Supporting Information

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SI Materials and Methods

Brain Organization and Structural Delineation. Within the chondrichthyan dataset, the caudal boundary of the telencephalon was set as a plane extending from the rostral edge of the optic chasm. The caudal boundary of the diencephalon was deemed to be a diagonal plane extending from the rostral pole of the optic tectum to the caudal pole of the infundibulum, and the mesencephalon was considered to include the tectum and tegmentum. The cerebellum was taken to be all of the tissue lying above the upper leaf of the cerebellar auricle, whereas the medulla extended from the lower leaf (including the dorsal and medial octavolateral nuclei) to the caudal boundary of this structure, which was set at the level of the first complete cervical spinal nerve, based on divisions reported by Northcutt (1, 2) and Yopak et al. (3). Mass data were compiled for 51 chondrichthyan species across 22 families for which data on brain size and brain organization were available in the literature that overlapped with species for which we had mass data on the olfactory bulbs (*Materials and Methods*). Please note that six species names have changed since the publication of those previous studies. Brain organization data published for *Centroscymnus owstoni*, *Galeus boardmani*, *Carcharhinus falciformes*, *Rhinobatos typus*, *Okamejei lemprieri*, *Dasyatis kuhlii* (3–5) are referred to herein as data for *Centroscymnus owstonii*, *Figaro boardmani*, *Carcharhinus falciformis*, *Glaucostegus typus*, *Dentiraja lemprieri*, and *Neotrygon kuhlii*, respectively (6–8).

Brain mass and brain structure data for 160 mammalian species were compiled from reports of Stephen et al. (9), Baron et al. (10), and Reep et al. (11). To allow comparison of the mammalian and chondrichthyan brain datasets, the following structural delineations for analogous mammalian brain areas were used. Similar to the regional boundaries for the chondrichthyan brain structures, the olfactory bulb included the olfactory tract. The mammalian "telencephalon" included summed mass data from the hippocampus, septum, subicular cortex, striatum, and neocortex. The rostral boundary of the diencephalon was set where the third ventricle and anterior commisure were present together, and did not include the optic nerve, pituitary, or third ventricle. The mesencephalon, or midbrain, comprised the visual cortex and the cerebral peduncle. The cerebellum included all tissue of the cerebellar cortex. The rostral boundary of the medulla was set at cranial nerve VII, and the caudal boundary was set at the appearance of cells of the inferior olive (11, 12).

Phylogenetic Information. Independent contrasts were calculated using our own custom-written software and phylogenies of Shirai (13, 14) and McEachran and Aschliman (15), with additional information for orectolobiformes (16), lamniformes (17), carcharhiniformes (18), carcharhinids and sphyrnids (19), chimaeriformes (20) and batoids (21) (Figs. S1 and S2). Because the branch lengths for many taxa are unknown, arbitrary branch lengths were assigned (22).

Controversy surrounds the evolutionary relationships among various groups within the chondrichthyes, particularly the positions of members of *Batoidea* (15, 23, 24). However, if further information changes the phylogenies used here, then moving the batoids changes one contrast. Errors in trees tends to decrease relationships between variables; thus, true relationships between variables are likely at least as high as stated here.

Relative Versus Absolute Sizes When Comparing Brain Structures. For all of the analyses presented here, absolute sizes of the brain and its corresponding components were used. We chose to control for variables like brain size by standard methods involving regression and partial correlation, rather than expressing structures as a percentage of brain size. The theoretical ideal would be to control for brain size by studying many species with the same brain size, which is not possible when dealing with large comparative datasets. It is well known that given reasonable assumptions, this ideal is approximated by regression and partial correlation methods, whereas percentages can obscure simple relationships and give very different results.

SI Discussion

Factor Analysis of Data on Brains of Sharks and Their Relatives. Factor analysis on the brains of chondrichthyans yielded eigenvalues, the first five of which were 5.7323, 0.3998, 0.1477, 0.1176, and 0.0449. Factor analysts like to find a "simple structure" pattern, in which each entry in the pattern matrix is either high or low. This matrix reflects a high degree of simple structure; with only one exception, every entry in the matrix is either >0.6 or <0.05 in absolute value. The single exception is the loading of the medulla on factor 1. Ignoring this, the telencephalon, diencephalon, and cerebellum load highly on factor 1, the olfactory bulbs load highly on factor 2, and the mesencephalon and medulla load highly on factor 3.

Table S7 presents correlations among oblique factors. The correlations among the factors are what we would expect, with all being high but those involving factor 2 (the olfactory factor) being the lowest by far.

Hyperallometry. Here we report the results of two different analyses on hyperallometry, each analysis performed very differently with corroborating results. The first analysis used species values, and the second used contrast values. The first used 81 species, whereas the second used just 51. In the first analysis, the measure of relative hyperallometry was the regression slope predicting the logged structure size from the logged size of the nonolfactory brain. In the second analysis, the measure was the structure's mean contrast value. The results demonstrate that the five nonolfactory structures fall in the exact same order in the two analyses (Table S1). For those five structures, the correlation between the two result columns was 0.942. Thus, the results are essentially the same by the two methods. Table S2 gives the results of significance tests testing each structure for hyperallometry against every other structure.

Corrections for multiple comparisons are usually done when just a few tests are significant out of many and there is a serious possibility that those tests might have turned out to be significant just by chance (25). That is obviously not the case here; out of 30 tests, two had $P < 0.00006$ and five more had $P < 0.005$ (Table S2). That is far beyond the number that would be expected by chance. Furthermore, the significant P values are not scattered randomly, as might be expected had they occurred by chance. As we noted, six of them occurred in a 3×2 block of six cells, and most of the rest occurred in a single row involving the olfactory bulbs; three of the five entries in that row were significant.

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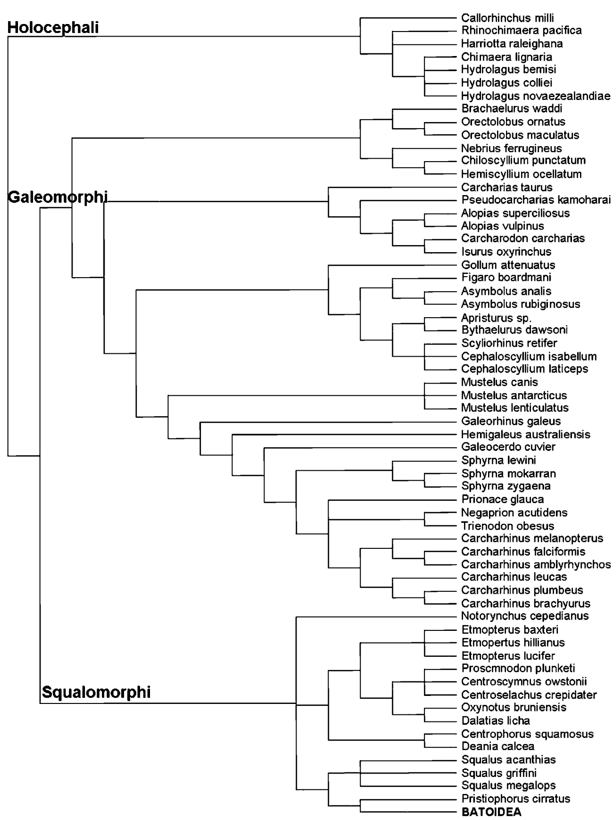

Fig. S1. A phylogenetic tree of 57 shark and holocephalan species used in this study, indicating the placement of the batoids on the dendrogram. The relationships between species are based primarily on the phylogeny of Shirai (13, 14), with additional information from Compagno (18), Martin et al. (17), Naylor (19), Didier (20), and Goto (16).

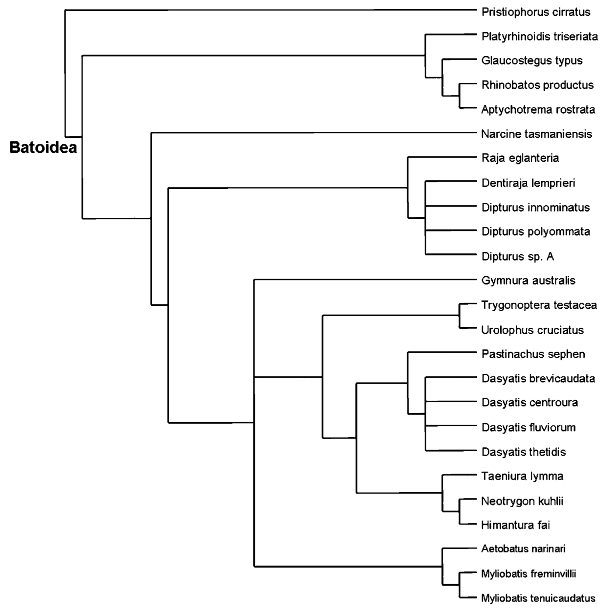

Fig. S2. A phylogenetic tree of the 24 batoid species used in this study. The relationships between major groups are based primarily on the phylogeny of Shirai (13, 14), whereas relationships within families are based on the phylogeny of McEachran and Aschliman (15), with additional information from Rosenberger (21).

Table S1. Slope relative to whole brain and mean absolute contrast value for each brain structure, where available

	Slopes	Mean absolute contrast
Body	–	1.50
Olfactory bulbs	–	0.95
Telencephalon	1.14	0.85
Cerebellum	1.02	0.84
Brain (excluding olf)	1.00	0.77
Diencephalon	0.92	0.75
Medulla	0.78	0.64
Mesencephalon	0.86	0.62

Table S2. One-tailed *P* values, showing the significance of the Wilcoxon rank sums

	Telencephalon	Diencephalon	Cerebellum	Mesencephalon	Medulla	Olfactory bulbs
Telencephalon	0	0.02305	0.309297	0.000057	0.002158	0.772606
Diencephalon	0.977486	0	0.873459	0.004558	0.019041	0.993893
Cerebellum	0.694075	0.128562	0	0.000244	0.00155	0.877435
Mesencephalon	0.999946	0.995576	0.999765	0	0.645524	0.999948
Medulla	0.997978	0.981417	0.998502	0.358047	0	0.999677
Olfactory bulbs	0.230305	0.006284	0.124542	0.000054	0.000336	0

Low values suggest that the structure on the left is hyperallometric to the structure on the top. The telencephalon, diencephalon, and cerebellum are all hyperallometric relative to the mesencephalon and medulla oblongata. Tests within those two blocks are all nonsignificant, except those between the telencephalon and diencephalon. The olfactory bulbs are significantly hyperallometric relative to the diencephalon, mesencephalon, and medulla, but not to the telencephalon and cerebellum.

Table S3. Correlations among logged structure sizes from 51 chondrichthyan species, including SDs of logged structure sizes

	Body	Forebrain + Cer	Core	Olfactory bulbs	SD
Body	1	0.82	0.87	0.81	2.1425
Forebrain + cer	0.82	1	0.94	0.87	1.4903
Core	0.89	0.94	1	0.86	1.1209
Olfactory bulbs	0.81	0.87	0.86	1	1.3159

"Forebrain + cer" includes the telencephalon, diencephalon, and cerebellum, and "core" includes the mesencephalon and medulla. Sizes were acquired by adding the unlogged mass of all components, after which the sum was logged. Among the forebrain + cer, core, and olfactory bulbs, core was most highly correlated with body size. Core has the smallest SD.

Table S4. Mass data for the olfactory bulbs for 36 sharks and 15 batoid species

Order	Family	Species	Olfactory bulb mass (×2), g
Sharks			
Squaliformes	Squalidae	*Squalus acanthias*	0.2322*
	Centrophoridae	*Centrophorus squamosus*	0.30
		Deania calcea	0.56
	Etmopteridae	*Etmopterus baxteri*	0.41
		Etmopterus lucifer	0.12
	Somniosidae	*Centroscymnus owstonii*	0.47
		Centroselachus crepidater	0.44
		Proscymnodon plunketi	0.72
	Dalatiidae	*Dalatias licha*	0.07
Orectolobiformes		*Orectolobus ornatus*	0.11
		Chiloscyllium punctatum	0.26
		Hemiscyllium ocellatum	0.16
		Nebrius ferrugineus	0.79
Lamniformes		*Alopias superciliosus*	0.84
		Pseudocarcharias kamoharai	0.27
		Carcharodon carcharias	5.53
		Carcharias taurus	1.87
		Isurus oxyrinchus	0.54
Carcharhiniformes	Scyliorhinidae	*Apristurus* sp.	0.45
		Asymbolus analis	0.18
		Asymbolus rubiginosus	0.14
		Bythaelurus dawsoni	0.10
		Figaro boardmani	0.16
	Pseudotriakidae	*Gollum attenuatus*	0.36
	Carcharhinidae	*Carcharhinus amblyrhynchos*	1.39
		Carcharhinus falciformis	1.85
		Carcharhinus leucas	3.06
		Carcharhinus melanopterus	1.14
		Carcharhinus plumbeus	1.27
		Galeocerdo cuvier	7.36
		Negaprion acutidens	0.33
		Prionace glauca	3.38
		Triaenodon obesus	0.49
	Sphyrnidae	*Sphyrna lewini*	2.91
		Sphyrna mokarran	10.60
		Sphyrna zygaena	7.41
Batoids			
Rajiformes	Rajidae	*Dipturus polyommata*	0.11
		Raja eglanteria	0.0498*
	Rhinobatidae	*Aptychotrema rostrata*	0.09
		Rhinobatos productus	0.4555*
		Glaucostegus typus	1.59
	Platyrhinidae	*Platyrhinoidis triseriata*	0.0959*
	Dasyatidae	*Dasyatis centroura*	1.5888*
		Dasyatis fluviorum	0.74
		Neotrygon kuhlii	0.53
		Himantura fai	1.69
		Pastinachus sephen	1.20
		Taeniura lymma	0.13
	Myliobatidae	*Aetobatos narinari*	1.00
		Myliobatis freminvillii	1.5708*
	Gymnuridae	*Gymnura australis*	0.20

*Data obtained from Northcutt (1, 5).

Table S5. Species and tree from independent contrasts analysis

Abbreviation	Species	Taxonomic tree
OO	*Orectolobus ornatus*	1 1 1
NF	*Nebrius ferrugineus*	1 1 2 1
CP	*Chiloscyllium punctatum*	1 1 2 2 1
HO	*Hemiscyllium ocellatum*	1 1 2 2 2
CT	*Carcharias taurus*	1 2 1 1
PK	*Pseudocarcharias kamoharai*	1 2 1 2 1
AS	*Alopias superciliosus*	1 2 1 2 2 1
CC	*Carcharodon carcharias*	1 2 1 2 2 2 1
IO	*Isurus oxyrinchus*	1 2 1 2 2 2 2
GA	*Gollum attenuatus*	1 2 2 1 1
GB	*Figaro boardmani*	1 2 2 1 2 1 1
AA	*Asymbolus analis*	1 2 2 1 2 1 2 1
ARU	*Aptychotrema rostrata*	1 2 2 1 2 1 2 2
AP	*Apristurus* sp.	1 2 2 1 2 2 1
BD	*Halaelurus dawsoni*	1 2 2 1 2 2 2
GC	*Galeocerdo cuvier*	1 2 2 2 1
SL	*Sphyrna lewini*	1 2 2 2 2 1 1
SMo	*Sphyrna mokarran*	1 2 2 2 2 1 2 1
SZ	*Sphyrna zygaena*	1 2 2 2 2 1 2 2
PG	*Prionace glauca*	1 2 2 2 2 2 1 1
NA	*Negaprion acutidens*	1 2 2 2 2 2 1 2 1
TO	*Triaenodon obesus*	1 2 2 2 2 2 1 2 2
CMe	*Carcharhinus melanopterus*	1 2 2 2 2 2 2 1 1
CF	*Carcharhinus falciformis*	1 2 2 2 2 2 2 1 2 1
CA	*Carcharhinus amblyrhynchos*	1 2 2 2 2 2 2 1 2 2
CLe	*Carcharhinus leucas*	1 2 2 2 2 2 2 2 1
CPl	*Carcharhinus plumbeus*	1 2 2 2 2 2 2 2 2
EB	*Etmopterus baxteri*	2 1 1 1 1
EL	*Etmopterus lucifer*	2 1 1 1 2
PP	*Proscymnodon plunketi*	2 1 1 2 1 1
CO	*Centroscymnus owstonii*	2 1 1 2 1 2 1
CCr	*Centroselachus crepidater*	2 1 1 2 1 2 2
DLi	*Dalatias licha*	2 1 1 2 2
CS	*Centrophorus squamosus*	2 1 2 1
DC	*Deania calcea*	2 1 2 2
SA	*Squalus acanthias*	2 2 1
PT	*Platyrhinoidis triseriata*	2 2 2 1 1
RT	*Glaucostegus typus*	2 2 2 1 2 1
RPr	*Rhinobatos productus*	2 2 2 1 2 2 1
AR	*Asymbolus rubiginosus*	2 2 2 1 2 2 2
RE	*Raja eglanteria*	2 2 2 2 1 1
DP	*Dipturus polyommata*	2 2 2 2 1 2
GAU	*Gymnura australis*	2 2 2 2 2 1 1
PS	*Pastinachus sephen*	2 2 2 2 2 1 2 1 1
DCe	*Dasyatis centroura*	2 2 2 2 2 1 2 1 2 1
DF	*Dasyatis fluviorum*	2 2 2 2 2 1 2 1 2 2
TL	*Taeniura lymma*	2 2 2 2 2 1 2 2 1
DK	*Neotrygon kuhlii*	2 2 2 2 2 1 2 2 2 1
HF	*Himantura fai*	2 2 2 2 2 1 2 2 2 2
AN	*Aetobatus narinari*	2 2 2 2 2 2 1
MF	*Myliobatis freminvillii*	2 2 2 2 2 2 2

For dendrograms of phylogenetics relationships, see Figs. S1 and S2.

Table S6. Rotated pattern matrix (OBLIMIN, $\gamma = 0.0$)

	Factor 1	Factor 2	Factor 3
Olf	0.0148	0.0055	1.1655
Tel	1.087	−0.0048	0.0213
Die	0.8978	0.0496	0.0323
Cer	1.0946	−0.0058	0.0149
Mes	−0.0507	0.8712	0.0494
Med	0.292	0.6267	−0.0232

Table S7. Correlations among oblique factors

	Factor 1	Factor 2	Factor 3
Factor 1	1.0000	—	—
Factor 2	0.9051	1.0000	—
Factor 3	0.7913	0.7523	1.0000