of the region's ecosystem functioning could be established. Much of the oceanographic knowledge is also dated, with no dedicated surveys and significant measurements undertaken since 1989. The overarching theme of the KZN Bight project was to examine the relative importance of sources of nutrients to the central KZN coast and how these are taken up and recycled in the ecosystem, and to describe aspects of the benthic biodiversity, which is poorly described in much of this region. An ambitious project, its accessibility to a ship-based research platform and the diverse scientific skills of the participating scientists allowed considerable success, as reflected in the papers that follow.

Fernández, J. M., Meunier, F. J., Cloutier, R., Clément, G., & Laurin, M. (2022). Life history and ossification patterns in Miguashaia bureaui reveal the early evolution of osteogenesis in coelacanths. *Peerj,* 10, e13175. https://doi.org/10.7717/peerj.13175

The study of development is critical for revealing the evolution of major vertebrate lineages. Coelacanths have one of the longest evolutionary histories among osteichthyans, but despite access to extant representatives, the onset of their weakly ossified endoskeleton is still poorly understood. Here we present the first palaeohistological and skeletochronological study of Miguashaia bureaui from the Upper Devonian of Canada, pivotal for exploring the palaeobiology and early evolution of osteogenesis in coelacanths. Cross sections of the caudal fin bones show that the cortex is made of layers of primary bone separated by lines of arrested growth, indicative of a cyclical growth. The medullary cavity displays remnants of calcified cartilage associated with bony trabeculae, characteristic of endochondral ossification. A skeletochronological analysis indicates that rapid growth during a short juvenile period was followed by slower growth in adulthood. Our new analysis highlights the life history and palaeoecology of Miguashaia bureaui and reveals that, despite differences in size and habitat, the poor endoskeletal ossification known in the extant Latimeria chalumnae can be traced back at least 375 million years ago.

Fraser, M. D., Henderson, B. A. S., Carstens, P. B., Fraser, A. D., Henderson, B. S., Dukes, M. D., & Bruton, M. N. (2020). Live coelacanth discovered off the KwaZulu-Natal South Coast, South Africa. *South African Journal of Science,* 116(3/4), 1-3. https://doi.org/10.17159/sajs.2020/7806

When a living coelacanth was trawled off East London, South Africa, at a depth between 72 m and 100 m on 22 December 1938, it caused an international sensation. The specimen was saved for science by the young curator of the East London Museum, Marjorie Courtenay-Latimer8 and identified by JLB Smith of Rhodes University College. Smith named it Latimeria chalumnae, after Courtenay-Latimer and the river off which it was caught, and it is listed in the official Coelacanth Conservation Council (CCC) inventory as CCC 1. L. chalumnae is classified in the family Latimeriidae and the suborder Latimerioidea. Hans Fricke and his team from Germany were the first to study the living coelacanth in detail from their research submersible Jago. They compiled an extraordinary data series on the living coelacanth in the Comoros spanning 21 years and including 145 specimens that had been individually identified using the unique patterns of white spots on their bodies.

Gao, B., Sang, Y. T., Zong, W. C., Diaby, M., Shen, D., Wang, S. S., . . . Song, C. Y. (2020). Evolution and Domestication of Tc1/mariner transposons in the African coelacanth (Latimeria chalumnae) genome. *Genome,* 63(8), 375-386. https://doi.org/10.1139/gen-2019-0216

Here, we comprehensively analysed the abundance, diversity, and activity of Tc1/mariner transposons in African coelacanth (Latimeria chalumnae). Fifteen Tc1/mariner autonomous transposons were identified and grouped into six clades: DD34E/Tc1, DD34D/manner, DD35D/Fot, DD31D/pogo, DD30-31D/pogo-like, and DD32-36D/Tigger, belonging to three known families: DD34E/Tc1, DD34D/mariner, and DDxD/pogo (DD35D/Fot, DD31D/pogo, DD30-31D/pogo-like, and DD32-36D/Tigger). Thirty-one miniature inverted-repeat transposable element (MITE) transposons of Tc1/mariner were also identified, and 20 of them display similarity to the identified autonomous transposons. The structural organization of these full Tc1/mariner elements includes a transposase gene flanked by terminal inverted repeats (Tilts) with TA dinucleotides. The transposases contain N-terminal DNA binding domain and a C-terminal catalytic domain characterized by the presence of a conservative D(Asp)DE(Glu)/D triad that is essential for transposase activity. The Tc1/mariner superfamily in coelacanth exhibited very low genome coverage (0.3%), but it experienced an extraordinary difference of proliferation dynamics among the six clades identified; moreover, most of them exhibited a very recent and current proliferation, suggesting that some copies of these transposons are putatively active. Additionally, at least four functional genes derived from Tc1/mariner transposons were found. We provide an up-to-date overview of Tc1/mariner in coelacanth, which may be helpful in determining genome and gene evolution in this living fossil.

Huby, A., Mansuit, R., Herbin, M., & Herrel, A. (2021). Revision of the muscular anatomy of the paired fins of the living coelacanth Latimeria chalumnae (Sarcopterygii: Actinistia). *Biological Journal of the Linnean Society,* 133(4), 949-989. https://doi.org/10.1093/biolinnean/blab047

As a sarcopterygian fish, the extant coelacanth Latimeria has muscular paired fins, different in their skeletal and muscular anatomy from the paired fins of actinopterygians. Although the muscular anatomy of the pectoral and pelvic fins of Latimeria has been described by several studies, a detailed functional description of the muscles and their architecture has never been performed. Our detailed functional description of the muscles of the paired fins shows a more complex organization than previously described. The pectoral and pelvic fins have a different organization of their muscular anatomy, and the pelvic fin shows a more plesiomorphic configuration of the muscles since most of them are poly-articular and run from the pelvic girdle to the fin rays, an organization typical of actinopterygians. We found that the pectoral fins are stronger than the pelvic fins which is likely to be associated with the greater contribution of the pectoral fins to locomotion and manoeuvring. Finally, the study of the joint mobility of the paired fins showed that the pectoral fins show greater mobility than the pelvic fins. The reduced mobility of the pelvic fin is possibly a consequence of the morphology of the mesomeres and the large pre-axial radials.

Iwata, M., Yabumoto, Y., Saruwatari, T., Yamauchi, S., Fujii, K., Ishii, R., . . . Abe, Y. (2019). Observation of the first juvenile Indonesian coelacanth, Latimeria menadoensis from Indonesian waters with a comparison to embryos of Latimeria chalumnae. *Bulletin of the Kitakyushu Museum of Natural History and Human History, Series A (Natural History),* 17, 57-65. https://doi.org/10.34522/kmnh.17.0_57

The juvenile of Indonesian coelacanth, Latimeria menadoensis is here described for the first time in detail with comparison to embryos of Latimeria chalumnae. The juvenile was found in free swimming at 164.6 m depth off Manado, Indonesia on the 6th October in 2009. Because the total length of the juvenile is 31.5 cm, which is smaller than the embryos of L. chalumnae, it is speculated that not much time has passed from its birth. The depth at which the juvenile was found is within the range of the depth where adult L. menadoensis were observed, hidden in a narrow and long overhang where large predators could not enter. The juvenile has a more slender body, smaller orbit, shorter and deeper posterior part of the body (caudal peduncle) between the second dorsal and the anal fins and anterior ends of the dorsal and ventral lobes of the caudal fin (the third dorsal and second anal fins), longer dorsal and ventral lobes of the caudal fin (the third dorsal and second anal fins), broader peduncles of broader lobed fins, larger first dorsal fin and longer supplementary lobe of the caudal fin (caudal fin) than embryos of L. chalumnae. This indicates clear differences in the first ontogenetic stages of the two species, although adults have almost the same morphological features. Latimeria menadoensis appears to reproduce in a rather confined area, because both the juvenile and adults have been found within the same area inside of Manado Bay.

James, R., Jialiang, G., & Emily Jane, M. (2024). Phylogenetic Diversity Across the Complete Tree of Life. *Research Square*. https://doi.org/10.21203/rs.3.rs-4397985/v1

In the face of rapid biodiversity loss, many approaches have been developed to measure biodiversity in ways that go beyond species richness. One prominent example is Phylogenetic Diversity (PD), which measures evolutionary history by summing the branches required to connect a set of species on a dated phylogenetic tree. PD may also capture other biodiversity measures by proxy such as the richness of biological features and their potential future benefits for humanity, sometimes known as 'future options'. The total global PD is known for some well-studied groups, such as most vertebrates, but PD estimates are lacking for the majority of the tree of life. Here, we characterize the distribution of PD across the complete tree of life with over 2.2 million species. To do this we use data from the Open Tree of Life and a smoothing method to interpolate between nodes without date information. We estimate that the PD represented by all described species together is between 29 and 33 trillion years. We characterize the distribution of evolutionary distinctiveness, a measure of the fair share of PD captured by individual species, across all life and within selected clades. Many clades have bimodal distributions of evolutionary distinctiveness across species which may be due to changes in diversification rate within subclades. PD has previously been used as the basis for conservation prioritization schemes such as EDGE (Evolutionary Distinct and Globally Endangered) which synthesizes phylogenetic tree data with extinction risk data from the IUCN Red List of threatened species. Here we estimate EDGE scores for over 130,000 species, many more than have been done previously. The top EDGE species is Latimeria chalumnae, the critically endangered West Indian Ocean coelacanth. We hope this work will pave the way for more complete and automated analyses of PD and EDGE scores across the complete tree of life.

Johnston, P. (2022). The missing anatomy of the living coelacanth, Latimeria chalumnae (Smith, 1939). *Vertebrate Zoology,* 72, 513-531. https://doi.org/10.3897/vz.72.e84274

Anatomical features that have not been previously described in Latimeria were sought in histological section series, tissue-stained microCT scans, MRI scans, and synchrotron scan series. The spiracular organ, ultimobranchial endocrine gland, and m. cucullaris were identified in the expected locations. In addition, a muscle arising on the medial side of the pectoral girdle is identified and com-pared with a muscle in a similar location that attaches to the cranial rib in lungfish; these are proposed as homologues of the tetrapod m. omohyoideus. These findings are placed in evolutionary context by comparison with selected other groups of fish, lungfish and tetrapods. The position of Latimeria as a key taxon in the fish-to-tetrapod transition is emphasised by these findings, and the findings have potential to inform research on cranial structure in extinct taxa.

Kathleen, M. G., Tsvetan, R. B., & Rosemary, J. (2016). Expansion of eIF4E and 4E-BP Family Members in Deuterostomes. In *Evolution of the Protein Synthesis Machinery and Its Regulation.* (pp. 165-185) https://doi.org/10.1007/978-3-319-39468-8_8

Analysis of eIF4E sequences from the more than twenty fish genomes currently available, as well as those of select tetrapods, echinoderm (Strongylocentrotus purpuratus), tunicate (Ciona intestinalis), and cephalocordate (Branchiostoma lanceolatum), has allowed a glimpse of the origins and evolution of the eIF4E and 4E-BP families in vertebrates. Metazoan eIF4E family members group into three classes, with Class I containing the canonical cap-binding translational initiation factor, eIF4E-1. Class II and III eIF4E family members have distinct characteristics and have been shown to regulate the translation of particular mRNAs. All deuterostomes have at least one representative from each of the three classes of eIF4E. Outgroup deuterostomes such as sea urchins, tunicates, and lancelets have only one eIF4E from each class: eIF4E-1, eIF4E-2, and eIF4E-3. Evidence of the duplication of Class I eIF4Es can be seen in elephant shark (Callorhinchus milii), coelacanth (Latimeria chalumnae), and the basal ray-finned fish, spotted gar (Lepisosteus oculatus), which all have three eIF4E-1 subclasses: eIF4E-1A, -1B, and -1C. The emergence of eIF4E-1 subclasses is consistent with the duplication of Class I prior to the teleost-specific whole genome duplication (TGD), probably at one of the vertebrate genome duplications that occurred at ~550 Ma (VGD1) and 500 Ma (VGD2). eIF4E-1C has maintained the function of a prototypical initiation factor. It has been retained in all teleosts, but lost in tetrapods; eIF4E-1B has neofunctionalized to become a tissue-specific regulator of mRNA recruitment. It has been retained in tetrapods and most teleosts, but lost in the Tetraodontiforms such as Tetroadon and Takifugu species. Some percomorphs have acquired new cognates of eIF4E-1A and eIF4E-3 to give eIF4E-1A1 and -1A2 and eIF4E-3A and -3B. A duplication of class II eIF4Es occurred prior to the emergence of the tetrapod branch to give eIF4E-2A and -2B. eIF4E-2B is retained by amphibians and teleosts, but has been lost in coelacanth and amniotes. Overall, duplication within the different classes of eIF4E occurred early in vertebrate evolution with some neofunctionalization. Further duplication within teleosts of eIF4E-1A and eIF4E-3 occurred and has been retained in some teleost lineages. Asymmetric losses in different vertebrate classes also occurred. Similarly, expansion of the 4E-BPs took place in vertebrates to give three classes, 4E-BP1, -BP2, and -BP3, with further duplication in select teleosts to give six 4E-BP cognates, with asymmetric loss in more recently emerging teleosts.

Kélig, M., Bruno, E., & Marc, H. (2021). New scale analyses reveal centenarian African coelacanths. *Current Biology,* 31(16), 3621-3628.e3624. https://doi.org/10.1016/j.cub.2021.05.054

The extant coelacanth was discovered in 1938; its biology and ecology remain poorly known due to the low number of specimens collected. Only two previous studies have attempted to determine its age and growth. They suggested a maximum lifespan of 20 years, placing the coelacanth among the fastest growing marine fish. These findings are at odds with the coelacanth's other known biological features including low oxygen-extraction capacity, slow metabolism, ovoviviparity, and low fecundity, typical of fish with slow life histories and slow growth. In this study, we use polarized light microscopy to study growth on scales based on a large sample of 27 specimens. Our results demonstrate for the first time nearly imperceptible annual calcified structures (circuli) on the scales and show that maximal age of the coelacanth was underestimated by a factor of 5. Our validation method suggests that circuli are indeed annual, thus supporting that the coelacanth is among the longest-living fish species, its lifespan being probably around 100 years. Like deep-sea sharks with a reduced metabolism, the coelacanth has among the slowest growth for its size. Further reappraisals of age at first sexual maturity (in the range 40 to 69 years old) and gestation duration (of around 5 years) show that the living coelacanth has one of the slowest life histories of all marine fish and possibly the longest gestation. As long-lived species with slow life histories are extremely vulnerable to natural and anthropogenic perturbations, our results suggest that coelacanths may be more threatened than previously considered.

Kozhukhar, N., & Alexeyev, M. F. (2022). TFAM's Contributions to mtDNA Replication and OXPHOS Biogenesis Are Genetically Separable. *Cells,* 11(23). https://doi.org/10.3390/cells11233754

The ability of animal orthologs of human mitochondrial transcription factor A (hTFAM) to support the replication of human mitochondrial DNA (hmtDNA) does not follow a simple pattern of phylogenetic closeness or sequence similarity. In particular, TFAM from chickens (Gallus gallus, chTFAM), unlike TFAM from the "living fossil" fish coelacanth (Latimeria chalumnae), cannot support hmtDNA replication. Here, we implemented the recently developed GeneSwap approach for reverse genetic analysis of chTFAM to obtain insights into this apparent contradiction. By implementing limited "humanization" of chTFAM focused either on amino acid residues that make DNA contacts, or the ones with significant variances in side chains, we isolated two variants, Ch13 and Ch22. The former has a low mtDNA copy number (mtCN) but robust respiration. The converse is true of Ch22. Ch13 and Ch22 complement each other's deficiencies. Opposite directionalities of changes in mtCN and respiration were also observed in cells expressing frog TFAM. This led us to conclude that TFAM's contributions to mtDNA replication and respiratory chain biogenesis are genetically separable. We also present evidence that TFAM residues that make DNA contacts play the leading role in mtDNA replication. Finally, we present evidence for a novel mode of regulation of the respiratory chain biogenesis by regulating the supply of rRNA subunits.

Lambertz, M. (2017). The vestigial lung of the coelacanth and its implications for understanding pulmonary diversity among vertebrates: new perspectives and open questions. *Royal Society Open Science,* 4(11), 171518-171518. https://doi.org/10.1098/rsos.171518

The coelacanth, Latimeria chalumnae Smith, 1939 [1] (Sarcopterygii: Actinistia), together with the closely related L. menadoensis Pouyaud et al ., 1999 [2], remains the only living representative of one of the most basally-branching primary radiations of lobe-finned fishes (Sarcopterygii). Even though extant species cannot be considered ‘primitive’ due to the inherent logic of phylogenetic theory, the coelacanth nonetheless is invaluable for understanding evolutionary transformations in basal sarcopterygians as it can help in the determination of character polarity. The appearance of one novelty during early vertebrate evolution that had major implications for the success of a huge number of species is the origin of lungs. The conventional interpretation is that lungs evolved in basal bony fishes (Osteichthyes or Osteognathostomata), were maintained in the lobe-finned fishes, and eventually were transformed into a swimbladder among the ray-finned fishes (Actinopterygii) (e.g. [3]). However, the currently available data do not rule out separate origins of lungs and swimbladders from a common ‘respiratory pharynx’, even though this would require a slightly less parsimonious course of evolution [4,5]. The coelacanth is a key species in addressing this question and for this reason the data recently provided by Cupello and colleagues [6] are a very welcome addition to the discussion. Here, I would like to add a few points pertinent to lung evolution that appear to be a consequence of these exciting data. One of the most interesting aspects of the coelacanth is that it apparently exhibits an unpaired structure of putative homology with lungs [6–8]. In the Polypteriformes (bichir and reed fish), the lungs are paired [5,9,10], as are those of the lungfishes (Dipnoi) [11], except the Australian lungfish, Neoceratodus forsteri (Krefft, 1870) …

Lauridsen, H., Pedersen, J. M. H., Ringgaard, S., & Moller, P. R. (2022). Buoyancy and hydrostatic balance in a West Indian Ocean coelacanth Latimeria chalumnae. *BMC Biology,* 20(1), 180. https://doi.org/10.1186/s12915-022-01354-8

Background Buoyancy and balance are important parameters for slow-moving, low-metabolic, aquatic organisms. The extant coelacanths have among the lowest metabolic rates of any living vertebrate and can afford little energy to keep station. Previous observations on living coelacanths support the hypothesis that the coelacanth is neutrally buoyant and in close-to-perfect hydrostatic balance. However, precise measurements of buoyancy and balance at different depths have never been made. Results Here we show, using non-invasive imaging, that buoyancy of the coelacanth closely matches its depth distribution. We found that the lipid-filled fatty organ is well suited to support neutral buoyancy, and due to a close-to-perfect hydrostatic balance, simple maneuvers of fins can cause a considerable shift in torque around the pitch axis allowing the coelacanth to assume different body orientations with little physical effort. Conclusions Our results demonstrate a close match between tissue composition, depth range and behavior, and our collection-based approach could be used to predict depth range of less well-studied coelacanth life stages as well as of deep sea fishes in general.

Lauridsen, H., Pedersen, J. M. H., Ringgaard, S., & Moller, P. R. (2022). Buoyancy and Hydrostatic Balance in The West Indian Coelacanth Latimeria chalumnae. *Faseb Journal,* 36(S1). https://doi.org/10.1096/fasebj.2022.36.S1.0R901

Buoyancy and balance are important parameters for static or slow moving low-metabolic aquatic organisms. The extant coelacanths, a single genus (Latimeria) consisting of two species living at moderate depths (100 – 400 m) in the Western Indian Ocean and off Indonesia and representing an ancient group of lobe finned fishes dating back to the early Devonian (410 Myr), have among the lowest metabolic rates of any living vertebrate, and thus would be predicted to expend precious little energy to maintain buoyancy and balance. Previous observations on living coelacanths support the hypothesis that the coelcanth is neutrally buoyant and is in close to perfect hydrostatic balance in any body posture. Likewise, point-by-point measurements of tissue composition have shown a generally high lipid content of coelacanth tissue supporting neutral buoyancy without a gas filled bladder as found in other sarcopterygians (lungs) and in many actinopterygians (swim bladder). However, precise measurements of buoyancy and hydrostatic balance at different depths have never been made in the coelacanth. Here we show using non-invasive imaging that buoyancy of the coelacanth closely matches its depth distribution and a close-to-perfect balance can be used by the animal to change body posture with little effort. We found that the lipid filled "fatty organ" of the coelacanth is well adapted to support neutral buoyancy and simple maneuvers of fins can cause a considerable shift in torque around the pitch axis. This allows the coelacanth to assume and remain in any body posture like horizontal orientation, headstand or tail stand with little physical effort. Our results demonstrate a close match between tissue composition in the extant coelacanth, depth range and behavior (e.g. effortless vertical drift hunting with the electrosensitive rostral organ in close contact with the substrate). We anticipate our non-invasive technique of mapping tissue components to be a starting point for more sophisticated models of buoyancy and hydrostatic balance in aquatic vertebrates in general. Specifically, we suggest the technique can be used on the few late term and juvenile coelacanth specimens in existence to predict the most likely habitat depth of the juvenile life stage which is currently unknown.

Li, H. X., Zhang, L., Li, J. L., Yu, F., Wang, M. Y., Wang, Q., . . . Yu, J. H. (2021). Identification, expression and pro-inflammatory effect of interleukin-17 N in common carp (Cyprinus carpio L.). *Fish & Shellfish Immunology,* 111, 6-15. https://doi.org/10.1016/j.fsi.2020.11.024

Two interleukin (IL)-17 N genes (CcIL-17Na and b) present on different linkage groups were identified in the common carp (Cyprinus carpio) genome and confirmed by polymerase chain reaction (PCR) and real time (RT)-PCR in this experiment. Synteny analysis revealed that IL-17 N is transcribed by the complement sequence of TOP3B's intron 2. It is flanked by SDF2L and PPM1F in all fish studied to date, except fugu (Takifugu rubripes). The open reading frames of the two CcIL-17Ns are 411 base pairs long and encode 136 amino acids. The amino acid identity/similarity between CcIL-17Na and b is 91.2%/97.1%. The CcIL-17Ns share identity (46.8-90.4%) with their orthologs from other teleosts. Identities/similarities to other members of the IL-17 family in common carp were low at 21.4-30.2%/31.4-51.4%. In the phylogenetic tree, IL-17Ns from spotted gar (Lepisosteus oculatus, the ancestor of teleosts) and coelacanth (Latimeria chalumnae, the ancestor of tetrapods) were grouped within the same branch with a high bootstrap value of 97%, which indicates that IL-17 N is an ancient and conserved gene. Quantitative RT-PCR results showed that CcIL-17Ns were most highly expressed in the brain of healthy individuals. The expression in brain was significantly induced at 6 h post Aeromonas hydrophila infection; at 1 day post infection, expression in liver, muscle, skin, spleen, and head kidney was up-regulated. In addition, the upregulated expression of proinflammatory cytokines IL-1 beta, IFN-gamma, IL-6, chemokine CCL20, NF - kappa B and TRAF6 in kidney tissue by ccIL-17 N recombinant protein also indicate that IL-17 N can promote inflammation through NF-kappa B pathway and induce the expression of chemokines and inflammatory factors.

Li, H. Z., Shao, X. X., Wang, Y. F., Liu, Y. L., Xu, Z. G., & Guo, Z. Y. (2023). LEAP2 is a more conserved ligand than ghrelin for fish GHSRs. *Biochimie,* 209, 10-19. https://doi.org/10.1016/j.biochi.2023.01.010

Recently, liver-expressed antimicrobial peptide 2 (LEAP2) was identified as an endogenous antagonist and an inverse agonist of the ghrelin receptor GHSR. However, its functions in lower vertebrates are not well understood. Our recent study demonstrated that both LEAP2 and ghrelin are functional towards a fish GHSR from Latimeria chalumnae, an extant coelacanth believed to be one of the closest ancestors of tetrapods. However, amino acid sequence alignment identified that the 6.58 position (Ballesteros-Weinstein numbering system) of most fish GHSRs are not occupied by an aromatic Phe residue, which is absolutely conserved in all known GHSRs from amphibians to mammals, and is responsible for human GHSR binding to its agonist, ghrelin. To test whether these unusual fish receptors are functional, we studied the ligand binding properties of three representative fish GHSRs, two from Danio rerio (zebrafish) and one from Larimichthys crocea (large yellow croaker). After overexpression in human embryonic kidney 293T cells, the three fish GHSRs retained normal binding to all tested LEAP2s, except for a second LEAP2 from L. crocea. However, they displayed almost no binding to all chemically synthesized n-octa-noylated ghrelins, despite these ghrelins all retaining normal function towards human and coelacanth GHSRs. Thus, it seems that LEAP2 is a more conserved ligand than ghrelin towards fish GHSRs. Our re-sults not only provided new insights into the interaction mechanism of GHSRs with LEAP2s and ghrelins, but also shed new light on the functions of LEAP2 and ghrelin in different fish species.(c) 2023 Elsevier B.V. and Societe Francaise de Biochimie et Biologie Moleculaire (SFBBM). All rights reserved.

Li, H. Z., Shou, L. L., Shao, X. X., Li, N., Liu, Y. L., Xu, Z. G., & Guo, Z. Y. (2021). LEAP2 has antagonized the ghrelin receptor GHSR1a since its emergence in ancient fish. *Amino Acids,* 53(6), 939-949. https://doi.org/10.1007/s00726-021-02998-6

Recent studies have demonstrated that liver-expressed antimicrobial peptide 2 (LEAP2) antagonizes the ghrelin receptor GHSR1a in mammals. However, its antagonistic function in lower vertebrates has not yet been tested. LEAP2 orthologs have been identified from a variety of fish species; however, previous studies all focused on their antimicrobial activity. To test whether LEAP2 functions as a GHSR1a antagonist in the lowest vertebrates, we studied the antagonism of a fish LEAP2 from Latimeria chalumnae, an extant coelacanth that is one of the closest living fish relatives of tetrapods. Using binding assays, we demonstrated that the coelacanth LEAP2 and ghrelin bound to the coelacanth GHSR1a with IC50 values in the nanomolar range. Using activation assays, we demonstrated that the coelacanth ghrelin activated the coelacanth GHSR1a with an EC50 value in the nanomolar range, and this activation effect was efficiently antagonized by a nanomolar range of the coelacanth LEAP2. In addition, we also showed that the human LEAP2 and ghrelin were as effective as their coelacanth orthologs towards the coelacanth GHSR1a; however, the coelacanth peptides had moderately lower activity towards the human GHSR1a. Thus, LEAP2 serves as an endogenous antagonist of the ghrelin receptor GHSR1a in coelacanth and the ghrelin-LEAP2-GHSR1a system has evolved slowly since its emergence in ancient fish.

Li, H. Z., Wang, Y. F., Zheng, Y. S., Liu, Y. L., Xu, Z. G., & Guo, Z. Y. (2023). The ghrelin receptor GHSR has two efficient agonists in the lobe-finned fish Latimeria chalumnae. *Biochemical and Biophysical Research Communications,* 679, 110-115. https://doi.org/10.1016/j.bbrc.2023.09.002

The peptide hormone ghrelin (an agonist) and LEAP2 (an antagonist) play important functions in energy metabolism via their receptor GHSR, an A-class G protein-coupled receptor. Ghrelin, LEAP2, and GHSR are widely present from fishes to mammals. However, our recent study suggested that fish GHSRs have different binding properties to ghrelin: a GHSR from the lobe-finned fish Latimeria chalumnae (coelacanth) is efficiently activated by ghrelin, but GHSRs from the ray-finned fish Danio rerio (zebrafish) and Larimichthys crocea (large yellow croaker) have lost binding to ghrelin. Do fish GHSRs use another peptide as their agonist? In the present study we tested to two fish motilins from D. rerio and L. chalumnae because motilin is distantly related to ghrelin. In ligand binding and activation assays, the fish GHSRs from D. rerio and L. crocea displayed no detectable or very low binding to all tested motilins; however, the fish GHSR from L. chalumnae bound to its motilin with high affinity and was efficiently activated by it. Therefore, it seemed that motilin is not a ligand for GHSR in the rayfinned fish D. rerio and L. crocea, but is an efficient agonist for GHSR in the lobe-finned fish L. chalumnae, one of the closest fish relatives of tetrapods. The results of present study suggested that GHSR might have two efficient agonists, ghrelin and motilin, in ancient fishes; however, this feature might be only preserved in some extant fishes with ancient evolutionary origins.

Li, Y. C., Wang, R., Wang, H. H., Pu, F. Y., Feng, X. L., Jin, L., . . . Ma, X. X. (2021). Codon Usage Bias in Autophagy-Related Gene 13 in Eukaryotes: Uncovering the Genetic Divergence by the Interplay Between Nucleotides and Codon Usages. *Frontiers in Cellular and Infection Microbiology,* 11, 771010. https://doi.org/10.3389/fcimb.2021.771010

Synonymous codon usage bias is a universal characteristic of genomes across various organisms. Autophagy-related gene 13 (atg13) is one essential gene for autophagy initiation, yet the evolutionary trends of the atg13 gene at the usages of nucleotide and synonymous codon remains unexplored. According to phylogenetic analyses for the atg13 gene of 226 eukaryotic organisms at the nucleotide and amino acid levels, it is clear that their nucleotide usages exhibit more genetic information than their amino acid usages. Specifically, the overall nucleotide usage bias quantified by information entropy reflected that the usage biases at the first and second codon positions were stronger than those at the third position of the atg13 genes. Furthermore, the bias level of nucleotide 'G' usage is highest, while that of nucleotide 'C' usage is lowest in the atg13 genes. On top of that, genetic features represented by synonymous codon usage exhibits a species-specific pattern on the evolution of the atg13 genes to some extent. Interestingly, the codon usages of atg13 genes in the ancestor animals (Latimeria chalumnae, Petromyzon marinus, and Rhinatrema bivittatum) are strongly influenced by mutation pressure from nucleotide composition constraint. However, the distributions of nucleotide composition at different codon positions in the atg13 gene display that natural selection still dominates atg13 codon usages during organisms' evolution.

Luigi, M., Raphael, C., & Lionel, C. (2023). A 3D reconstruction of the skull of the West Indian Ocean coelacanth Latimeria chalumnae. *MorphoMuseuM,* 9(3), e211. https://doi.org/10.18563/journal.m3.211

We provide a 3D reconstruction of the skull of Latimeria chalumnae that can be easily accessed and visualized for a better understanding of its cranial anatomy. Different skeletal elements are saved as separate PLY files that can be combined to visualize the entire skull or isolated to virtually dissect the skull. We included some guidelines for a fast and easy visualization of the 3D skull.

Mahé, K., Ernande, B., & Herbin, M. (2021). New scale analyses reveal centenarian African coelacanths. *Current Biology,* 31(16), 3621-3628.e3624. https://doi.org/10.1016/j.cub.2021.05.054

The extant coelacanth was discovered in 1938; its biology and ecology remain poorly known due to the low number of specimens collected. Only two previous studies have attempted to determine its age and growth. They suggested a maximum lifespan of 20 years, placing the coelacanth among the fastest growing marine fish. These findings are at odds with the coelacanth?s other known biological features including low oxygen-extraction capacity, slow metabolism, ovoviviparity, and low fecundity, typical of fish with slow life histories and slow growth. In this study, we use polarized light microscopy to study growth on scales based on a large sample of 27 specimens. Our results demonstrate for the first time nearly imperceptible annual calcified structures (circuli) on the scales and show that maximal age of the coelacanth was underestimated by a factor of 5. Our validation method suggests that circuli are indeed annual, thus supporting that the coelacanth is among the longest-living fish species, its lifespan being probably around 100 years. Like deep-sea sharks with a reduced metabolism, the coelacanth has among the slowest growth for its size. Further reappraisals of age at first sexual maturity (in the range 40 to 69 years old) and gestation duration (of around 5 years) show that the living coelacanth has one of the slowest life histories of all marine fish and possibly the longest gestation. As long-lived species with slow life histories are extremely vulnerable to natural and anthropogenic perturbations, our results suggest that coelacanths may be more threatened than previously considered.

Mangora, M. M., Msangameno, D. J., & Woiso, J. F. (2024). *Transitioning to Blue Economy: Contribution of Coastal and Marine Environment*.State of the Coast for Mainland Tanzania Dodoma, Tanzania: National Environment Management Council (NEMC) Retrieved from https://www.wiomsa.org/publications/46792-2/

This State of the Coast for mainland Tanzania is the fourth in the series that provides an update of the status and trends in the condition and use of mainland Tanzania's coastal and marine environment and its contribution to improving livelihoods of coastal communities, local economies and national development. The first edition came out in 2001 featuring a theme on "People and the Environment" (TCMP 2001). The second edition followed in 2003 and carried a theme that provided a reflection to the "National Integrated Coastal Management Strategy and the Prospects for Poverty Reduction" (TCMP 2003). The third edition was released in 2009 taking back the theme of "People and the Environment" (NEMC 2009). This fourth edition's theme of "Transitioning to Blue Economy: Contribution of Coastal and Marine Environment" is drawn from the national agenda on blue economy that was first introduced in the second National Five-Year Development Plan 2016/17-2020/21 (URT 2016) and is being pursued in the third National Five-Year Development Plan 2021/22-2025/26 (URT 2021). The rationale for this edition's theme is based on the fact that most economic discussions in Tanzania are rarely centered on the importance of the ocean as a driver for economic growth. Tanzania is endowed with vast blue resources that bear a great potential to contribute towards the Vision 2025 (URT 1999). However, recognition of the ocean as an economic frontier and its contribution to food security, job creation, and sustainable economic growth through its main drivers of growth such as fisheries, coastal tourism, shipping, oil and gas exploitation, coastal mining, agriculture and urbanization etc. has remained limited. Many ocean-dependent communities in Tanzania are facing increasing economic hardships from the degradation of their resource base, due largely to increased resource over exploitation and environmental degradation, and growing pressures of development from infrastructure, extractive industries and population. The effects and impacts of global climate change exacerbate other sources of disturbance. This publication therefore provides a synthesis of the opportunities and constraints presented by blue resources in balancing the three pillars of sustainable development: environment, economy, and social.

Mansuit, R., Clément, G., Herrel, A., Dutel, H., Tafforeau, P., Santin, M. D., & Herbin, M. (2020). Development and growth of the pectoral girdle and fin skeleton in the extant coelacanth Latimeria chalumnae. *Journal of Anatomy,* 236(3), 493-509. https://doi.org/10.1111/joa.13115

The monobasal pectoral fins of living coelacanths and lungfishes are homologous to the forelimbs of tetrapods and are thus critical to investigate the origin thereof. However, it remains unclear whether the similarity in the asymmetrical endoskeletal arrangement of the pectoral fins of coelacanths reflects the evolution of the pectoral appendages in sarcopterygians. Here, we describe for the first time the development of the pectoral fin and shoulder girdle in the extant coelacanth Latimeria chalumnae, based on the tomographic acquisition of a growth series. The pectoral girdle and pectoral fin endoskeleton are formed early in development with a radially outward growth of the endoskeletal elements. The visualization of the pectoral girdle during development shows a reorientation of the girdle between the fetus and pup 1 stages, creating a contact between the scapulocoracoids and the clavicles in the ventro-medial region. Moreover, we observed a splitting of the pre- and post-axial cartilaginous plates in respectively pre-axial radials and accessory elements on one hand, and in post-axial accessory elements on the other hand. However, the mechanisms involved in the splitting of the cartilaginous plates appear different from those involved in the formation of radials in actinopterygians. Our results show a proportional reduction of the proximal pre-axial radial of the fin, rendering the external morphology of the fin more lobe-shaped, and a spatial reorganization of elements resulting from the fragmentation of the two cartilaginous plates. Latimeria development hence supports previous interpretations of the asymmetrical pectoral fin skeleton as being plesiomorphic for coelacanths and sarcopterygians.

Mansuit, R., Clément, G., Herrel, A., Dutel, H., Tafforeau, P., Santin, M. D., & Herbin, M. (2021). Development and growth of the pelvic fin in the extant coelacanth Latimeria chalumnae. *Anatomical Record-Advances in Integrative Anatomy and Evolutionary Biology,* 304(3), 541-558. https://doi.org/10.1002/ar.24452

The ontogeny of the paired appendages has been extensively studied in lungfishes and tetrapods, but remains poorly known in coelacanths. Recent work has shed light on the anatomy and development of the pectoral fin in Latimeria chalumnae. Yet, information on the development of the pelvic fin and girdle is still lacking. Here, we described the development of the pelvic fin and girdle in Latimeria chalumnae based on 3D reconstructions generated from conventional and X-ray synchrotron microtomography, as well as MRI acquisitions. As in other jawed vertebrates, the development of the pelvic fin occurs later than that of the pectoral fin in Latimeria. Many elements of the endoskeleton are not yet formed at the earliest stage sampled. The four mesomeres are already formed in the fetus, but only the most proximal radial elements (preaxial radial 0-1) are formed and individualized at this stage. We suggest that all the preaxial radial elements in the pelvic and pectoral fin of Latimeria are formed through the fragmentation of the mesomeres. We document the progressive ossification of the pelvic girdle, and the presence of a trabecular system in the adult. This trabecular system likely reinforces the cartilaginous girdle to resist the muscle forces exerted during locomotion. Finally, the presence of a preaxial element in contact with the pelvic girdle from the earliest stage of development onward questions the mono-basal condition of the pelvic fin in Latimeria. However, the particular shape of the mesomeres may explain the presence of this element in contact with the girdle.

Mansuit, R., Clément, G., Herrel, A., & Herbin, M. (2019, Jun). *Does the muscular anatomy of the pelvic fin of the extant coelacanth Latimeria chalumnae (Actinistia: Latimeriidae) provide information on its mobility and role during locomotion?* Paper presented at the 12th International congress of Vertebrate Morphology, Prague, Czech Republic. Retrieved from https://hal.science/hal-04546632v1

Cœlacanths are sarcopterygian fishes that were originally known only from their fossil record and assumed extinct since the Upper Cretaceous (70My ago). The discovery of a living coelacanth, Latimeria chalumnae, offshore South Africa in 1938, was a surprise for the scientific community, and provide a unique opportunity to study the anatomy of this close relative to tetrapods. Its paired fins are of special interest because of their mono-basal articulation and their proximal endoskeleton, homologous to that of tetrapods. A recent study on the functional anatomy of the musculature of the pectoral fin showed that it is more complex than previously thought. Here, we focus on the pelvic fin and hypothesize that the muscles are equally complex and allow complex movements of the fins. A detailed dissection and anatomical description of the pelvic fins was undertaken on an adult specimen of L. chalumnae preserved in the MNHN collections, Paris. According to previous descriptions, the pelvic fin musculature presents a three-layered organization: the adductor and abductor muscles form the superficial and middle layers, whereas the pronator and supinator form the deep layer. Amongst others, our preliminary results show that the muscle bundles of the superficial and middle layers lead to adduction or abduction movements, but also to the protraction or retraction of the fin. Moreover, whereas previous studies documented about twenty muscles, we observed and described more than 70 clearly individualized muscle bundles. This complex organization of the muscle bundles is congruent with a high mobility of the pelvic fin as quantified based on in-vivo video recording.

Marín, I. (2020). Tumor Necrosis Factor Superfamily: Ancestral Functions and Remodeling in Early Vertebrate Evolution. *Genome Biology and Evolution,* 12(11), 2074-2092. https://doi.org/10.1093/gbe/evaa140

The evolution of the tumor necrosis factor superfamily (TNFSF) in early vertebrates is inferred by comparing the TNFSF genes found in humans and nine fishes: three agnathans, two chondrichthyans, three actinopterygians, and the sarcopterygian Latimeria chalumnae. By combining phylogenetic and synteny analyses, the TNFSF sequences detected are classified into five clusters of genes and 24 orthology groups. A model for their evolution since the origin of vertebrates is proposed. Fifteen TNFSF genes emerged from just three progenitors due to the whole-genome duplications (WGDs) that occurred before the agnathan/gnathostome split. Later, gnathostomes not only kept most of the genes emerged in the WGDs but soon added several tandem duplicates. More recently, complex, lineage-specific patterns of duplications and losses occurred in different gnathostome lineages. In agnathan species only seven to eight TNFSF genes are detected, because this lineage soon lost six of the genes emerged in the ancestral WGDs and additional losses in both hagfishes and lampreys later occurred. The orthologs of many of these lost genes are, in mammals, ligands of death-domain-containing TNFSF receptors, indicating that the extrinsic apoptotic pathway became simplified in the agnathan lineage. From the patterns of emergence of these genes, it is deduced that both the regulation of apoptosis and the control of the NF-kappa B pathway that depends in modern mammals on TNFSF members emerged before the ancestral vertebrate WGDs.

Masamitsu, I., Yoshitaka, Y., Toshiro, S., Shinya, Y., Kenichi, F., Rintaro, I., . . . Yoshitaka, A. B. E. (2020). Field surveys on the Indonesian coelacanth, Latimeria menadoensis using remotely operated vehicles from 2005 to 2015. *Bulletin of the Kitakyushu Museum of Natural History and Human History, Series A (Natural History),* 17, 49-56. https://doi.org/10.34522/kmnh.17.0_49

Habitats of the Indonesian coelacanth, Latimeria menadoensis, were investigated by Remotely Operated Vehicles (ROVs) surveys in the northern coast of Sulawesi Island and southern coast of Biak Island by collaboration of Aquamarine Fukushima (Japan), and Indonesian Institute of Sciences and Sam Ratulangi University (Indonesia) from 2005 to 2015. The Remotely Operated Vehicles operations were conducted 1173 times and coelacanths were encountered 30 times. A total of 30 different individuals were observed at a depth range from 115.6 m to 218.9 m deep. The water temperature was between 12.4 to 21.5 ºC. Most of the individuals were found alone, however, schools of two, three and six individuals were also observed. The Indonesian coelacanth, L. menadoensis, was observed at a similar depth of the African coelacanth, Latimeria chalumnae, and the temperature range also seems to be very similar. However, Latimeria menadoensis was sometimes observed besides big rocks or the steep wall. It seems to be less sensitive to daylight than L. chalumnae. Here we report also, for the first time in the world, a juvenile coelacanth was observed in a small crack at 165 to 171 m depth during these surveys.

Masamitsu, I., Yoshitaka, Y., Toshiro, S., Shinya, Y., Kenichi, F., Rintaro, I., . . . Yoshitaka, A. B. E. (2020). Observation of the first juvenile Indonesian coelacanth, Latimeria menadoensis from Indonesian waters with a comparison to embryos of Latimeria chalumnae. *Bulletin of the Kitakyushu Museum of Natural History and Human History, Series A (Natural History),* 17, 57-65. https://doi.org/10.34522/kmnh.17.0_57

The juvenile of Indonesian coelacanth, Latimeria menadoensis is here described for the first time in detail with comparison to embryos of Latimeria chalumnae. The juvenile was found in free swimming at 164.6 m depth off Manado, Indonesia on the 6th October in 2009. Because the total length of the juvenile is 31.5 cm, which is smaller than the embryos of L. chalumnae, it is speculated that not much time has passed from its birth. The depth at which the juvenile was found is within the range of the depth where adult L. menadoensis were observed, hidden in a narrow and long overhang where large predators could not enter. The juvenile has a more slender body, smaller orbit, shorter and deeper posterior part of the body (caudal peduncle) between the second dorsal and the anal fins and anterior ends of the dorsal and ventral lobes of the caudal fin (the third dorsal and second anal fins), longer dorsal and ventral lobes of the caudal fin (the third dorsal and second anal fins), broader peduncles of broader lobed fins, larger first dorsal fin and longer supplementary lobe of the caudal fin (caudal fin) than embryos of L. chalumnae. This indicates clear differences in the first ontogenetic stages of the two species, although adults have almost the same morphological features. Latimeria menadoensis appears to reproduce in a rather confined area, because both the juvenile and adults have been found within the same area inside of Manado Bay.

Mesaki, S. (2024). The Coelacanth, its Conservation and Concerns in Tanzania. *Advances in Oceanography & Marine Biology,* 4(1). https://doi.org/10.33552/AOMB.2024.04.000576

Referred to as one of the world's best-known "living fossils" the Coelacanth (Latimeria chalumnae), was thought to have been extinct until it was "rediscovered" in South Africa in 1938, causing much excitement. Since 2003 Tanzania witnessed unprecedented catches of coelacanths which led to conservation measures of the species by establishing a marine park named after it. This short paper is about this unique fish, its ubiquitous capture in Tanzania, the prospects and threats for its conservation due to inherent and emergent factors particularly the construction of the 1,443 kilometres East African Crude Oil Pipeline from Hoima in Uganda to Chongoleani within the precincts of the park.

Meunier, F. J., Cupello, C., & ClÉMent, G. (2019). The skeleton and the mineralized tissues of the living coelacanths. *Bulletin of the Kitakyushu Museum of Natural History and Human History, Series A (Natural History),* 17, 37-48. https://doi.org/10.34522/kmnh.17.0_37

The present overview of the histological studies on Latimeria mineralized tissues, since the discovery of the first living coelacanth in 1938, allows some anatomical and evolutionary considerations. It enlightens: i) a drastic reduction of cartilage to bone transformation processes during evolution; ii) the persistence of large volume of cartilage in the endoskeleton at adult stage; iii) the bony nature of the plates that surround the lung diverticle; iv) the presence of a developed process of spheritic mineralization in various skeletal organs: in teeth, in odontodes of the tegumentary skeleton (scales, fin rays), in scales at the interface between the external layer and the basal plate, as well as in lung bony plates.

Miyake, T., Kumamoto, M., Iwata, M., Sato, R., Okabe, M., Koie, H., . . . Abe, Y. (2016). The pectoral fin muscles of the coelacanth Latimeria chalumnae: Functional and evolutionary implications for the fin-to-limb transition and subsequent evolution of tetrapods. *Anatomical Record-Advances in Integrative Anatomy and Evolutionary Biology,* 299(9), 1203-1223. https://doi.org/10.1002/ar.23392

To investigate the morphology and evolutionary origin of muscles in vertebrate limbs, we conducted anatomical dissections, computed tomography and kinematic analyses on the pectoral fin of the African coelacanth, Latimeria chalumnae. We discovered nine antagonistic pairs of pronators and supinators that are anatomically and functionally distinct from the abductor and adductor superficiales and profundi. In particular, the first pronator and supinator pair represents mono- and biarticular muscles; a portion of the muscle fibers is attached to ridges on the humerus and is separated into two monoarticular muscles, whereas, as a biarticular muscle, the main body is inserted into the radius by crossing two joints from the shoulder girdle. This pair, consisting of a pronator and supinator, constitutes a muscle arrangement equivalent to two human antagonistic pairs of monoarticular muscles and one antagonistic pair of biarticular muscles in the stylopod between the shoulder and elbow joints.

Our recent kinesiological and biomechanical engineering studies on human limbs have demonstrated that two antagonistic pairs of monoarticular muscles and one antagonistic pair of biarticular muscles in the stylopod (1) coordinately control output force and force direction at the wrist and ankle and (2) achieve a contact task to carry out weight-bearing motion and maintain stable posture. Therefore, along with dissections of the pectoral fins in two lungfish species, Neoceratodus forsteri and Protopterus aethiopicus, we discuss the functional and evolutionary implications for the fin-to-limb transition and subsequent evolution of tetrapods. Anat Rec, 299:1203-1223, 2016. (c) 2016 Wiley Periodicals, Inc.

Miyake, T., & Okabe, M. (2022). Roles of Mono- and Bi-articular Muscles in Human Limbs: Two-joint Link Model and Applications. *Integrative Organismal Biology,* 4(1), obac042. https://doi.org/10.1093/iob/obac042

Synopsis We review the two-joint link model of mono- and bi-articular muscles in the human branchium and thigh for applications related to biomechanical studies of tetrapod locomotion including gait analyses of humans and non-human tetrapods. This model has been proposed to elucidate functional roles of human mono- and bi-articular muscles by analyzing human limb movements biomechanically and testing the results both theoretically and mechanically using robotic arms and legs. However, the model has not yet been applied to biomechanical studies of tetrapod locomotion, in part since it was established based mainly on mechanical engineering analyses and because it has been applied mostly to robotics, fields of mechanical engineering, and to rehabilitation sciences. When we discovered and published the identical pairs of mono- and bi-articular muscles in pectoral fins of the coelacanth fish Latimeria chalumnae to those of humans, we recognized the significant roles of mono- and bi-articular muscles in evolution of tetrapod limbs from paired fins and tetrapod limb locomotion. Therefore, we have been reviewing the theoretical background and mechanical parameters of the model in order to analyze functional roles of mono- and bi-articular muscles in tetrapod limb locomotion. Herein, we present re-defined biological parameters including 3 axes among 3 joints of forelimbs or hindlimbs that the model has formulated and provide biological and analytical tools and examples to facilitate applicable power of the model to our on-going gait analyses of humans and tetrapods.

Nathan, H., & Helena Bailes Justin Marshall Shaun, C. (2016). Vision in Lungfish. In *The Biology of Lungfishes.* (pp. 463-492) https://doi.org/10.1201/b10357-21

All three extant genera of lungfish, Australian, African and South American, appear to possess unremarkable, even ‘degenerate eyes’ when viewed externally. Th e eyes of the Australian lungfish, Neoceratodus forsteri, are slightly larger than those of the other species (seven African species in the genus Protopterus and the single South American species Lepidosiren paradoxa). N. forsteri seems to be the most visually-oriented of the extant lungfishes. All three genera of lungfish, however, possess remarkable and beautiful retinal adaptations, including, coloured oil droplets, multiple cone spectral sensitivities and large photoreceptor inner segments, making them more closely aligned in design to modern amphibians and other terrestrial animals, than to teleosts. The tetrapod-like retinal features of N. forsteri provide the capability for tetrachromatic colour vision and add to the debate on the phylogenetic origin(s) of lungfish. They also suggest that the complex colour vision system of vertebrates on land, exemplified by birds, may have first evolved in the aquatic environment or at least close to the time when aquatic life emerged onto land. Other ocular adaptations in dipnoans include a non-spherical lens, the anatomical mechanism for accommodation, a mobile pupil and giant retinal cells. This eye design suggests a need to increase light flux, rather than for a reliance on high spatial acuity, a conclusion supported by the relatively low ganglion cell densities. Future work should certainly aim at a better understanding of the visual biology, behaviour and ecology of all lungfish, especially in light of their disappearing habitat worldwide. Both African and South American species also need a full description of their visual system before they are properly consigned to being 'less well developed', than N. forsteri.

Newbrey, M. G., Woolfolk, F. R., Martin-Abad, H., & Maisey, J. G. (2020). Chronological ages of the coelacanths Latimeria chalumnae and Axelrodichthys araripensis by comparing ages from scales and bones. *Integrative and Comparative Biology,* 60, E388-E388. Retrieved from https://sicb.org/abstracts/chronological-ages-of-the-coelacanths-latimeria-chalumnae-and-axelrodichthys-araripensis-by-comparing-ages-from-scales-and-bones/

Coelacanth age and growth has been argued for the last 22 years and there are only two published papers on their age and growth. Previously published literature suggests longevities of 20 years old or 40 years old based on ages from scales; an examination of their data suggests very irregular growth. A more recent hypothesis suggests a 100-year lifespan from a 21-year in situ study where larger individuals had little to no observable growth. Previous studies also suggest 3 years gestation period based on examination of embryos found in a Latimeria chalumnae female. The largest known individuals of L. chalumnae grow to 1.8 m TL. Our objective is to determine the number of years it takes to attain maximum size. Previous studies have failed to describe growth cessation marks adequately and there were no other structures to compare assigned ages. We used new criteria to identify growth cessation marks on scales of extant (Latimeria chalumnae) and extinct (Axelrodichthys araripensis) individuals. New age assignments for L. chalumnae resulted in higher individual ages than previously noted in the literature. We also compared chronological ages of scales and bones in A. araripensis and found that they agree. Our age assignments suggest a lifespan that exceeds 40 years, and we do not refute the 100 year lifespan hypothesis. The results suggest that coelacanths grow much more slowly than previously reported. This study provides new numerical data that supports the idea of low metabolic rate and slow growth in coelacanths.

Noia, M., Fontenla-Iglesias, F., Valle, A., Blanco-Abad, V., Leiro, J. M., & Lamas, J. (2021). Characterization of the turbot Scophthalmus maximus (L.) myeloperoxidase. An insight into the evolution of vertebrate peroxidases. *Developmental and Comparative Immunology,* 118. https://doi.org/10.1016/j.dci.2021.103993

We have completed the characterization of the turbot (Scophthalmus maximus) myeloperoxidase (mpx) gene and protein, which we partially described in a previous study. The turbot mpx gene has 15 exons that encode a protein of 767 aa, with a signal peptide, propeptide and light and heavy chains, and also with haem cavities, a Ca+2-binding motif and several N- and O-glycosylation sites. The mature protein forms homodimers of about 150 kDa and is very abundant in turbot neutrophils. In addition to the mpx (epx2a) gene, another three peroxidase genes, named epx1, epx2b1 and epx2b2, were identified in the turbot genome. Epx1, Epx2b1 and Epx2b2 proteins also have signal peptides and many structural characteristics of mammalian MPO and eosinophil peroxidase (EPX). Mpx was strongly expressed in head kidney, while epx2b1 and epx2b2 were strongly expressed in the gills, and epx1 was not expressed in any of the tissues or organs analysed. In vitro stimulation of head kidney leucocytes with the parasite Philasterides dicentrarchi caused a decrease in mpx expression and an increase in epx2b1 expression over time. In turbot infected experimentally with P. dicentrarchi a significant increase in mpx expression in the head kidney was observed on day 7 postinfection, while the other genes were not regulated. However, mpx, epx2b1 and epx2b2 were downregulated in the gills of infected fish, and epx1 expression was not affected. These results suggest that the four genes responded differently to the same stimuli. Interestingly, BLAST analysis revealed that Epx1 and Mpx showed greater similarity to mammalian EPX than to MPO. Considering the phylogenetic and synteny data obtained, we concluded that the epx/mpx genes of Gnathostomes can be divided into three main clades: EPX1, which contains turbot epx1, EPX2, which contains turbot mpx (epx2a) and epx2b1 and epx2b2 genes, and a clade containing mammalian EPX and MPO (EPX/MPO). EPX/MPO and EPX2 clades share a common ancestor with the chondrichthyan elephant shark (Callorhinchus milii) and the coelacanth (Latimeria chalumnae) peroxidases. EPX2 was only found in fish and includes two sister groups. One of the groups includes turbot mpx and was only found in teleosts. Finally, the other group contains epx2b1 and epx2b2 genes, and epx2b1-2b2 loci share orthologous genes with other teleosts and also with holosteans, suggesting that these genes appeared earlier on than the mpx gene.

Nye, T. M. W., Tang, X. X., Weyenberg, G., & Yoshida, R. (2017). Principal component analysis and the locus of the Fr,chet mean in the space of phylogenetic trees. *Biometrika,* 104(4), 901-922. https://doi.org/10.1093/biomet/asx047

Evolutionary relationships are represented by phylogenetic trees, and a phylogenetic analysis of gene sequences typically produces a collection of these trees, one for each gene in the analysis. Analysis of samples of trees is difficult due to the multi- dimensionality of the space of possible trees. In Euclidean spaces, principal component analysis is a popular method of reducing high- dimensional data to a low-dimensional representation that preserves much of the sample's structure. However, the space of all phylogenetic trees on a fixed set of species does not form a Euclidean vector space, and methods adapted to tree space are needed. Previous work introduced the notion of a principal geodesic in this space, analogous to the first principal component. Here we propose a geometric object for tree space similar to the kth principal component in Euclidean space: the locus of the weighted Frechet mean of k + 1 vertex trees when the weights vary over the k- simplex. We establish some basic properties of these objects, in particular showing that they have dimension k, and propose algorithms for projection onto these surfaces and for finding the principal locus associated with a sample of trees. Simulation studies demonstrate that these algorithms perform well, and analyses of two datasets, containing Apicomplexa and African coelacanth genomes respectively, reveal important structure from the second principal components.

Oliver, J.-C., Shum, P., Mariani, S., Sink, K. J., Palmer, R., & Matcher, G. F. (2024). Enhancing African coelacanth monitoring using environmental DNA. *Biology Letters,* 20(10), 20240415. https://doi.org/10.1098/rsbl.2024.0415

Coelacanths are rare, elusive, ancient lobe-finned fish species, residing in poorly accessible tropical marine caves and requiring close monitoring and protection. Environmental DNA (eDNA) approaches are being increasingly applied in the detection of rare and threatened species. Here we devise an eDNA approach to detect the presence of African coelacanths (Latimeria chalumnae) off the eastern coast of South Africa. Novel coelacanth-specific primers were designed to avoid cross-amplification with other fish lineages and validated for specificity. These primers were tested on field samples in conjunction with remotely operated vehicle (ROV) visual surveys. Samples were collected from a known coelacanth habitat and two adjacent slope habitats a few kilometres apart. Coelacanth DNA was detected from three of 15 samples collected. Two of these positive eDNA detections occurred in the presence of coelacanths, as evidenced by ROV footage, while the third positive detection was at a station where coelacanths had not been previously observed. eDNA detections are discussed in relation to the species' metabolic rate, movement patterns and population size, as well as the local oceanographic features. We demonstrate that eDNA can provide a non-invasive method to extend the knowledge of coelacanth distribution ranges and boost research efforts around these iconic fishes.

Osuka, K. E., McClean, C., Stewart, B. D., Bett, B. J., Le Bas, T., Howe, J., . . . Samoilys, M. (2021). Characteristics of shallow and mesophotic environments of the Pemba Channel, Tanzania: Implications for management and conservation. *Ocean & Coastal Management,* 200. https://doi.org/10.1016/j.ocecoaman.2020.105463

Information on the spatial distribution of habitats and vulnerable species is important for conservation planning. In particular, detailed knowledge on connectivity of marine ecosystems in relation to depth and seafloor characteristics is crucial for any proposed conservation and management actions. Yet, the bulk of the seafloor remains under-sampled, unstudied and unmapped, thereby limiting our understanding of connections between shallow and deep-water communities. Recent studies on mesophotic coral ecosystems (MCEs) have highlighted the Western Indian Ocean as a particularly understudied marine region. Here we utilise an autonomous underwater vehicle (AUV) to collect in-situ temperature, oxygen concentration, bathymetry, acoustic backscatter and photographic data on benthic communities from shallow (<30 m) and mesophotic (30–150 m) depths at selected sites in the Greater Pemba Channel, Tanzania. Further, we use generalised additive models (GAMs) to determine useful predictors of substratum (hard and sand) and benthic community type (coral, turf algae, fleshy algae, fish). Our results revealed the presence of a complex seafloor characterised by pockmarks, steep slopes, submarine walls, and large boulders. Photographs confirmed the presence of MCE composed of corals, algae and fishes on the eastern margins of the Pemba Channel. The GAMs on the presence and absence of benthic community explained 35%–91% of the deviance in fish and fleshy algae assemblages, respectively. Key predictors of the distribution of hard substrata and the coral reef communities were depth, showing the upper boundary of MCEs present at 30–40 m, and seafloor slope that showed more occurrences on steep slopes. The upper 100 m of water column had stable temperatures (25–26 °C) and oxygen concentrations (220–235 µmol/l). We noted the presence of submarine walls, steeply inclined bedrock, which appeared to support a highly bio-diverse community that may be worthy of particular conservation measures. Our results also highlight the capability of using marine robotics, particularly autonomous vehicles, to fill the knowledge gap for areas not readily accessible by divers or with surface vessels, and their potential application for the initial survey and subsequent monitoring of Marine Protected Areas.

Page, R., Yoshida, R., & Zhang, L. (2020). Tropical principal component analysis on the space of phylogenetic trees. *Bioinformatics,* 36(17), 4590-4598. https://doi.org/10.1093/bioinformatics/btaa564

Motivation: Due to new technology for efficiently generating genome data, machine learning methods are urgently needed to analyze large sets of gene trees over the space of phylogenetic trees. However, the space of phylogenetic trees is not Euclidean, so ordinary machine learning methods cannot be directly applied. In 2019, Yoshida et al. introduced the notion of tropical principal component analysis (PCA), a statistical method for visualization and dimensionality reduction using a tropical polytope with a fixed number of vertices that minimizes the sum of tropical distances between each data point and its tropical projection. However, their work focused on the tropical projective space rather than the space of phylogenetic trees. We focus here on tropical PCA for dimension reduction and visualization over the space of phylogenetic trees. Results: Our main results are 2-fold: (i) theoretical interpretations of the tropical principal components over the space of phylogenetic trees, namely, the existence of a tropical cell decomposition into regions of fixed tree topology; and (ii) the development of a stochastic optimization method to estimate tropical PCs over the space of phylogenetic trees using a Markov Chain Monte Carlo approach. This method performs well with simulation studies, and it is applied to three empirical datasets: Apicomplexa and African coelacanth genomes as well as sequences of hemagglutinin for influenza from New York.

Painter, S. C., Sekadende, B., Michael, A., Noyon, M., Shayo, S., Godfrey, B., . . . Kyewalyanga, M. (2021). Evidence of localised upwelling in Pemba Channel (Tanzania) during the southeast monsoon. *Ocean & Coastal Management,* 200. https://doi.org/10.1016/j.ocecoaman.2020.105462

Oceanographic and biogeochemical observations collected in Pemba Channel, a deep-water (800 m) channel separating Pemba Island from mainland Tanzania, during the South East monsoon indicate the presence of active upwelling along the western edge of Pemba Island. Surface salinity values, nutrient concentrations and the presence of coccolithophore species previously reported from the mid to lower euphotic zone all suggest upwelling from at least 80–100 m depth. The surface waters of the channel were characterised with low NO3−:PO43− (0.68:1) and NO3−:Si (0.04:1) ratios far below the Brzezinski-Redfield ratio indicating the presence of N-limitation and the possibility that these waters may be susceptible to anthropogenic N inputs. Surface NO3− concentrations averaged 0.09 ± 0.10 µmol L−1 but increased to 0.5 µmol L−1 in the centre of upwelling where coincidentally both integrated nutrient concentrations and surface POC/PON pools were approximately 2-fold higher than the channel average. Despite its significance for local productivity upwelling is tentatively estimated, via stoichiometric assumptions, to enhance local productivity by only 20%. The modest productivity response to upwelling may be explained by picoplankton (0.2–2 µm) dominance of the phytoplankton community with this size-class representing ~80% of total chlorophyll-a. Nevertheless, important spatial variability was identified in larger size fractions and supported by taxonomic analyses with indications that the distribution of Chaetoceros spp. alone may be particularly relevant for understanding the variability in larger (>20 µm) chlorophyll-a size fractions. The location of upwelling has previously been shown to host large concentrations of small pelagic fish thus management of this regionally important resource would benefit from additional investigation of the underlying physical mechanism driving upwelling and subsequently how trophic interactions and ecosystem productivity are influenced.

Pulfrich, A. (2018). *Environmental impact assessment (EIA) for a proposed exploration drilling campaign within Block ER236 off the east coast of South Africa: Marine and coastal ecology assessment.* Pisces Environmental Services for Eni South Africa B.V., URL not available.

This specialist report was compiled as a desktop study on behalf of ERM, for their use in compiling an Environmental Impact Assessment (EIA) and EMPr for the proposed exploration drilling off the South African East Coast.

Pulfrich, A. (2018). *Proposed Speculative 2D and 3D Seismic Surveys off the South and East Coast of South Africa: Environmental Management Plan Amendment for Speculative 3D Seismic Survey Offshore of Kwazulu-Natal: Marine Faunal Assessment.* Pisces Environmental Services (Pty) Ltd for SLR Environmental Consulting (Pty) Ltd, URL not available.

Hydrocarbon deposits occur in reservoirs in sedimentary rock layers. Being lighter than water they accumulate in traps where the sedimentary layers are arched or tilted by folding or faulting of the geological layers. Marine seismic surveys are the primary tool for locating such structures and are thus an indispensable component of offshore oil or gas exploration. Seismic survey programmes comprise data acquisition in either two-dimensional (2D) and/or three dimensional (3D) scales, depending on information requirements. 2D surveys are typically applied to obtain regional data from widely spaced survey grids and provide a vertical slice through the seafloor geology along the survey track-line. Infill surveys on closer grids subsequently provide more detail over specific areas of interest. In contrast, 3D seismic surveys are conducted on a very tight survey grid, and provide a cube image of the seafloor geology along each survey track–line. Such surveys are typically applied to promising petroleum prospects to assist in fault line interpretation. The nature of the sound impulses utilised during seismic surveys have resulted in concern over their potential impact on marine fauna, particularly marine mammals, fish, and turtles (McCauley et al. 2000). Consequently, it has been proposed that environmental management already be applied at the exploration stage of the life cycle of a hydrocarbon field project (Duff et al. 1997, in Salter & Ford 2001). For this investigation Petroleum Geo-Services (PGS) is proposing to undertake a speculative 3D seismic survey offshore of the KwaZulu-Natal coast, South African (Figure 1). SLR Consulting (South Africa) (Pty) Ltd (SLR) has been appointed by PGS to compile an Amendment to the Environmental Management Programme (EMP) to be submitted as part of the application for surveying within the approved Reconnaissance Permit area. SLR in turn has approached Pisces Environmental Services (Pty) Ltd to provide a specialist report on potential impacts of the proposed operations on marine fauna in the area.

Queiros, A. M., Talbot, E., Msuya, F. E., Kuguru, B., Jiddawi, N., Mahongo, S., . . . Popova, E. (2024). A sustainable blue economy may not be possible in Tanzania without cutting emissions. *Science of the Total Environment,* 947, 174623. https://doi.org/10.1016/j.scitotenv.2024.174623

Balancing blue growth with the conservation of wild species and habitats is a key challenge for global ocean management. This is exacerbated in Global South nations, such as Tanzania, where climate-driven ocean change requires delicate marine spatial planning (MSP) trade-offs to ensure climate resilience of marine resources relied upon by coastal communities. Here, we identified challenges and opportunities that climate change presents to the near-term spatial management of Tanzania's artisanal fishing sector, marine protected areas and seaweed farming. Specifically, spatial meta-analysis of climate modelling for the region was carried out to estimate the natural distribution of climate resilience in the marine resources that support these socially important sectors. We estimated changes within the next 20 and 40 years, using modelling projections forced under global emissions trajectories, as well as a wealth of GIS and habitat suitability data derived from globally distributed programmes. Multi-decadal analyses indicated that long-term climate change trends and extreme weather present important challenges to the activity of these sectors, locally and regionally. Only in few instances did we identify areas exhibiting climate resilience and opportunities for sectoral expansion. Including these climate change refugia and bright spots in effective ocean management strategies may serve as nature-based solutions: promoting adaptive capacity in some of Tanzania's most vulnerable economic sectors; creating wage-gaining opportunities that promote gender parity; and delivering some economic benefits of a thriving ocean where possible. Without curbs in global emissions, however, a bleak future may emerge for globally valuable biodiversity hosted in Tanzania, and for its coastal communities, despite the expansion of protected areas or curbs in other pressures. Growing a sustainable ocean economy in this part of the Global South remains a substantial challenge without global decarbonization.

Raycraft, J. (2020). The (un)making of marine park subjects: Environmentality and everyday resistance in a coastal Tanzanian village. *World Development,* 126. https://doi.org/10.1016/j.worlddev.2019.104696

This paper focuses on local conflicts over marine conservation in southeastern Tanzania. It draws from ethnographic fieldwork conducted in 2014 and 2015 in a coastal village located inside the boundaries of a marine park. The paper first examines why villagers have come to contest the park, and subsequently outlines the various forms of resistance they employ to mobilize their opposition. Some people are willing to protest openly, as evidenced by the destruction of the park's gatehouse office and directory signs in 2013. However, an immediate violent response to such acts from state paramilitary forces has instilled fear in villagers. The swift crackdown, coupled with ongoing surveillance from ranger patrols, has engendered a degree of discipline in some people. Rather than risking further repercussions, many villagers engage in 'everyday forms of resistance' through subtle acts of noncompliance to the conservation regulations. These practices are entangled with material benefits and moral statements about customary rights to resources. They may also facilitate political mobility by destabilizing conservation management, while simultaneously avoiding open confrontation with governing authorities. I refer to this overall process as the (un)making of marine park subjects.

Robert, P., Leon, Z., & Ruriko, Y. (2019). Tropical principal component analysis on the space of ultrametrics. *arXiv*. https://doi.org/10.48550/arxiv.1911.10675

In 2019, Yoshida et al. introduced a notion of tropical principal component analysis (PCA). The output is a tropical polytope with a fixed number of vertices that best fits the data. We here apply tropical PCA to dimension reduction and visualization of data sampled from the space of phylogenetic trees. Our main results are twofold: the existence of a tropical cell decomposition into regions of fixed tree topology and the development of a stochastic optimization method to estimate the tropical PCA using a Markov Chain Monte Carlo (MCMC) approach. This method performs well with simulation studies, and it is applied to three empirical datasets: Apicomplexa and African coelacanth genomes as well as sequences of hemagglutinin for influenza from New York.

Robertson, M. D., Midway, S. R., West, L., Tillya, H., & Rivera-Monroy, V. H. (2018). Fishery characteristics in two districts of coastal Tanzania. *Ocean & Coastal Management,* 163, 254-268. https://doi.org/10.1016/j.ocecoaman.2018.06.015

Nearshore marine fisheries provide the main source of protein for nearly 9 million people in coastal villages of Tanzania, yet for decades the fisheries have shown signs of overexploitation. These fisheries are small-scale and co-managed by local coastal communities and governmental authorities in groups known as Beach Management Units (BMUs). BMUs record individual fishing trip data (e.g. gear, vessel, taxa); however, the catch data have only been analyzed in nationally aggregated statistics. The objective of this study was to determine if BMU catch-assessment surveys can provide information on the fishing characteristics of small-scale fishing communities in Tanzania. We collected all available landings data from 2014 to 2017 from BMUs in fourteen villages in two spatially, socially, and ecologically distinct districts (Pangani and Rufiji) of the country. Our results show that each village had unique patterns for vessel-use, gear-use, and taxa landed, and that every village was specialized in some measure. Specifically, two villages in Pangani district landed octopus or parrotfish almost exclusively, suggesting potential trophic cascades after years of overexploitation. Furthermore, village fisheries had shared characteristics within their district, thus describing how fishing patterns vary at multiple spatial scales along the coast. Although imperfect, the catch data collected by the community organizations have generated the first descriptions of how village-based fisheries in Tanzania function. Using these findings, we suggest implementing local monitoring data and analysis into the fisheries management plans at the village and district scale. Continuing to collect and analyze community collected data is necessary to gain insights into the range of characteristics of small-scale fisheries to improve current management programs.

Roux, D. E. (2015). *An Eco-Umuzi.* (M.Arch.), University of the Free State, Bloemfontein, SA. Retrieved from http://hdl.handle.net/11660/11639

Sodwana Bay has been a tourist attraction since the late 1970's. It is known for its sandy beaches and abundance of marine and wild life. This dissertation is proposing a multi-functional project which includes a crafts market, restaurant, information centre and scuba diving school that will enhance the tourists and locals' experience of the beauty and diversity of the location. This dissertation aims to cater on various levels to different needs in order to ensure their integration, for example: to recognise the fossil-like fish, the coelacanth; to incorporate the existing scubadiving and tourist industry; and to include the local inhabitants' culture and crafts. Consequently, this project will recognise and respect these different components, it will be inclusive while, simultaneously, working as sensitively as possible on the site.

Sakaue, J., Maeda, K., Miller, M. J., Sakai, R., Tahara, K. I., Abe, H., . . . Ida, H. (2021). New Insights About the Behavioral Ecology of the Coelacanth Latimeria chalumnae Video Recorded in the Absence of Humans Off South Africa. *Frontiers in Marine Science,* 8. https://doi.org/10.3389/fmars.2021.755275

South African coelacanths, Latimeria chalumnae, were intensively studied using submersibles in the Comoros Islands before recent progress in deep-diving techniques led to the discovery of coelacanths living at shallower depths off Sodwana Bay, South Africa, which were then studied by divers in close encounters or from underwater vehicles. However, all previous observations were made under intense human influence, so the "natural" behaviors of coelacanths have never been observed. Here we sought to record the natural behaviors of coelacanths by minimizing anthropogenic influences using trimix-gas diving and remote recording techniques. We thus set fixed camera and current/temperature recorders at 98 and 113 m to monitor the behaviors of fishes and oceanographic parameters over a 6-day period. Time-lapse video observations succeeded to record one coelacanth that entered the cave during the coldest-water period, two sand tiger sharks, and many other smaller fishes entering a cave. An extensive analysis of the footage led to an interesting discovery that the first dorsal fin angle of the coelacanth corelated with the presence-or-absence of a large shark that frequently passed through the cave. When no shark was present, the coelacanth's dorsal fin was folded similar to 3/4 of the time, but when the shark entered the cave, its dorsal fin was unfolded > 95% of the time, while no such reactions were observed with other observed fishes. The erected coelacanth first dorsal fin posture is an important part of the iconic symbol of these ancient fish, but it may be reflecting stressful situations such as responses to potential predators. Our observation clearly showed that the dorsal fin is in a folded position during a steady relaxed state of the fish and it can be unfolded in response to external stimuli. Use of non-biased observation systems is strongly recommended when observing the natural behavior of coelacanths.

Salema, F. G., Mbije, N. E., Mwakalapa, E. B., & Rija, A. A. (2022). Patterns of fish community structure in protected and non-protected marine areas of mainland Tanzania. *Western Indian Ocean Journal of Marine Science,* 21(1), 91-101. https://doi.org/10.4314/wiojms.v21i1.7

Information on the benefits of Marine Protected Areas (MPAs) for the condition of fish stocks is not well documented in Tanzania. Fish landing sites located in Tanga and Mtwara regions were surveyed to assess patterns of fish community structure; particularly fish abundance, species diversity, growth patterns, and maturity stages, based on catches landed at sites with different protection status. Fish abundance in the catch from protected areas was significantly lower than in non-protected areas ($p=0.002$). Species diversity was relatively higher in catches from non-protected ($H=2.742$) compared to protected areas ($H=2.232$). A high percentage of species (63.24 %) exhibiting negative allometric growth was observed in catches from non-protected areas. Further, a large number of mature fish was observed in catches from protected areas compared to non-protected areas ($p<0.01$). These indices are useful indicators of the performance of MPAs. The observed negative allometric growth and reduced number of mature fishes in the non-protected areas suggest that extractive pressure and disturbances from fishing gears have negative impacts on the fish stock. Continued high extraction may induce a decline in general fish size due to the constant selection for large-trait fish specimens, potentially causing evolutionally change in morphological traits. In contrast, the lower abundance and species diversity from the protected areas reflected low catch effort as a result of regulated fishing pressure in MPAs, rather than indicating the actual diversity in the fish stocks in these protected waters. Based on these findings it is recommended that more regulatory strategies are implemented in non-protected waters to allow more time for fish to attain appropriate harvest sizes and to ensure the effective protection of marine resources.

Sherman, V. R., Quan, H. C., Yang, W., Ritchie, R. O., & Meyers, M. A. (2017). A comparative study of piscine defense: The scales of Arapaima gigas, Latimeria chalumnae and Atractosteus spatula. *Journal of the Mechanical Behavior of Biomedical Materials,* 73, 1-16. https://doi.org/10.1016/j.jmbbm.2016.10.001

We compare the characteristics of the armored scales of three large fish, namely the Arapaima gigas (arapaima), Latimeria chalumnae (coelacanth), and Atractosteus spatula (alligator gar), with specific focus on their unique structure-mechanical property relationships and their specialized ability to provide protection from predatory pressures, with the ultimate goal of providing bio-inspiration for manmade materials. The arapaima has flexible and overlapping cycloid scales which consist of a tough Bouligand-type arrangement of collagen layers in the base and a hard external mineralized surface, protecting it from piranha, a predator with extremely sharp teeth. The coelacanth has overlapping elasmoid scales that consist of adjacent Bouligand-type pairs, forming a double-twisted Bouligand-type structure. The collagenous layers are connected by collagen fibril struts which significantly contribute to the energy dissipation, so that the scales have the capability to defend from predators such as sharks. The alligator gar has inflexible articulating ganoid scales made of a hard and highly mineralized enamel-like outer surface and a tough dentine-like bony base, which resist powerful bite forces of self-predation and attack by alligators. The structural differences between the three scales correspond with the attack of their predators, and show refined mechanisms which may be imitated and incorporated into superior bioinspired and biomimetic designs that are specialized to resist specific modes of predation.

Subir Ranjan, K. (2021). Chapter 4 One small step for amphibious fish, one evolutionary leap for moving tetrapods on Earth. In *The Evolutionary Biology of Extinct and Extant Organisms.* (pp. 41-51) https://doi.org/10.1016/b978-0-12-822655-1.00005-2

According to the evolutionary biologists, the first tetrapods were amphibians in nature, originated around 395 mya during the Devonian period and evolved a few times in the last millions of years, which supposedly evolved from the lobe-finned fish or Sarcopterygians (those are phylogenetically integrated to coelacanth and lungfish) (Schoch, 2014). The evolutionary biologists observed that Tiktaalik roseae was the transitional form or evolutionary link between fish and amphibians, supposedly roaming around in shallow water, around 375 mya. The comparative genomic analysis between African lungfish and African coelacanth has helped the scientists to resolve this complex phylogenetic puzzle as lungfish has emerged with respiratory organs like lungs, to be accustomed to the aerial breathing, surviving in terrestrial habitats and evolved as the phylogenetic predecessor as well as "extant sister group to the maiden land vertebrates" on Earth (Meyer and Dolven, 1992; Brinkmann et al., 2004; Amemiya et al., 2013).

Tansheq Limited. (2024). *Environmental and social impact assessment report for the proposed installation of 132KV power trasmission line from the existing 132/33/11KV Majani Mapana Substation in Tanga region to 132/33KV Wesha Substation in Pemba Island.* National Environment Management Council Dar Es Salaam, Tanzania. Retrieved from https://www.tanesco.co.tz/attachments/investments/environment_reports/KYCWqJShT7dfz087aqRslr5_HgQU96Ay_2024_08_12_10_46_55.pdf

Tanzania Electric Supply Company Limited (TANESCO) owns most of the generation, transmission and distribution facilities in mainland Tanzania and sells bulk power to the Zanzibar Electricity Corporation (ZECO), which in turn sells it to the public on the islands of Unguja and Pemba. Power supply to Zanzibar is conveyed through No. 2 (two) existing 132 kV Transmission lines with submarine cable component from Dar es Salaam to Unguja and 33 kV distribution line with submarine cable component from Tanga to Pemba. Considering the existing power supply to Pemba Island, there is need to develop and implement another high voltage Transmission line with submarine cable from Tanzania Mainland to Zanzibar (Pemba) to be operated at 132 kV. Hence, TANESCO with engagement of ZECO decided to initiate the Project of increasing power supply to Zanzibar to meet the increasing demand. Currently the Consultant CESI S.p.A. (Italy) in joint venture with ELC Electroconsult S.p.A. (Italy) and Colenco Consulting Ltd. (Nigeria) are undertaking the assignment under the financing of African Development Bank (AfDB), with the following proposed scope of work: - 132 kV transmission line from Tanga (Tanzania mainland) to supply Pemba Island. In order to comply with the requirements of Registration and Practice of Environmental Expert Regulations, 2021; Consultant CESI S.p.A. (Italy) in joint venture with ELC Electroconsult S.p.A. (Italy) and Colenco Consulting Ltd. (Nigeria) contracted Tansheq Limited a local consulting firm to conduct the Environmental and Social Impact Assessment for the proposed project as per law requires The ultimate goal of the project is to improve the livelihood of the people as well as the quality of the socioeconomic development environment for Tanzania and Zanzibar, through increased availability and affordability of electricity supply.

Tao, Z., Qunfu, W., Yicheng, M., Wenjing, L., Chengang, Z., & Zhigang, Z. (2021). Evolution of ACE2 and SARS-CoV-2 Interplay Across 247 Vertebrates. *bioRxiv*, 2021.2001.2028.428568. https://doi.org/10.1101/2021.01.28.428568

Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) cause the most serious pandemics of Coronavirus Disease 2019 (COVID-19), which threatens human health and public safety. SARS-CoV-2 spike (S) protein uses angiotensin-converting enzyme 2 (ACE2) as recognized receptor for its entry into host cell that contributes to the infection of SARS-CoV-2 to hosts. Using computational modeling approach, this study resolved the evolutionary pattern of bonding affinity of ACE2 in 247 jawed vertebrates to the spike (S) protein of SARS-CoV-2. First, high-or-low binding affinity phenotype divergence of ACE2 to the S protein of SARS-CoV-2 has appeared in two ancient species of jawed vertebrates, Scyliorhinus torazame (low-affinity, Chondrichthyes) and Latimeria chalumnae (high-affinity, Coelacanthimorpha). Second, multiple independent affinity divergence events recur in fishes, amphibians-reptiles, birds, and mammals. Third, high affinity phenotypes go up in mammals, possibly implying the rapid expansion of mammals might accelerate the evolution of coronaviruses. Fourth, we found natural mutations at eight amino acid sites of ACE2 can determine most of phenotype divergences of bonding affinity in 247 vertebrates and resolved their related structural basis. Moreover, we also identified high-affinity or low-affinity-associated concomitant mutation group.The group linked to extremely high affinity may provide novel potentials for the development of human recombinant soluble ACE2 (hrsACE2) in treating patients with COVID-19 or for constructing genetically modified SARS-CoV-2 infection models promoting vaccines studies. These findings would offer potential benefits for the treatment and prevention of SARS-CoV-2.

Tatsumi, N., Kobayashi, R., Yano, T., Noda, M., Fujimura, K., Okada, N., & Okabe, M. (2016). Molecular developmental mechanism in polypterid fish provides insight into the origin of vertebrate lungs. *Scientific Reports,* 6, 30580. https://doi.org/10.1038/srep30580

The lung is an important organ for air breathing in tetrapods and originated well before the terrestrialization of vertebrates. Therefore, to better understand lung evolution, we investigated lung development in the extant basal actinopterygian fish Senegal bichir (Polypterus senegalus). First, we histologically confirmed that lung development in this species is very similar to that of tetrapods. We also found that the mesenchymal expression patterns of three genes that are known to play important roles in early lung development in tetrapods (Fgf10, Tbx4, and Tbx5) were quite similar to those of tetrapods. Moreover, we found a Tbx4 core lung mesenchyme-specific enhancer (C-LME) in the genomes of bichir and coelacanth (Latimeria chalumnae) and experimentally confirmed that these were functional in tetrapods. These findings provide the first molecular evidence that the developmental program for lung was already established in the common ancestor of actinopterygians and sarcopterygians.

Toriño, P., Soto, M., & Perea, D. (2021). A comprehensive phylogenetic analysis of coelacanth fishes (Sarcopterygii, Actinistia) with comments on the composition of the Mawsoniidae and Latimeriidae: evaluating old and new methodological challenges and constraints. *Historical Biology,* 33(12), 3423-3443. https://doi.org/10.1080/08912963.2020.1867982

The phylogeny of coelacanths (Devonian-Recent) has been a matter of discussion at least since 1940s following the discovery of Latimeria chalumnae, and it remains as a revisited issue in most recent works. In this contribution, an updated phylogenetic analysis based on a new consensual data matrix is presented, merging most of the emendations proposed over the past two decades, and including a completely reviewed character scoring for some genera. Also, a complete Stratigraphic Tree Analysis is introduced, calibrating divergence times, branch lengths, potential ghost ranges and quantifying the stratigraphic fit of the trees. The topologies are congruent with previous analyses, with exceptions: Mawsoniidae and Latimeriidae include some genera previously not considered as such. Implied weights analysis indicates that this result is influenced by homoplasies. Time-scaled phylogenies show a great proportion of cladogenetic events concentrated in the Permian-Triassic transition, leading to the diversification of the Mesozoic modern stock of the group (Latimerioidei). In spite of some large ghost ranges (e.g. Latimeria, ranging from Middle-Upper Jurassic), the metrics indicate relatively good stratigraphic fits. Although additional reviews of both the character codings and the scorings of several taxa are still needed, these preliminary results can constitute an input for future macroevolutionary studies.

UNEP-Nairobi Convention, & WIOMSA. (2021). *Western Indian Ocean Marine Protected Areas Outlook: Towards achievement of the Global Biodiversity Framework Targets.* United Nations Environment Programme/Nairobi Convention Secretariat, Nairobi, Kenya. Retrieved from https://www.wiomsa.org/publications/western-indian-ocean-wio-marine-protected-areas-outlook/

The Western Indian Ocean region has declared 143* marine and coastal areas as protected – an area covering 553,163 square kilometers, representing 7 percent of the total Exclusive Economic Zone (EEZ) for the region – according to the WIO MPA outlook publication released by the UN Environment Programme (UNEP)-Nairobi Convention and the Western Indian Ocean Marine Science Association. The MPA Outlook documents progress made by countries in the region towards the achievement of Sustainable Development Goal 14.5 and provides lessons and opportunities to increase momentum for achieving post-2020 Global Biodiversity Framework targets.
The Marine Protected Areas Outlook, indicates that almost half of the total area – an estimated 63 percent of the overall square kilometers – was brought under protection in the seven years since the 2015 adoption of Sustainable Development Goal 14.5, which committed countries to conserving at least 10 percent of their marine and coastal areas by 2020.
This Outlook examines the current and future status of Marine Protected Areas (MPAs) in Comoros, Kenya, France (in its Western Indian Ocean territories), Madagascar, Mauritius, Mozambique, Seychelles, South Africa, and Tanzania, emphasizing the increased commitment of countries to strengthen marine protection. In 2019 alone, Seychelles brought 30 percent of its Exclusive Economic Zone under protection, safeguarding the habitats of 2,600 species, while South Africa declared 20 new MPAs – enabling both countries to exceed the 10 percent target. Comoros has developed new MPA-specific legislation, while over three hundred Locally Managed Marine Areas – i.e., areas in which coastal communities shoulder the mantle of conservation – have been declared across the region.

Xiao, L., Guo, Y., Wang, D. D., Zhao, M., Hou, X., Li, S. H., . . . Zhang, Y. (2020). Beta-Hydroxysteroid Dehydrogenase Genes in Orange-Spotted Grouper (Epinephelus coioides): Genome-Wide Identification and Expression Analysis During Sex Reversal. *Frontiers in Genetics,* 11, 161. https://doi.org/10.3389/fgene.2020.00161

Beta-hydroxysteroid dehydrogenases (beta-HSDs) are a group of steroidogenic enzymes that are involved in steroid biosynthesis and metabolism, and play a crucial role in mammalian physiology and development, including sex determination and differentiation. In the present study, a genome-wide analysis identified the numbers of beta-hsd genes in orange-spotted grouper (Epinephelus coioides) (19), human (Homo sapiens) (22), mouse (Mus musculus) (24), chicken (Gallus gallus) (16), xenopus (Xenopus tropicalis) (24), coelacanth (Latimeria chalumnae) (17), spotted gar (Lepisosteus oculatus) (14), zebrafish (Danio rerio) (19), fugu (Takifugu rubripes) (19), tilapia (Oreochromis niloticus) (19), medaka (Oryzias latipes) (19), stickleback (Gasterosteus aculeatus) (17) and common carp (Cyprinus carpio) (27) samples. A comparative analysis revealed that the number of beta-hsd genes in teleost fish was no greater than in tetrapods due to gene loss followed by a teleost-specific whole-genome duplication event. Based on transcriptome data from grouper brain and gonad samples during sex reversal, six beta-hsd genes had relatively high expression levels in the brain, indicating that these genes may be required for neurogenesis or the maintenance of specific biological processes in the brain. In the gonad, two and eight beta-hsd genes were up- and downregulated, respectively, indicating their important roles in sex reversal. Our results demonstrated that beta-hsd genes may be involved in the sex reversal of grouper by regulating the synthesis and metabolism of sex steroid hormones.

Yellan, I., Yang, A. W. H., & Hughes, T. R. (2021). Diverse Eukaryotic CGG-Binding Proteins Produced by Independent Domestications of hAT Transposons. *Molecular Biology and Evolution,* 38(5), 2070-2075. https://doi.org/10.1093/molbev/msab007

The human transcription factor (TF) CGGBP1 (CGG-binding protein) is conserved only in amniotes and is believed to derive from the zf-BED and Hermes transposase DNA-binding domains (DBDs) of a hAT DNA transposon. Here, we show that sequence-specific DNA-binding proteins with this bipartite domain structure have resulted from dozens of independent hAT domestications in different eukaryotic lineages. CGGBPs display a wide range of sequence specificity, usually including preferences for CGG or CGC trinucleotides, whereas some bind AT-rich motifs. The CGGBPs are almost entirely nonsyntenic, and their protein sequences, DNA-binding motifs, and patterns of presence or absence in genomes are uncharacteristic of ancestry via speciation. At least eight CGGBPs in the coelacanth Latimeria chalumnae bind distinct motifs, and the expression of the corresponding genes varies considerably across tissues, suggesting tissue-restricted function.

Yue, H. M., Ye, H., Ruan, R., Du, H., Li, C. J., & Wei, Q. W. (2019). Feedback regulation of 17β-estradiol on two kisspeptin genes in the Dabry's sturgeon (Acipenser dabryanus). *Comparative Biochemistry and Physiology B-Biochemistry & Molecular Biology,* 230, 1-9. https://doi.org/10.1016/j.cbpb.2019.01.006

In tetrapods, kisspeptins are a group of peptides that play essential roles in the regulation of the Gonadotropin-releasing hormone secretion, and may participate in the feedback regulation of sex steroids as well. In this study, two kiss paralogs, designated as dskiss1 and dskiss2 were identified in Acipenser dabryanus. The full-length cDNA sequences of dskissl and dskiss2 are 1265 and 744 base pairs (bp), encoding 130 and 146 amino acids, respectively. Multiple sequence alignment indicated that both Kiss1 and Kiss2 decapeptides were highly conserved among vertebrates. Besides, Kissl of Dabry's sturgeon shared closer evolutionary relationship with the holostean species spotted gar (Lepisosteus oculatus), while Kiss2 of Acipenser dabryanus was conservatively grouped with the early sarcopterygian coelacanth (Latimeria chalumnae) in the phylogenetic analysis. Tissue distribution analysis showed that dskissl transcribed exclusively in the brain, whereas dskiss2 exhibited wider tissue distribution including brain, testis and ovary. Furthermore, male Dabry's sturgeons were intraperitoneally injected with 17 beta-estradiol (E2) and the effect of E2 on hypothalamus kiss and its receptors kissr mRNA levels was evaluated by relative real-time PCR. The transcription levels of dskiss2 and dskissrl were significantly increased by E2 injection (P <.05). However, the mRNA levels of dskiss1 and dskissr2 were not changed in E2-treated group compared to the control group. These results indicate that E2 exerts positive feedback effects through dskiss2/dskissr1 in male Dabry's sturgeon.

Yunfeng, S. (2022). Three Genome-scale Approaches Support that Lungfish is the Closest Living Relative of Land Vertebrate, but not Coelacanth. *Authorea*. https://doi.org/10.22541/au.165760392.21011351/v1

The origin of tetrapod has been one of intense debating open questions for decades between coelacanth(Latimeria chalumnae) and lungfish (Protopterus annectens). For resolving this incongruence in phylogenies, a genome-wide data mining approach is used to retrieve 43 shared genes of seven taxa from GenBank and further 1001 orthologous genes of ten taxa from the Ensembl and NCBI. We used the maximum gene-support tree approach and the majority-rule branch approach to analyze 43 nuclear genes encoding amino acid residues and compared these results to those inferred with the concatenation approach. Our results successfully provide strong evidence in favor of the lungfish-tetrapod hypothesis, but rejecting the coelacanth-tetrapod hypothesis based on significantly fewer gene supports and lower taxon jackknife probabilities for the coelacanth-tetrapod clade than the lungfish-tetrapod one with the maximum gene-support tree approach and the jackknife method for taxon subsampling. When more and more genomic data become available in recent years, sequence data of 1001 shared genes was mined. We used the maximum gene-support approach with this larger dataset successfully to infer that lungfish is the closest relative of land vertebrates with a significant difference at $p < 0.01$ (Chi-Square test) in gene support values between a maximum gene-support tree and the second most gene support tree with ML methods. The second most support to the maximum (SM ratio), a relative value, is a better support index than a single absolute value of support to show the insight of the phylogenetic support. Our results also show increasing the number of shared genes is much more effective than increasing the number of taxa.

Yunfeng, S., Guo, L., Xiu-Qing, L., Robin, G., & Youjun, Z. (2022). *Data-Mining with Three Genome-Scale Approaches Supports that Lungfish is the Closest Living Relative of Land Vertebrate, but not Coelacanth.* Paper presented at the 2022 International Conference on Computational Science and Computational Intelligence (CSCI). https://doi.org/10.1109/csci58124.2022.00110

The origin of tetrapod has been one of intense debating open questions for decades between coelacanth (Latimeria chalumnae) and lungfish (Protopterus annectens). For resolving this incongruence in phylogenies, a genome-wide data mining approach is used to retrieve 43 shared genes of seven taxa from GenBank and further 1001 orthologous genes of ten taxa from the Ensembl and NCBI. We used the maximum gene-support tree approach and the majority-rule branch approach to analyze 43 nuclear genes encoding amino acid residues, and compared these results to those inferred with the concatenation approach. Our results successfully provide strong evidence in favor of the lungfish-tetrapod hypothesis, but reject the coelacanth-tetrapod hypothesis based on significantly fewer gene support frequency and lower taxon jackknife probabilities for the coelacanth-tetrapod clade than the lungfish-tetrapod one with the maximum gene-support tree approach and the jackknife method for taxon subsampling. When more genomic data became available in recent years, sequencing data of 1001 shared genes was mined. We used the maximum gene-support approach with this larger dataset successfully to infer that lungfish is the closest relative of land vertebrates with a significant difference at $p < 0.01$ (Chi-Square test) in gene support values between the maximum gene-support tree and the second most gene-support tree with ML methods. The second most gene support frequency to the maximum gene support frequency (SM ratio), a combined index, is a better support measure than a single absolute value of support to reveal the insight of the phylogenetic support. Our results also show increasing the number of shared genes is much more effective than increasing the number of taxa.

Zakon, H. H., Li, W. M., Pillai, N. E., Tohari, S., Shingate, P., Ren, J. F., & Venkatesh, B. (2017). Voltage-gated sodium channel gene repertoire of lampreys: gene duplications, tissue-specific expression and discovery of a long-lost gene. *Proceedings of the Royal Society B-Biological Sciences,* 284(1863). https://doi.org/10.1098/rspb.2017.0824

Studies of the voltage-gated sodium (Nav) channels of extant gnathostomes have made it possible to deduce that ancestral gnathostomes possessed four voltage-gated sodium channel genes derived from a single ancestral chordate gene following two rounds of genome duplication early in vertebrates. We investigated the Nav gene family in two species of lampreys (the Japanese lamprey Lethenteron japonicum and sea lamprey Petromyzon marinus) (jawless vertebrates-agnatha) and compared them with those of basal vertebrates to better understand the origin of Nav genes in vertebrates. We noted six Nav genes in both lamprey species, but orthology with gnathostome (jawed vertebrate) channels was inconclusive. Surprisingly, the Nav2 gene, ubiquitously found in invertebrates and believed to have been lost in vertebrates, is present in lampreys, elephant shark (Callorhinchus milii) and coelacanth (Latimeria chalumnae). Despite repeated duplication of the Nav1 family in vertebrates, Nav2 is only in single copy in those vertebrates in which it is retained, and was independently lost in ray-finned fishes and tetrapods. Of the other five Nav channel genes, most were expressed in brain, one in brain and heart, and one exclusively in skeletal muscle. Invertebrates do not express Nav channel genes in muscle. Thus, early in the vertebrate lineage Nav channels began to diversify and different genes began to express in heart and muscle.

Zheng, P. H., Wang, L., Wang, A. L., Zhang, X. X., Ye, J. M., Wang, D. M., . . . Xian, J. A. (2019). cDNA cloning and expression analysis of glutaredoxin (Grx) 2 in the Pacific white shrimp Litopenaeus vannamei. *Fish & Shellfish Immunology,* 86, 662-671. https://doi.org/10.1016/j.fsi.2018.12.011

Glutaredoxin (Grx) is a class molecule oxidoreductase, which can regulate the redox state of proteins and plays a key role in antioxidant defense. However, the informations of Grx cDNA sequences and their functions are lack in decapod crustacea. In the present study, the cDNA of LvGrx 2 was cloned from the Pacific white shrimp, Litopenaeus vannamei. The open reading frame (ORF) of LvGrx 2 was 360 bp, which encoded a polypeptide of 119 amino acids. The molecular mass of the predicted protein is 12.87 kDa with an estimated pI of 8.22. Sequence alignment showed that the amino acid sequence of LvGrx 2 shares 59%, 59% and 58% identity with that of the coelacanth Latimeria chalumnae, the plateau frog

Nanorana parked and the half-smooth tongue sole Cynoglossus semilaevis, respectively. Quantitative real-time PCR analysis revealed that LvGrx 2 were detected in a wide range of tissues, with highest expression in gill, hepatopancrea and intestine, and weakest expression in muscle. The expression responses of LvGrx 2 were analyzed in hepatopancrea and gill after ammonia-N stress or lipopolysaccharide (LPS) injection. During ammonia-N exposure, the LvGrx 2 transcriptions in hepatopancrea and gill significantly up-regulated, and the peak value appeared after 12 h and 24 h exposure respectively. After LPS injection, expression levels of LvGrx 2 in hepatopancrea obviously increased in the early and late stages, while LvGrx 2 transcription in gill sharply up-regulated in the middle period. These results suggest that LvGrx 2 may play a vital role in shrimp defense system against environmental stress and pathogen infection. RNA interference experiment was designed to further probe roles of LvGrx 2 during ammonia-N exposure. Ammonia-N induced obvious improvement in expression levels of LvGrx 2, LvGrx 3, GPx, GST and Trx, accompanied by increases of protein carbonyl and malondialdehyde (MDA) contents. However, transcription of GPx and GST were much weaker in LvGrx 2 interfered-shrimp, and oxidative damage in both lipid and protein were more serious. These results further suggest that LvGrx 2 in shrimp participates in oxidative defence and regulation of antioxidant system.