Table S1: Characteristics of the fish individuals used in this study

sample_id	Species	Standard length (mm)	Body mass (g)	Gut length (mm)	Relative gut length	Diet category
F_F268	Boops_boops	175	98	329	2.14	Selective_plankton_feeding
F_F272	Boops_boops	140	27	342	2.44	Selective_plankton_feeding
F_F275	Boops_boops	171	48	315	1.84	Selective_plankton_feeding
F_F264	Diplodus_annularis	156	160	166	1.02	Hunting_macrofauna
F_F267	Diplodus_annularis	160	143	176	1.10	Hunting_macrofauna
F_F319	Diplodus_annularis	166	211	155	0.94	Hunting_macrofauna
F_F218	Diplodus_puntazzo	238	223	194	0.82	Hunting_macrofauna
F_F298	Diplodus_puntazzo	191	254	281	1.47	Hunting_macrofauna
F_F084	Diplodus_sargus	200	299	251	1.26	Hunting_macrofauna
F_F214	Diplodus_sargus	170	210	141	0.83	Hunting_macrofauna
F_F519	Diplodus_sargus	250	469	196	0.80	Hunting_macrofauna
F_F219	Diplodus_vulgaris	140	44	197	1.04	Hunting_macrofauna
F_F234	Diplodus_vulgaris	174	200	227	1.31	Hunting_macrofauna
F F266	Diplodus vulgaris	200	293	178	0.89	Hunting macrofauna
F F283	Diplodus vulgaris	192	343	238	1.24	Hunting macrofauna
F F291	Diplodus vulgaris	212	367	157	0.74	Hunting macrofauna
F F293	Diplodus vulgaris	202	334	198	0.98	Hunting macrofauna
F F310	Diplodus vulgaris	184	154	205	1.12	Hunting macrofauna
F F311	Diplodus vulgaris	171	233	176	1.03	Hunting macrofauna
F F316	Lithognathus mormyrus	223	127	120	0.54	Hunting macrofauna
F F318	Lithognathus mormyrus	236	335	183	0.78	Hunting macrofauna
F F323	Lithognathus mormyrus	282	476	143	0.62	Hunting macrofauna
F F468	Lithognathus mormyrus	235	321	124	0.53	Hunting macrofauna
F F324	Oblada melanura	236	350	243	1.03	Hunting macrofauna
F F520	Oblada melanura	215	251	329	1.53	Hunting macrofauna
F F522	Oblada melanura	200	196	286	1.28	Hunting macrofauna
F F325	Pagellus acarne	175	135	110	0.63	Hunting macrofauna
F F475	Pagellus acarne	185	145	110	0.63	Hunting macrofauna
F_F476	Pagellus_acarne	180	143	110	0.63	Hunting_macrofauna
F F487	Pagellus acarne	130	54	110	0.63	Hunting macrofauna
F F200	Pagellus erythrinus	168	100	107	0.64	Hunting macrofauna
F_F201	Pagellus_erythrinus	185	131	138	0.75	Hunting_macrofauna
F_F202	Pagellus_erythrinus	165	100	103	0.59	Hunting_macrofauna
F_F238	Pagellus_erythrinus	160	116	64	0.40	Hunting_macrofauna
F F207	Pagrus pagrus	186	151	180	0.88	Hunting macrofauna
F_F215	Pagrus_pagrus	205	261	180	0.88	Hunting_macrofauna
F F521	Pagrus pagrus	190	209	180	0.88	Hunting macrofauna
F F523	Pagrus pagrus	155	114	180	0.88	Hunting macrofauna
F F104	Sarpa salpa	236	431	706	2.99	Grazing aquatic plants
F F116	Sarpa salpa	203	203	554	2.73	Grazing aquatic plants
F F121	Sarpa salpa	246	453	474	1.93	Grazing aquatic plants
F F252	Sarpa salpa	283	523	440	1.56	Grazing aquatic plants
F F256	Sarpa salpa	251	411	783	3.12	Grazing aquatic plants
F F216	Sparus aurata	220	288	125	0.57	Hunting macrofauna
F F232	Sparus [–] aurata	213	286	138	0.65	Hunting macrofauna
F F309	Sparus [–] aurata	161	102	194	1.21	Hunting macrofauna
F F313	Sparus aurata	222	297	201	0.90	Hunting macrofauna
F_F315	Sparus_aurata	195	188	140	0.72	Hunting_macrofauna

Table S2: Average trait values per species

Species	Gut_length	Relative_gut_length	Diet_category
Boops boops	329	2.14	Selective_plankton_feeding
Diplodus annularis	166	1.02	Hunting_macrofauna
Diplodus puntazzo	238	1.15	Hunting_macrofauna
Diplodus sargus	196	1.04	Hunting_macrofauna
Diplodus vulgaris	197	1.04	Hunting_macrofauna
Lithognathus mormyrus	143	0.61	Hunting_macrofauna
Oblada melanura	286	1.28	Hunting_macrofauna
Pagellus acarne	110	0.63	Hunting_macrofauna
Pagellus erythrinus	103	0.59	Hunting_macrofauna
Pagrus pagrus	180	0.88	Hunting_macrofauna
Sarpa salpa	591	2.46	Grazing_aquatic_plants
Sparus aurata	160	0.81	Hunting_macrofauna

Table S3: Phylogenetic conservatism of morphological traits

Phylogenetic signal was tested using Abouheif test.

Trait	Obs	Std.Obs	p-value
Gut length	0.19	2.25	0.027
Relative gut length	0.34	2.82	0.021

Figure S1: Abundance-occurrence distribution of ASVs and identification of core ASVs

The figure below represents the relationship between occurrence (number of samples in which the ASV occurs) and average abundance of ASVs across samples (%). Green ASVs are core ones.



Figure S2: Phylogenetic conservatism of morphological traits

Gut length and relative gut length were significantly related with phylogeny. Trait values were scaled for the representation.



Figure S3: Composition of the core gut microbiome in Mediterranean Sparidae



Relative abundance in the core microbiome (%)

Figure S4: Determinants of gut microbiome structure in Sparidae

Differences in gut microbiome structure between groups were tested using Wd test. Each barplot represents the logged p-values of the test for six different dissimilarity methods (see main text). Blue lines correspond to p-values = 0.05 and red lines to p-values = 0.01. Left plots depict raw p-values and right plots logged p-values.



Figure S5: Gut traits explain the differences in phylogenetic structure of the microbiome better than host phylogeny

We tested for relationship between dissimilarity of the gut microbiome for specific bacterial taxa (Y axes) and host dissimilarity (X axis) using Mantel tests (for each subplot: r = correlation between X and Y variables and p-val. = p-value of the Mantel test). Gut microbiome dissimilarity, here estimated using abundance-weighted Hill numbers phylogenetic index with q = 2, was computed at six different levels of taxonomic resolution (row names on the right of the figure). Each point represents a pair of fish species. Pairs within the *Diplodus* genus are depicted in blue, pair within the *Pagellus* genus is depicted in pink, pair between *Sarpa salpa* and *Boops boops* is depicted in black and other pairs that included *S. salpa* and *B. boops* are depicted in green and orange, respectively.



Host dissimilarity

Table S4: Importance of morphological traits and diet items in differentiating Sparidae gut microbiome

This table summarizes the number of time each variable was determined as a significant contributor to the dissimilarity of the gut microbiome composition across the 36 CAP analysis models tested (*i.e.* 6 dissimilarity indices times 6 bacterial taxonomic ranks). Average F values were computed using only the models in which the variables were significant.

Explanatory variable	% significant tests	F values		
Gut length	53	4.9	±	2.3
Echinoderms	8	2.2	±	0.1
Mollusks	8	1.8	±	0.2
Relative gut length	8	1.8	±	0.2

Figure S6: Association between microbiome, gut morphological traits and diet items in Sparidae

Ordinations showing the results of a Constrained Analysis on Principal coordinates (CAP). Fish individuals are represented by big dots colored according to the species (legend as in Figure 2 in main text), explaining variables are represented by italicized labels and arrows, bacterial taxa are represented by grey squares. Microbial data were agglomerated at the taxonomic level serving as title of each plot and dissimilarity between fish microbiome composition was estimated using Hill' numbers abundance-weighted taxonomic dissimilarity (q = 1). Only the traits that were identified as explaining a significant proportion of total microbiome variation are depicted (ANOVA.CCA, p-value < 0.05).

