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Global taxonomic diversity of sharks, rays, and chimaeras: Family-level patterns and changes in species classification

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Abstract

Quantifying the current taxonomic structure of sharks, rays, and chimaeras (Chondrichthyes) provides an essential, albeit classification-dependent, baseline for biodiversity research and conservation management. In this study, family-level genus and species counts extracted from Eschmeyer's Catalog of Fishes (21 September 2026) were systematically analysed and validated. The consistency of the taxonomic hierarchy and associated subtotals was assessed, and the resulting taxonomic inventory was compared with two historical benchmarks: the 2015 dataset reported by Weigmann (2016) and the classification reflecting the taxonomic status as of 31 December 2023 compiled by Weigmann *et al*. (2024). The 2026 extract contains 1,331 accepted species in 218 genera, 68 families, and 14 orders. Batoids account for 702 species (52.7%), sharks for 568 (42.7%), and chimaeras for 61 (4.6%). Carcharhiniformes, Rajiformes, and Myliobatiformes together encompass 871 species (65.4%); the ten richest families contain 788 (59.2%). Species richness is highly unequal among families (median=9; mean=19.6; Gini=0.640), corresponding to an entropy-based effective richness of 31.9 equally represented families. Genus and species count covary across families (Spearman's $\rho = 0.704$), but this association is descriptive because both counts share a hierarchical definition. Compared with the 2023 classification, recognized richness increased by a net 65 species (+5.1%), and by 143 (+12.0%) relative to the earlier published checklist with a 2015 cutoff. Family-level changes include taxonomic redistribution: Dichichthyidae was established after the 2023 benchmark and cannot be counted as five entirely new discoveries. One genus-count anomaly (Mitsukurinidae, two genera but one accepted living species) warrants clarification of counting conventions. The audited census documents strong taxonomic concentration and emphasizes that temporal inventory differences should not be equated directly with rates of species discovery.

Keywords: Cartilaginous fishes, Batoidea, Elasmobranchii, Holocephali, Taxonomic inventory, Species richness, Taxonomic change, Classification

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Introduction

Living chondrichthyans (cartilaginous fishes) including sharks, rays, skates, and chimaeras form an evolutionarily distinctive lineage of jawed vertebrates with a deep Paleozoic history, wide variation in body form and reproductive biology, and important ecological roles in marine and some freshwater ecosystems (Stein *et al*., 2018; Gayford and Jambura, 2025). Extant Chondrichthyes comprise two major lineages, Holocephali (chimaeras) and Elasmobranchii (sharks and batoids). In conventional classifications, the latter comprises Selachii (sharks, traditionally subdivided into Galeomorphii and Squalomorphii) and Batoidea (rays and skates). Although these groups are widely used in taxonomy and biodiversity assessments, some of their deepest branching relationships remain contested.

Recent phylogenomic investigations have clarified many relationships within Chondrichthyes but have also exposed conflicts between genomic markers. Using 4,452 single-copy exons from 98 species, Huang *et al*. (2025; bioRxiv preprint) found that analyses of unfiltered loci placed Hexanchiformes at the base of Elasmobranchii, whereas filtering loci according to relative branch-length properties supported the monophyly of major superordinal groups, including sharks (Selachii) and batoids (Batoidea). A separate analysis of genomic data from 48 chondrichthyan species recovered contrasting relationships from different marker classes: ultraconserved elements placed Hexanchiformes as sister to all other elasmobranchs, implying shark paraphyly, whereas conserved protein-coding orthologues supported the traditional monophyly of sharks (Brownstein and Near, 2026; bioRxiv preprint). These results should be viewed as provisional because the two phylogenomic studies have not undergone journal peer review; nevertheless, their contrasting inferences illustrate how locus selection, evolutionary-rate heterogeneity and compositional bias can influence estimates of deep relationships.

The phylogenetic uncertainty is relevant to taxonomic inventories because classifications based on different evolutionary hypotheses need not delimit the same higher taxa. It does not, however, invalidate the practical use of a clearly identified nomenclatural and classification reference. Moreover, differences in extant species richness among lineages should not be interpreted directly as differences in evolutionary diversification rates. A peer-reviewed synthesis of elasmobranch macroevolution concluded that past diversity patterns have been shaped by interacting factors, including trait evolution, biotic interactions, climatic change and tectonic events; available studies do not identify a single universally dominant driver (Gayford and Jambura, 2025). Much of the evolutionary history represented by living elasmobranch lineages reflects diversification during

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the Mesozoic, particularly the Jurassic, but crown ages and deeper topologies are still subjects of investigation (Gayford and Jambura, 2025; Brownstein and Near, 2026).

The deep evolutionary history of Chondrichthyes, its phylogenetic distinctiveness and ecological importance make species and family-level inventories essential reference points for systematic biology and conservation (Stein *et al*., 2018; Weigmann *et al*., 2024). The evolutionary relationships among taxa and their classification are related but distinct questions: a dated catalogue documents the taxa accepted under a stated taxonomic treatment, whereas a phylogenetic hypothesis addresses historical relationships among lineages. Reliable names and counts underpin identification tools, distributional assessments and the interpretation of fisheries and conservation data. Nevertheless, recognised diversity changes with new species descriptions, revalidation or synonymisation of names, transfers among genera and revisions of family boundaries (Naylor *et al*., 2012; Weigmann *et al*., 2024).

A robust and versioned taxonomic baseline is particularly important because chondrichthyans face extensive anthropogenic pressures. A global reassessment of 1,199 chondrichthyan species identified 391 (32.6%) as threatened and estimated a threatened fraction of 37.5% after accounting for Data Deficient species (Dulvy *et al*., 2021). More recent work has emphasised the impacts of deepwater fisheries and the continuing need to link accepted taxon names to up-to-date conservation assessments (Finucci *et al*., 2024, 2026). Counts in a taxonomic catalogue should not be conflated with counts of assessed taxa in the IUCN Red List because the databases differ in purpose, temporal coverage and taxonomic treatment.

Weigmann (2016) reported 1,188 living chondrichthyan species in 61 families and 199 genera using information available to 7 November 2015. Weigmann *et al*. (2024) subsequently assembled a classification recognising approximately 1,266 species, 67 families and 215 genera as of 31 December 2023. Eschmeyer's Catalog of Fishes (Sep. 2026) provides a separately maintained, frequently updated reference for fish names and their classification (Fricke *et al*., 2026). Comparisons among these inventories can identify changes in accepted taxonomic richness only when the source version, temporal cutoff and classification differences are explicitly documented.

The objectives of the present study are to (i) describe the distribution of accepted living chondrichthyan genera and species among orders and families in the Catalog extract dated 21 September 2026; (ii) assess variation and evenness in the distribution of genera and species across families using complementary inequality and entropy-based measures; (iii) compare the census with published inventories having 2015 and 2023 taxonomic cutoffs; and (iv) identify data-integrity issues and interpretative

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limitations relevant to subsequent species-level reconciliation. The analysis is a descriptive census of a defined classification, not a phylogenetic reconstruction, an estimate of diversification rates or an extinction-risk assessment.

Materials and methods

Taxonomic source and scope

Family-level chondrichthyan data attributed to the 21 September 2026 release of Eschmeyer's Catalog of Fishes (Fricke *et al*., 2026) were extracted and analysed. The official Catalog website identifies that release date. The 92 taxonomic entries comprise two major-lineage headings (Elasmobranchii and Holocephali), 14 orders, 68 families and eight subfamilies. The order assignments of the source were retained for descriptive purposes; orders were additionally grouped as sharks (nine orders), batoids (four orders) and chimaeras (one order). These three groups are analysis-defined aggregates and were not separate fields in the source extract. This grouping provides continuity with earlier inventories without assuming that all higher-level phylogenetic relationships are resolved.

Validation and quantitative summaries

Internal consistency of the dataset was evaluated by checking that each family name appeared only once, family-level counts summed correctly to their respective orders and major lineages, subfamily totals agreed with those of their parent families, and the species counts across all 68 families reconciled with the overall number of accepted species. Descriptive statistics, including the mean, median, quartiles, standard deviation, and coefficient of variation, were calculated to summarize variation in family-level species richness.

To characterize patterns of inequality and evenness in the distribution of accepted species among families, the relative contributions of the most species-rich families were examined, and complementary inequality- and entropy-based measures were calculated. Inequality in family-level species richness was quantified using the Gini coefficient: $G = \Sigma_i\Sigma_j|x_i - x_j| / (2n\Sigma_i x_i)$**;** where x_i and x_j represent the numbers of accepted species in families i and j, respectively, and n denotes the total number of recognized families (n = 68). The Gini coefficient provides a summary of inequality in taxonomic richness, with values approaching zero indicating a relatively uniform distribution of species among families and higher values indicating progressively greater inequality. Although originally developed for economic applications, the Gini coefficient has also been employed in ecological and ichthyological research, including analyses of marine fish biomass distributions (Rufino *et al*., 2018), freshwater food-web structure (Liew *et al*., 2018), and geographical sampling inequality in marine biodiversity datasets encompassing Chondrichthyes (Ikari *et al*., 2026).

Complementary measures included Shannon entropy ($H=-\Sigma_i p_i \ln p_i$), the

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Gini–Simpson index ($1 - \Sigma_i p_i^2$), and the exponential of Shannon entropy [exp(H)], where $p_i = x_i / \Sigma_i x_i$ represents the proportion of accepted species assigned to family i. The exponential of Shannon entropy expresses the observed distribution as an effective number of equally species-rich families, whereas the Gini–Simpson index summarizes the probability that two species drawn independently from the catalogue species distribution belong to different families. Together, these complementary measures characterize variation, inequality, and evenness in the allocation of accepted species among families within the defined taxonomic classification. They should not be interpreted as measures of ecological alpha diversity, species abundance, evolutionary diversification rates, or extinction risk.

The association between the numbers of accepted genera and species per family was examined using Pearson's correlation coefficient (r) and Spearman's rank correlation coefficient (ρ). Because genera are nested within families and both variables represent related properties of the same taxonomic classification, these associations were interpreted descriptively rather than as evidence that genus richness independently predicts speciation or evolutionary diversification. No significance tests or bootstrapped confidence intervals were applied to the census-wide summaries, as the 68 families constituted the complete set recognized in the selected classification rather than a probabilistic sample. To evaluate the influence of a potential data inconsistency, a sensitivity analysis was conducted by recalculating the genus–species association after changing the anomalous genus count for Mitsukurinidae from two to one, while retaining the original catalogue value in the primary dataset.

Historical comparison and attribution of change

The September 2026 totals were compared with the checklist of Weigmann (2016; taxonomic cutoff 7 November 2015) and Table 1 of Weigmann *et al*. (2024; cutoff 31 December 2023). Each inventory is identified by its underlying cutoff rather than solely by the year of publication. For the comparison with 2023, 67 families were matched by name, and the newly recognised Dichichthyidae was considered separately. Net differences represent changes in accepted counts between the two sources, not independently verified numbers of newly described species. Individual changes could not be assigned to description, revalidation, synonymisation or reassignment because the supplied data and the 2023 family-level table lack a complete species-level crosswalk.

Results

Composition of living Chondrichthyes

The September 2026 extract contains 1,331 accepted living species, 218 genera, 68 families and 14 orders. Elasmobranchii comprise 1,270 species, 212 genera, 65 families and 13 orders

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(95.4% of the accepted species). Chimaeriformes accounts for the remaining 61 species in six genera and three families (4.6%). Batoids are more species-rich than sharks (702 vs. 568 species), whereas sharks are slightly richer in both genera (107 vs. 105) and families (39 vs. 26; Table 1).

Table 1: Composition of living Chondrichthyes in the 21 September 2026 Catalog extract; the sharks–batoids–chimaeras partition is an author-assigned grouping.

Group	Orders	Families	Genera	Species	% species	Sp./family
Sharks	9	39	107	568	42.7	14.6
Batoids	4	26	105	702	52.7	27.0
Chimaeras	1	3	6	61	4.6	20.3
Total	14	68	218	1,331	100.0	19.6

Uneven distribution among orders

Three orders including Carcharhiniformes (307 species; 23.1%), Rajiformes (306; 23.0%) and Myliobatiformes (258; 19.4%) encompass 871 species (65.4% of all living Chondrichthyes in the dataset). Including Squaliformes (146 species) increases the cumulative share to 76.4%. At the opposite extreme, Echinorhiniformes comprises two species and Hexanchiformes seven. Totals for the 14 orders were reconstructed from family entries and reconciled with the overall count of 1,331 species (Table 2; Fig. 2).

Table 2: Family, genus and species richness by order in September 2026, with differences from the 31 December 2023 classification of Weigmann et al. (2024).

Order	Families	Genera	Species	% total	2023	Net Δ
Carcharhiniformes	12	52	307	23.1	296	+11
Rajiformes	4	40	306	23.0	302	+4
Myliobatiformes	12	38	258	19.4	234	+24
Squaliformes	6	22	146	11.0	137	+9
Rhinopristiformes	5	12	70	5.3	68	+2
Torpediniformes	5	15	68	5.1	63	+5
Chimaeriformes	3	6	61	4.6	53	+8
Orectolobiformes	7	13	46	3.5	45	+1
Squatiniformes	1	1	24	1.8	24	+0
Lamniformes	8	11	16	1.2	15	+1
Heterodontiformes	1	1	10	0.8	10	+0
Pristiophoriformes	1	2	10	0.8	10	+0
Hexanchiformes	2	4	7	0.5	7	+0
Echinorhiniformes	1	1	2	0.2	2	+0
Total	68	218	1331	100.0	1266	+65

Family-level concentration and taxonomic entropy

Accepted species are unevenly allocated among the 68 families. Family richness ranges from one to 162 species, with a mean of 19.57 and a median of nine (interquartile range, 2.75–19). The coefficient of variation is 1.54, and species-level concentration has a Gini coefficient of 0.640. Eleven families (16.2%) have one species, while 27 (39.7%) are monogeneric. The five

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richest families contain 551 species (41.4%), and the ten richest contain 788 (59.2%; Table 3). The contrast between the observed 68 families and an entropy-based effective number of 31.9 equally represented families (Shannon H = 3.461) further captures the uneven taxonomic allocation (Fig. 1). Genus counts are less concentrated among families (Gini = 0.480).

Table 3: The ten most species-rich families in the September 2026 Catalog extract.

Rank	Family	Order	Genera	Species	% total	Cum. %
1	Rajidae	Rajiformes	18	162	12.2	12.2
2	Pentanchidae	Carcharhiniformes	12	113	8.5	20.7
3	Arhynchobatidae	Rajiformes	14	111	8.3	29.0
4	Dasyatidae	Myliobatiformes	19	105	7.9	36.9
5	Carcharhinidae	Carcharhiniformes	10	60	4.5	41.4
6	Etmopteridae	Squaliformes	4	57	4.3	45.7
7	Chimaeridae	Chimaeriformes	2	47	3.5	49.2
8	Triakidae	Carcharhiniformes	9	46	3.5	52.7
9	Potamotrygonidae	Myliobatiformes	5	45	3.4	56.0
10	Squalidae	Squaliformes	2	42	3.2	59.2

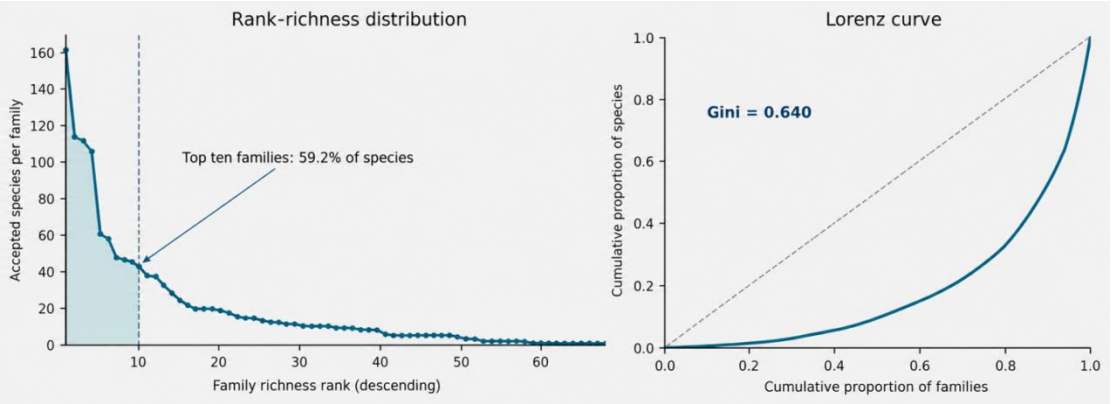

Figure 1: Uneven distribution of accepted species among 68 families in the September 2026 Catalog extract. Left: ranked family richness, with the ten largest families highlighted. Right: Lorenz curve and Gini coefficient. Family richness is taxonomic abundance, not local ecological abundance.

Association between family genus and species counts

The number of genera and accepted species per family covaries strongly on the untransformed scale (Pearson r=0.886). The rank association is more moderate (Spearman ρ=0.704), as is the log–log Pearson association (r=0.756), indicating that large families affect the raw linear association disproportionately. Families with high species-per-genus ratios include Squatinidae (24 species; one genus), Chimaeridae (47; two genera) and Etmopteridae (57; four genera). The overall ratio is 6.11 species per genus, but this aggregate is not interchangeable with the unweighted average across families. Replacing the Mitsukurinidae value of two genera with one changes Spearman ρ from 0.704 to 0.722, while the source data remain unmodified.

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Differences among the 2015, 2023 and 2026 inventories

Relative to the inventory with a 7 November 2015 cutoff (Weigmann, 2016), the 2026 extract contains 143 more recognized species (1,331 versus 1,188; +12.0%), 19 more genera (218 versus 199; +9.5%) and seven more families (68 versus 61). Species-count differences are +59 in sharks, +72 in batoids and +12 in chimaeras. Changes in order number (16 in the historical checklist versus 14 in the 2026 extract) should not be interpreted as lineage losses, since higher-level classification has changed substantially.

Relative to the 31 December 2023 classification, the net increase is 65 species (1,266 to 1,331; +5.1%), three genera (215 to 218) and one family (67 to 68). Sharks increased by 22 species (546 to 568), batoids by 35 (667 to 702), and chimaeras by eight (53 to 61). Among 67 family names shared between the benchmarks, 20 show higher counts, three lower counts and 44 no change, yielding a net +60 species across matched families. Dichichthyidae (five species in the September 2026 extract) accounts for the remaining five species in the arithmetic comparison. Species-by-species provenance cannot be inferred from these totals. Family richness rankings are remarkably similar across the two classifications (Spearman ρ=0.995); species concentration likewise differs little (family-level Gini=0.638 in 2023 and 0.640 in 2026) (Table 4; Fig. 2).

able 4: Selected family-level changes in recognized species between the 31 December 2023 classification and the 21 September 2026 Catalog extract. Changes are net differences, not counts of newly described species.

Family	2023 species	2026 species	Net Δ
Dasyatidae	93	105	+12
Etmopteridae	50	57	+7
Dichichthyidae	Not listed	5	New family[1]
Potamotrygonidae	40	45	+5
Chimaeridae	42	47	+5
Carcharhinidae	56	60	+4
Sphyrnidae	9	12	+3
Torpedinidae	18	21	+3
Rajidae	159	162	+3
Arhynchobatidae	108	111	+3
Urotrygonidae	16	19	+3
Rhinochimaeridae	8	11	+3
Squalidae	40	42	+2
Narcinidae	30	32	+2
Glaucostegidae	7	9	+2
Anacanthobatidae	16	14	-2
Gymnuridae	12	14	+2
Atelomycteridae	14	13	-1
Proscylliidae	7	6	-1

[1] Dichichthyidae contains five accepted species in 2026; a new family does not imply that all included species were newly described since the benchmark.

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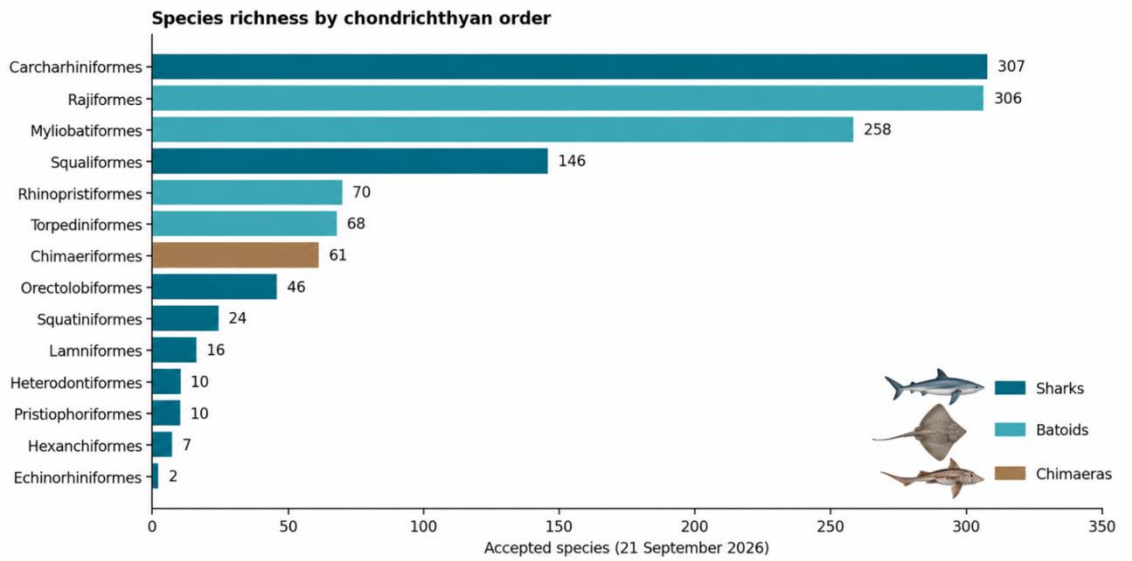

Figure 2: Number of accepted species assigned to the 14 orders of living Chondrichthyes in the 21 September 2026 Catalog extract. Shark, batoid and chimaera groupings are for descriptive visualization.

Data-integrity findings

All family totals reconciled with their respective orders and with the overall 1,331-species census. The eight subfamily rows likewise reconciled with their parent families: Triakidae, nine genera/46 species; Dasyatidae, 19/105; and Potamotrygonidae, five/45. No duplicate family names or missing family count values were detected. Mitsukurinidae is reported as two valid genera but one valid species in the extract, consistent with the Catalog's indexed family-statistics table. The apparent discrepancy could reflect the inclusion or treatment of fossil-related genus names; that possibility must be checked against the individual Catalog genus records before calling the entry an error or changing the accepted-genus total. The published 2023 comparison listed one genus and one species (Weigmann *et al*., 2024).

Discussion

The present study provides a dated, quantitative account of the taxonomic composition and family-level richness structure of living Chondrichthyes recognized in *Eschmeyer's Catalog of Fishes* on 21 September 2026. Beyond updating the numbers of accepted species, genera, families, and orders, the analysis shows that recognized richness is unevenly distributed among major lineages and taxonomic ranks. These patterns are informative for comparative systematics, historical inventory assessment, and conservation data management, but they are conditional on the classification and taxonomic decisions adopted by the source. The following discussion therefore distinguishes the measurable properties of an accepted taxonomic inventory from hypotheses about evolutionary diversification, ecological diversity, and extinction risk that require additional evidence.

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Strong taxonomic concentration is a central property of the accepted classification

The family-level census reveals a taxonomic structure characterized by a small number of exceptionally species-rich families and numerous species-poor families. The ten richest families collectively account for 59.2% of accepted species, while family-level species richness has a Gini coefficient of approximately 0.64. Shannon entropy expressed as its exponential corresponds to 31.9 equally represented families, compared with the 68 recognized families. Genus richness is less concentrated among families (Gini = 0.48). Considered together, these complementary statistics characterize the uneven allocation of accepted species and genera among named families more fully than the class-wide total alone. They do not establish differences in rates of speciation, extinction, or phenotypic evolution. The contrast between genus and species concentration is particularly relevant to comparative systematics. Some families combine high species richness with numerous recognized genera, whereas others contain many accepted species within comparatively few genera. Such contrasts may reflect differences in lineage age, historical diversification, species-delimitation practices, generic circumscription, and the intensity of taxonomic investigation; aggregate counts cannot separate these explanations. Reviews of shark and ray diversification emphasize the multiplicity of potential evolutionary drivers and the dependence of inferred patterns on analytical choices (Gayford and Jambura, 2025). Moreover, fossil-based reconstructions that explicitly address sampling variation can yield diversity trajectories that differ from those suggested by uncorrected or higher-rank counts (Gardiner *et al*., 2026). Consequently, neither the observed inequality nor correlations between nested taxonomic counts should be interpreted as evidence of particular diversification mechanisms without dated phylogenies and appropriate models of taxonomic and fossil sampling.

Batoid richness and the importance of taxonomic rank

Batoids account for 702 accepted species (52.7%) in the September 2026 extract, compared with 568 sharks (42.7%) and 61 chimaeras (4.6%). Despite their species-level predominance, batoids comprise slightly fewer accepted genera than sharks (105 versus 107), and sharks also exceed batoids in recognized family number. This pattern is consistent with earlier accounts emphasizing the exceptional species richness of skates and rays (Weigmann, 2016; Weigmann *et al*., 2024), while demonstrating that the ranking of major lineages depends on whether species, genera, or families are compared. Differences in the circumscription of genera, families, and orders among successive classifications further complicate comparisons at higher taxonomic ranks. Species richness also represents only one

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dimension of biodiversity. For example, de Oliveira *et al*. (2026) compared taxonomic, functional, and phylogenetic diversity of marine elasmobranchs across major fishing areas and examined the potential consequences of species loss. Such multidimensional analyses address questions that cannot be resolved from family-level species totals, including whether losses of equally numerous species represent similar losses of evolutionary history or functional attributes. The present results therefore provide an inventory-level complement to, rather than a substitute for, spatial, trait-based, and phylogenetic assessments. Historical comparisons of batoid and shark richness should prioritize reconciled species-level records and clearly state the classifications used.

Net inventory growth is not synonymous with taxonomic discovery

The September 2026 inventory exceeds the 1,188 species reported for 7 November 2015 by 143 species (Weigmann, 2016) and the end-of-2023 benchmark by 65 species (Weigmann *et al*., 2024). These are differences between accepted inventory totals, not direct counts of species newly described during the corresponding periods. New descriptions can increase the number of accepted species, but taxonomic resurrection, revised synonymy, reassignment, and differences in inclusion rules may also affect the total. Conversely, synonymization may offset additions. A complete explanation of the net changes therefore requires tracking individual taxon names and their accepted statuses across inventory versions. The recognition of Dichichthyidae illustrates the distinction between species discovery and higher-rank restructuring. White *et al*. (2024) resurrected *Dichichthys* for species previously placed in *Parmaturus*, established Dichichthyidae, and described a new species. Thus, a five-species family appearing in the 2026 inventory should not be interpreted as the discovery of five species during the comparison period. Likewise, the family-level changes reported here are uneven: Dasyatidae increased by 12 accepted species, Etmopteridae by seven, and Chimaeridae and Potamotrygonidae by five each relative to the end-of-2023 benchmark. Such net differences identify lineages meriting further examination but cannot independently distinguish newly described taxa from revised taxonomic treatments. The increase in recognized chimaera richness is similarly a change in accepted inventory size, not direct evidence of a higher rate of biological diversification or intensified deep-sea exploration. Explicit species-level reconciliation is essential before calculating valid description trajectories or attributing net gains to particular taxonomic events.

Relevance to conservation assessments

Stable, transparent, and versioned taxonomic information is indispensable for conservation assessment and fisheries reporting because species names and concepts determine which

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biological entities are linked to occurrence records, exploitation data, and Red List assessments. The global reassessment by Dulvy *et al*. (2021) demonstrated the high extinction risk faced by sharks and rays under fishing pressure. More recent analyses have documented worsening extinction-risk indicators and loss of ecological function, while a broader review has highlighted persistent geographic and taxonomic data gaps and the need for species-level monitoring and conservation action (Dulvy *et al*., 2024, 2026). Studies of deepwater sharks and rays further illustrate the importance of accurately resolving poorly known and heavily exploited taxa (Finucci *et al*., 2024). These findings establish the conservation significance of reliable taxonomic infrastructure but do not imply that the families with the greatest numbers of accepted species necessarily have the highest proportional extinction risk. Taxonomic revision creates particular challenges when accepted names, synonymies, and species concepts differ among data systems. Finucci *et al*. (2026) emphasize the importance of taxonomic information in the history and practice of chondrichthyan Red List assessments; a wider review of assessment practice likewise identifies taxonomy as a recurring source of difficulty for Red List specialists (Garnett *et al*., 2026). The present family-level dataset identifies where accepted richness is concentrated and where family totals differ among inventories, but it cannot determine which individual taxa are unassessed, assessed under alternative names, or affected by revised species limits. A reproducible crosswalk among accepted Catalog names, authorship and original descriptions, synonymies, and dated IUCN assessment identifiers would be necessary to identify genuine assessment gaps. The conservation concern surrounding wedge fishes and giant guitarfishes illustrates the practical importance of reliable species identification and taxonomic recognition in vulnerable lineages (Kyne *et al*., 2020).

Accordingly, conservation interpretation should be based on matched species records rather than comparisons between independently compiled totals. Even when two databases report similar species numbers, unmatched synonymies, taxonomic splits, or different assessment dates may obscure biologically important discrepancies. The 2026 inventory is best regarded as a taxonomic reference point for constructing such comparisons, rather than as an independent estimate of extinction risk.

Beyond their exploitation in commercial fisheries, sharks and rays are also utilized in the ornamental aquarium trade and displayed in public aquaria, representing an additional dimension of their economic, educational, and conservation significance. Public aquaria maintain diverse elasmobranch assemblages for exhibition, environmental education, research, and ex situ conservation. A survey of European zoo and aquarium

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collections documented 102 chondrichthyan species, of which 47.1% had reproduced in captivity, highlighting both the diversity maintained in these institutions and the potential for captive breeding programs to reduce dependence on wild populations (Janse *et al*., 2017). Furthermore, aquarium-based research has contributed substantially to understanding elasmobranch reproductive biology, including reproductive cycles, parthenogenesis, and assisted reproductive techniques (Feldheim *et al*., 2022). Nevertheless, the conservation sustainability of maintaining sharks and rays in captivity remains an important concern, particularly for threatened species that depend on continued collection from the wild. Buckley *et al*. (2018) emphasized the need for species-specific sustainability assessments, while Carlisle *et al*. (2026) highlighted the biological, ethical, and management concerns associated with the international aquarium trade of the globally threatened sand tiger shark, *Carcharias taurus*.

Freshwater stingrays, particularly members of the family Potamotrygonidae, constitute another distinctive component of the ornamental fish trade. South American river stingrays of the genus *Potamotrygon* are maintained and commercially bred for the international aquarium market. However, their movement beyond native ranges introduces additional conservation and biosecurity concerns. Jerikho *et al*. (2023) documented the commercial trade and cultivation of South American freshwater stingrays in Indonesia and reported evidence consistent with their establishment in the Brantas River, Java, illustrating the potential for ornamental trade to facilitate biological invasions. These findings demonstrate that the conservation implications of ornamental exploitation extend beyond harvesting pressure to include animal welfare, species identification, trade regulation, and the ecological consequences of non-native introductions. For the present study, the taxonomic inventory provides a reference for identifying potentially relevant lineages, but the extent of ornamental use, numbers of traded species, and associated conservation risks cannot be quantified without species-specific trade, husbandry, and conservation-assessment data.

Quality control and interpretation of genus totals

The apparent counting of two genera but only one living accepted species in Mitsukurinidae highlights a definitional problem: a catalogue count of taxonomically recognized genera may not be identical to a count of genera represented by at least one accepted extant species. Fossil-associated generic names, including *Scapanorhynchus*, offer a possible explanation, but the underlying genus entries must be checked before the discrepancy can be assigned to a particular name or cataloguing rule. In a sensitivity analysis, reducing the Mitsukurinidae genus count by one decreases the class-

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wide genus total from 218 to 217 and changes the accepted species-per-genus ratio only from 6.11 to 6.13. The principal patterns of taxonomic concentration are therefore insensitive to this single-count adjustment. Nevertheless, the primary results appropriately retain the source value, with the alternative reported transparently rather than substituted without documented justification.

Limitations and future analytical directions

Several methodological and conceptual limitations qualify the interpretation of this study. First, the underlying dataset is a dated extract of aggregate family-level taxonomic counts, not a species-level record of taxonomic acts; the acceptance history, synonymy, year of description, and distribution of individual species cannot be independently reconstructed from it. Second, the dataset was checked for internal consistency and selectively compared with the September 2026 Catalog display, but complete independent verification against a separately archived official species-by-family table was not undertaken. Third, the 2015, 2023, and 2026 inventories represent successive, non-independent summaries compiled under related but not identical taxonomic concepts and classification schemes. Their differences should therefore be interpreted as net changes in recognized inventories rather than statistically independent observations of biodiversity change. Fourth, Linnaean ranks are partly conventional, and their constituent lineages share evolutionary history. Measures such as the Gini coefficient and Shannon entropy describe the allocation of accepted taxa among named categories, not ecological alpha diversity, phylogenetic diversity, or rates of evolutionary diversification. The sensitivity of reconstructions to sampling and analytical assumptions, emphasized by Gardiner *et al*. (2026), further cautions against assigning evolutionary causes to richness patterns alone. Finally, phylogenomic hypotheses concerning relationships among major elasmobranch lineages, including shark monophyly, remain subject to reassessment; relevant analyses include studies disseminated as preprints (Huang *et al*., 2025; Brownstein and Near, 2026). Such uncertainty does not invalidate the inventory-level findings, but it affects any attempt to interpret the named orders or families as fixed, comparable evolutionary units.

A logical next phase would be a documented, species-by-species reconciliation of historical and current catalogs, retaining stable identifiers wherever possible and classifying each observed change as a new description, resurrection, synonymization, reassignment, or correction. This would permit separate estimation of new-species description rates and net changes in accepted inventories, which are not equivalent. Linking harmonized names to the IUCN Red List and to habitat, regional distribution, and publication-year information would enable reproducible identification of

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assessment gaps and comparisons of taxonomic coverage (Garnett *et al*., 2026). Extending the database with occurrence records, functional traits, and dated phylogenetic information would also allow analyses of complementary biodiversity dimensions, as demonstrated for marine elasmobranchs by de Oliveira *et al*. (2026). Where appropriate, sampling-aware fossil and phylogenetic models could then test hypotheses about the processes underlying extant family-richness disparities (Gardiner *et al*., 2026). These extensions require different underlying observations and analytical assumptions and should be treated as a distinct research phase rather than inferred retrospectively from the aggregate census presented here.

Conclusions

The present study provides an updated quantitative assessment of the taxonomic composition and diversity structure of living Chondrichthyes based on Eschmeyer's Catalog of Fishes as of 21 September 2026. The inventory comprises 1,331 accepted species distributed among 218 counted genera, 68 families, and 14 orders. Taxonomic richness is markedly uneven, with batoids accounting for 52.7% of all accepted species, the three most species-rich orders collectively representing 65.4%, and the ten richest families encompassing 59.2%. The pronounced concentration of species among families (Gini coefficient=0.640), together with the comparatively more even distribution of genera, highlights substantial heterogeneity in the structure of the accepted classification. Although family-level richness rankings remain broadly consistent with the end-of-2023 benchmark, the net increase of 65 accepted species reflects changes in the recognized taxonomic inventory rather than exclusively new species discoveries. These findings demonstrate the value of quantitative measures in characterizing taxonomic structure beyond conventional species counts. They also emphasize the importance of maintaining transparent, date-specific, and systematically validated taxonomic inventories as reference points for biodiversity research and conservation assessments. Future species-level reconciliation of historical and contemporary classifications, integrated with phylogenetic information, geographic distributions, and conservation assessments, will be essential for distinguishing taxonomic revisions from genuine discovery patterns and for evaluating their broader evolutionary and conservation implications.

Data and code availability

The taxonomic data analyzed in this study were derived from a dated extract of *Eschmeyer's Catalog of Fishes* (21 September 2026), maintained by the California Academy of Sciences and publicly accessible at https://research.calacademy.org/research/ichthyology/catalog/fishcatmain.asp. The accompanying Microsoft Excel workbook contains the species and genus counts for all 68 recognized

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families, order-level summaries, comparisons with the end-of-2023 taxonomic inventory, and internal validation checks. Data processing, statistical analyses, and graphical summaries were performed using Microsoft Excel and R statistical software. The dated source dataset, accompanying Excel workbook, and R scripts used to generate the reported results are available from the author upon reasonable request. Because the online Catalog is periodically updated, the dated extract provides the reference dataset necessary for reproducing the analyses.

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Ethics approval and consent to participate

This study was based exclusively on published taxonomic information and publicly available secondary data. No live animals or human participants were involved, and no experimental procedures were conducted. Therefore, ethical approval and informed consent were not required.

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Declaration of competing interests

The author declares that there are no financial or non-financial competing interests that could have influenced the research presented in this manuscript.

Declaration of generative AI and AI-assisted technologies

During the preparation of this manuscript, the author used ChatGPT (OpenAI) to assist with scientific language editing, improving the clarity and organization of the text, and refining graphical presentations. AI-assisted outputs were subject to author review and revision. The author retains full responsibility for the accuracy and integrity of the taxonomic data, statistical analyses, references, scientific interpretations, and final published content. AI was also used to enhance the visual presentation of figures.

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