

Biometric data to facilitate the diet reconstruction of piscivorous fauna

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Abstract. Biometric data are presented for common freshwater fish species in England and Wales. These enable the lengths and weights of fish in the diet of piscivorous fauna to be estimated from measurements of bones and scales that are recovered from faeces and stomach contents. Use of these data was demonstrated by reconstructing the length composition of species in the diet of cormorants from their faeces and an otter from its stomach contents. Both species were shown to be exploiting common size classes of abundant fish species in their home range.

Key words: key bones, scales, dietary analysis, otter, cormorant

Introduction

Investigations into the diet of piscivorous species are critical to understanding their ecology and has enabled, for example, calculation of their daily food intake, diet preferences and assessment of their impact on prey stocks (Mann & Beaumont 1980, Chanin 1981, Britton et al. 2002, Copp & Kováč 2003). Furthermore, the depredation by piscivorous fauna on fish populations in inland, recreational fisheries has long been a contentious fishery management issue (Britton et al. in press), so information on their diet is crucial in managing the overall resource.

The diet of piscivorous fauna can be reconstructed from analysis of stomach contents and faeces. Prey remains – in particular, the morphology of key bones and scales – enables species identification from published keys and guides (e.g. Steinmetz & Müller 1991, Conroy et al. 1993). Following identification, measurements of the structures enables estimates of the lengths and weights of prey to be determined from biometric relationships (Feltham & Marquiss 1989, Prenda & Granada-Lorenzo 1992, Hájková et al. 2003). Reliable biometric data required to convert measurements of bones and scales into fish lengths and weights are often scarce, especially as comprehensive data are regularly required. This is because the diet of many piscivorous species is opportunistic and catholic (e.g. Britton et al. 2002, Britton et al. in press). Yet for species encountered in England and Wales, data are only available for certain species, such as pike *Esox lucius* L., chub *Leuciscus cephalus* (L.) and perch *Perca fluviatilis* L. (Mann & Beaumont 1980, Copp & Kováč 2003). Moreover, for species such as eel *Anguilla anguilla* L. – fish that can be important dietary components of species such as the otter *Lutra lutra* (L.) – there are no published data available. Therefore, the aim of this paper was to provide biometric data for the scales and key bones of common freshwater fish species that are encountered in the diet of piscivorous fauna in England and Wales, and also for regions with a similar fish fauna. To demonstrate how the data can be utilised, two case studies are presented that involved the reconstruction of the diet of a piscivorous species.

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Materials and Methods

For the biometric relationship of scale radius (mm) against fish length (fork length, mm), data were available from scale ageing carried out as part of the stock assessment of over 100 river and stillwater fisheries completed in England and Wales between 2001 and 2004. The location of scale removal from each fish and the direction of scale measurement were as per Steinmetz & Müller (1991). Specimens for obtaining data for the relationship between bone length (mm) and fish length were available from samples of fish populations that had undergone parasitological investigations. The flesh was removed from the bones by boiling in water until it was easily detached, with cleaning of the bones completed by soaking for approximately 15 minutes in a solution of one third 50% sodium hydroxide and two third water. The bones used were the opercula, maxillae, pharyngeal teeth and caudal vertebrae. Measurement of the head bones followed Prenda & Granado-Lorenco (1992), although three dimensions of the pharyngeal teeth were measured as per Mann & Beaumont (1980). This was because recovered pharyngeal teeth are often damaged, resulting in some of their dimensions being unsuitable for measurement. There were more species data available for the scale radius: length relationships than bone: length relationships.

The data were analysed using simple linear regression of bone length (L_B) or scale radius (S_R) against fish length (L_f), with fish length derived from $L_f = bL_B + a$ and $L_f = bS_R + a$, where a and b were the constants from the regression relationship. Conversion of fish length to weight was through length-weight relationships. Fish length (fork length, mm) and weight (nearest g) data were available from individual fish that were being investigated for their parasitological status. The relationships were developed by linear regression of log weight against log length for each species. These produced values for the parameters a and b in the length-weight equation $W = aL^b$.

The use of the biometric relationships to reconstruct diet was demonstrated using cormorant *Phalacrocorax carbo carbo* (L.) faeces and the contents of an otter stomach. Cormorant faeces were collected in December 1997 from a night roost located in Nottingham, England (Britton et al. 2002). Species were identified from the morphology of scales in the faeces, with fish lengths determined from their measurements. Few bones were recovered. The reconstructed fish lengths by species were then compared to fish population data collected by boat mounted electric fishing from fisheries in the locality of the cormorant roost in October 1997. An otter carcass was recovered in August 2003 close to the River Inny, Cornwall. The stomach was removed, dissected and the fish remains separated. Species were identified from key bones, with fish lengths determined from their measurements. The size range and species composition of the fish population in the adjacent stretch of the River Inny was available for comparison following a stock assessment exercise completed in July 2003 using electric fishing.

Results

The biometric relationships of scale radius and fork length, key bones and fork length, and fork length and weight were significant for each species (Tables 1 to 3). Scales recovered from the faeces of cormorants at the Nottingham night roost suggested roach *Rutilus rutilus* (L.) and common bream *Abramis brama* (L.) were the principal species in their diet at that

Table 1. Regression parameters, a and b , for use in the scale radius (S_R): fork length (L_F) relationship $L_F = bS_R + a$. $P < 0.01$ for all r^2 values.

Species	n	a	b	r^2
<i>Rutilus rutilus</i>	2023	38.54	24.85	0.94
<i>Abramis brama</i>	347	55.82	11.77	0.95
<i>Leuciscus leuciscus</i>	1723	48.09	21.07	0.94
<i>Abramis bjoerkna</i>	245	33.78	31.16	0.96
<i>Barbus barbus</i>	504	84.28	46.63	0.95
<i>Esox lucius</i>	603	87.00	75.20	0.95
<i>Gymnocephalus cernuus</i>	84	30.91	26.69	0.93
<i>Sander lucioperca</i>	201	67.69	54.83	0.94
<i>Salmo salar</i> (juvenile)	347	74.95	51.13	0.91
<i>Thymallus thymallus</i>	502	56.23	71.44	0.94
<i>Leuciscus cephalus</i>	1038	41.95	23.07	0.97
<i>Cyprinus carpio</i>	159	40.35	9.68	0.97
<i>Perca fluviatilis</i>	548	47.31	15.30	0.95
<i>Gobio gobio</i>	401	39.22	21.12	0.94
<i>Alburnus alburnus</i>	328	36.41	37.70	0.98
<i>Salmo trutta</i>	789	22.33	168.54	0.95

time. Cormorant observations had suggested the majority of these birds foraged at Holme Pierrepont Rowing Course, Nottingham (Britton et al. 2002). Comparison of the reconstructed fish lengths with those available in the fishery, as revealed by electric fishing, revealed that cormorants were foraging on the principal species and size classes present (Fig. 1). However, larger bream of up to 380 mm were also present, size classes that were not exploited by the birds (Fig. 1).

The majority of bones recovered from the stomach of the otter were caudal vertebrae, with the majority still aligned in the vertebral column. Few thoracic vertebrae and no atlas bones (1st vertebra) were recovered. The caudal vertebrae suggested a minimum of 54 individuals of brown trout *Salmo trutta* and salmon *Salmo salar* L. had been recently ingested. These vertebrae did not allow further taxonomic differentiation. The remaining bones, including maxillae and opercula, indicated that a maximum of only 6 fish had been ingested. This suggested that either the otter discarded the heads of the majority of fish prior to ingestion or these body parts were digested and their bones passed at a faster rate than the caudal vertebrae. Fish length reconstruction suggested that the otter had depredated upon all of the size classes of salmonids present (Fig. 1). However, a disproportionate percentage of fish were consumed in the size range 100 to 115 mm (Fig. 1). Furthermore, although electric fishing revealed minnows *Phoxinus phoxinus* (L.) and bullheads *Cottus gobio* L. were also present in similar abundance to the salmonid species in the river, no remains of these species were found within the stomach. This suggested selective foraging by the otter during its last foraging bout prior to death.

Discussion

These outputs indicated that the species identification and measurement of key bones and scales found within the stomachs and faeces of piscivorous fauna are able to provide

Table 2. Regression parameters, *a* and *b*, for use in the bone (L_B): fork length (L_F) relationship $L_F=bL_B+a$. $P<0.01$ for all r^2 values.

Caudal vertebrae				
Species	n	a	b	r^2
<i>R. rutilus</i>	50	3.61	55.18	0.94
<i>A. brama</i>	15	11.92	66.77	0.98
<i>L. leuciscus</i>	15	25.12	67.12	0.94
<i>L. cephalus</i>	15	28.23	69.98	0.93
<i>C. carpio</i>	15	27.53	73.12	0.95
<i>P. fluviatilis</i>	15	15.74	61.31	0.97
<i>P. phoxinus</i>	20	4.53	39.15	0.92
<i>Barbatula barbatula</i>	20	5.38	47.54	0.93
<i>C. gobio</i>	20	2.15	45.21	0.96
<i>A. anguilla</i>	10	19.12	89.23	0.92
<i>G. gobio</i>	15	7.27	53.19	0.95
<i>S. trutta</i>	20	18.61	80.52	0.91

Opercula				
Species	n	a	b	r^2
<i>R. rutilus</i>	50	-10.85	10.48	0.95
<i>A. brama</i>	15	-5.67	10.57	0.95
<i>L. leuciscus</i>	15	2.13	8.23	0.93
<i>L. cephalus</i>	15	4.34	9.53	0.98
<i>C. carpio</i>	15	5.29	17.21	0.94
<i>P. fluviatilis</i>	15	-3.21	10.11	0.99
<i>P. phoxinus</i>	20	-1.24	10.12	0.94
<i>G. gobio</i>	15	-12.34	14.18	0.98
<i>S. trutta</i>	20	5.74	11.48	0.93

Pharyngeal teeth									
Species	Shank			Gape			Tip		
	a	b	r^2	a	b	r^2	a	b	r^2
<i>R. rutilus</i>	-26.63	26.56	0.94	13.72	12.72	0.97	7.95	12.24	0.95
<i>A. brama</i>	18.46	19.47	0.99	20.75	18.92	0.99	19.23	13.07	0.99
<i>L. leuciscus</i>	-42.57	28.53	0.99	-40.76	26.27	0.99	-18.77	28.04	0.97
<i>L. cephalus</i>	-28.13	27.21	0.94	-21.15	29.13	0.95	-9.14	27.47	0.92
<i>P. phoxinus</i>	-1.57	21.45	0.96	-2.63	19.29	0.97	11.15	13.17	0.93
<i>C. carpio</i>	13.32	31.37	0.95	16.42	19.13	0.96	9.48	21.42	0.95
<i>G. gobio</i>	-30.09	36.359	0.98	12.05	21.12	0.99	-9.71	19.29	0.99

Maxilla				
Species	n	a	b	r^2
<i>R. rutilus</i>	50	-1.37	13.74	0.92
<i>A. brama</i>	15	-2.31	14.72	0.94
<i>L. leuciscus</i>	15	3.1	12.45	0.96
<i>L. cephalus</i>	15	1.2	14.12	0.95
<i>C. carpio</i>	15	-1.43	16.23	0.93
<i>P. fluviatilis</i>	15	-3.15	15.71	0.94
<i>P. phoxinus</i>	20	1.18	11.19	0.97
<i>S. trutta</i>	20	1.27	12.13	0.95

Table 3. Regression parameters, a and b , for use in the length-weight relationship $W=aL^b$ to produce expected weight (g) from fork length (mm). $P<0.01$ for all r^2 values.

Species	n	a	b	r^2
<i>Rutilus rutilus</i>	5645	0.00000290	3.32	0.94
<i>Abramis brama</i>	1231	0.00000610	3.18	0.95
<i>Leuciscus leuciscus</i>	769	0.00000651	3.13	0.94
<i>Abramis bjoerkna</i>	201	0.00000401	3.28	0.96
<i>Barbus barbus</i>	127	0.00001210	2.98	0.95
<i>Esox lucius</i>	131	0.00000650	3.05	0.95
<i>Anguilla anguilla</i>	87	0.00001130	2.85	0.93
<i>Sander lucioperca</i>	107	0.00001200	3.01	0.94
<i>Salmo salar</i>	134	0.00002210	2.86	0.91
<i>Thymallus thymallus</i>	89	0.00000311	3.32	0.94
<i>Leuciscus cephalus</i>	549	0.00000430	3.21	0.97
<i>Cyprinus carpio</i>	3452	0.00001510	3.01	0.97
<i>Gymnocephalus cernuus</i>	197	0.00001614	3.02	0.96
<i>Phoxinus phoxinus</i>	145	0.00001047	3.02	0.94
<i>Cottus gobio</i>	117	0.00001324	3.02	0.98
<i>Perca fluviatilis</i>	327	0.00000461	3.23	0.95
<i>Barbatula barbatula</i>	113	0.00001290	3.05	0.97
<i>Gobio gobio</i>	159	0.00000790	3.08	0.94
<i>Salmo salar</i> (juvenile)	203	0.00002201	2.86	0.96
<i>Alburnus alburnus</i>	98	0.00000801	3.04	0.98
<i>Salmo trutta</i>	209	0.00001101	3.02	0.95

important dietary data. However, the content analysis of the otter stomach highlighted the limitations when reliant upon only one method of dietary analysis. The principal bone that allows taxonomic differentiation between salmonid species is the atlas (F e l t h a m & M a r q u i s s 1989, C a r s s & E l s t o n 1996). However, no atlas bones were recovered from the stomach, with identification reliant upon the abundant caudal vertebrae. Yet, vertebrae have limited usefulness in identification for they rarely allow taxonomic differentiation to species level (P r e n d a & G r a n a d o - L o r e n c i o 1993, C o n r o y et al. 1993, C o p p & K o v á ě 2003, H á j k o v á et al. 2003). This resulted in the analysis not being able to differentiate between brown trout and salmon. Further, the considerable size range that exists in vertebrae according to the position on the vertebral column can result in inaccurate length estimates (C o p p & K o v á ě 2003, H á j k o v á et al. 2003). Additional problems that exist when relying upon key bones is the size-related recovery of fish bones in faeces, the influence of activity on digestion rate (regarding bone resistance and recovery) and the problem of shrinkage during air drying (C a r s s & E l s t o n 1996, C a r s s & N e l s o n 1998, C a r s s et al. 1998, H á j k o v á et al. 2003). These factors can all result in both inaccurate back-calculation of fish lengths and incomplete diet reconstruction. Furthermore, unless feeding and activity observations complement dietary analysis, the feeding sites of piscivorous fauna may remain unconfirmed and limit the usefulness of any comparison with prey fish populations. For example, although the dead otter was recovered from close to the River Inny, it may have recently foraged elsewhere in its territory, for otters are able to travel long distances between feeding (C h a n i n 2003).

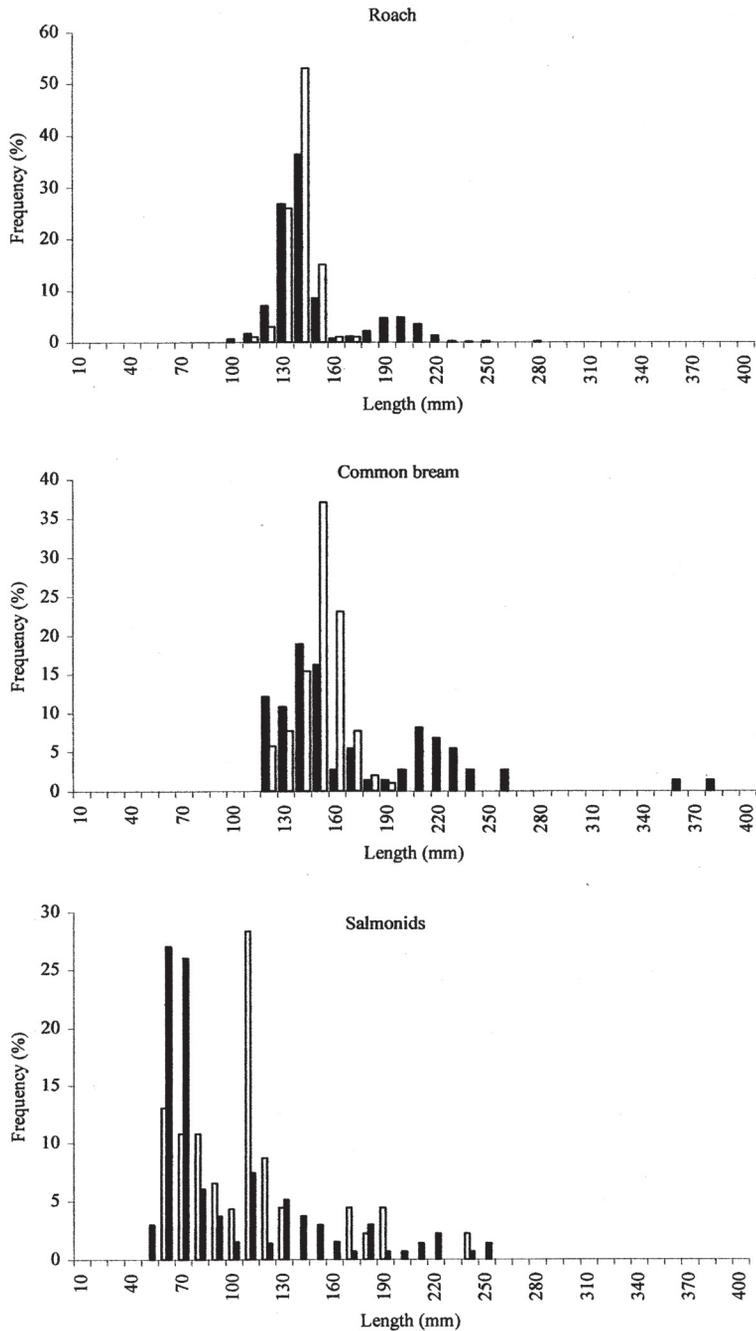


Fig. 1. Top/ middle: Length frequency of roach and common bream in the diet of cormorants in the Nottingham night roost in December 1997 (□) compared to the length composition of the fish population of Holme Pierrepont Rowing Course in October 1997 (■). Bottom: Length composition of salmonids in the stomach of an otter recovered from the River Inny in August 2003 (□) compared to the length composition of salmonids in the river in July 2003 (■).

This highlights the requirement to obtain estimates of species, and their lengths and weights, in the diet of piscivorous species from multiple sources and over extended time periods in order for temporal and spatial trends to be identified. When diet is being reconstructed, complementary data from both stomach contents and faeces will provide a greater insight into diet than one method in isolation. In the case of piscivorous birds, information from these methods can complement data collected during direct feeding observations (Feltham et al. 1999). In the case studies presented here, there was only one source of fish remains available from which diet could be reconstructed. Within these, there was only one principal identification source, namely scales (cormorant) and caudal vertebrae (otter). Therefore, the output from such work must acknowledge the limitations of the methodology used. Nevertheless, even where only one otter stomach is available for content analysis, the data obtained remains a source of dietary and ecological information that might otherwise have remained absent. Therefore, the use of biometric relationships to facilitate diet reconstruction remains a vital tool for the vertebrate ecologist, with the data presented here assisting by providing data for a more comprehensive range of fish species.

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