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Gymnocephalus ambriaelacus, a new species of ruffe from Lake Ammersee, southern Germany

(Teleostei, Perciformes, Percidae)

Matthias F. Geiger & Ulrich K. Schliewen

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A new ruffe of the genus *Gymnocephalus* (Teleostei, Perciformes, Percidae) is described from Lake Ammersee (Bavaria, Germany). *G. ambriaelacus*, new species, belongs to the subgenus *Acerina* and is distinguished from *G. (Acerina) cernua* (Linnaeus, 1758) by a smaller angle between the posterior dorsal fin margin and the caudal peduncle (90-110° vs. 113-154°), by a larger eye diameter (10.2-12.3 % SL vs. 7.9-10.5 % SL) and by an irregular pattern of large dorsolateral dark blotches vs. a pattern of small dots. It is distinguished from *G. (Acerina) baloni* Holčík & Hensel, 1974 by the combination of a larger eye diameter (10.2-12.3 % SL vs. 8.2-10.5 % SL), a smaller caudal peduncle depth (7.7-8.9 % SL vs. 7.4-10.1 % SL), and a higher mean and modal number of pectoral fin rays (15 vs. 13). Further, it is distinguished from all *Gymnocephalus* species by a unique nuclear LdhA6 intron haplotype. According to phylogenetic analysis of both nuclear and mitochondrial sequence data the new species is the sistertaxon to *G. baloni*. With *Salvelinus evasus* Freyhof & Kottelat, 2005 and *Coregonus bavaricus* Hofer, 1909, this is the third endemic species from Lake Ammersee.

Matthias F. Geiger (corresponding author) & Ulrich K. Schliewen, Bavarian State Collection of Zoology (ZSM), Department of Ichthyology, Münchhausenstr. 21, 81247 Munich, Germany;
e-mail: matthias.f.geiger@t-online.de; schliewen@zsm.mwn.de

Introduction

It has long been known that Lake Ammersee in Bavaria harbours a ruffe *(Gymnocephalus)* species. This has been known to local fishermen for at least the last 200 years (W. Ernst, pers. comm.), and at least for approximately one hundred years to ichthyologists, because Wagler mentioned a ruffe from Lake Ammersee as *Acerina cernua*. He must have caught ruffes in Lake Ammersee for an unpublished growth study (unpubl. manuscript from 1926) already around 1900, as pictures and scale samples from this time are present in the Bavarian State Collection of Zoology (ZSM). In combination, these sparse data show that it is very likely that ruffe has always been an element of Lake Ammersee, despite the fact that already Siebold (1863) states that ruffe are almost absent from prealpine lakes. Recently, the question about the species identity and status of Lake Ammersee ruffe arose in the course of a graduate study (Geiger 2006), dealing with ruffe diversity in Germany and Europe because it was not possible to convincingly identify the Ammersee ruffe either as *G. cernua* or as *G. baloni*.

Apart from this new species, the Eurasian genus *Gymnocephalus* currently contains four species: the widespread *G. cernua* (*cernua* is the correct spelling, see Kottelat & Freyhof 2009) with a natural range from northern and central Europe with the North East of France, Great Britain without Scotland

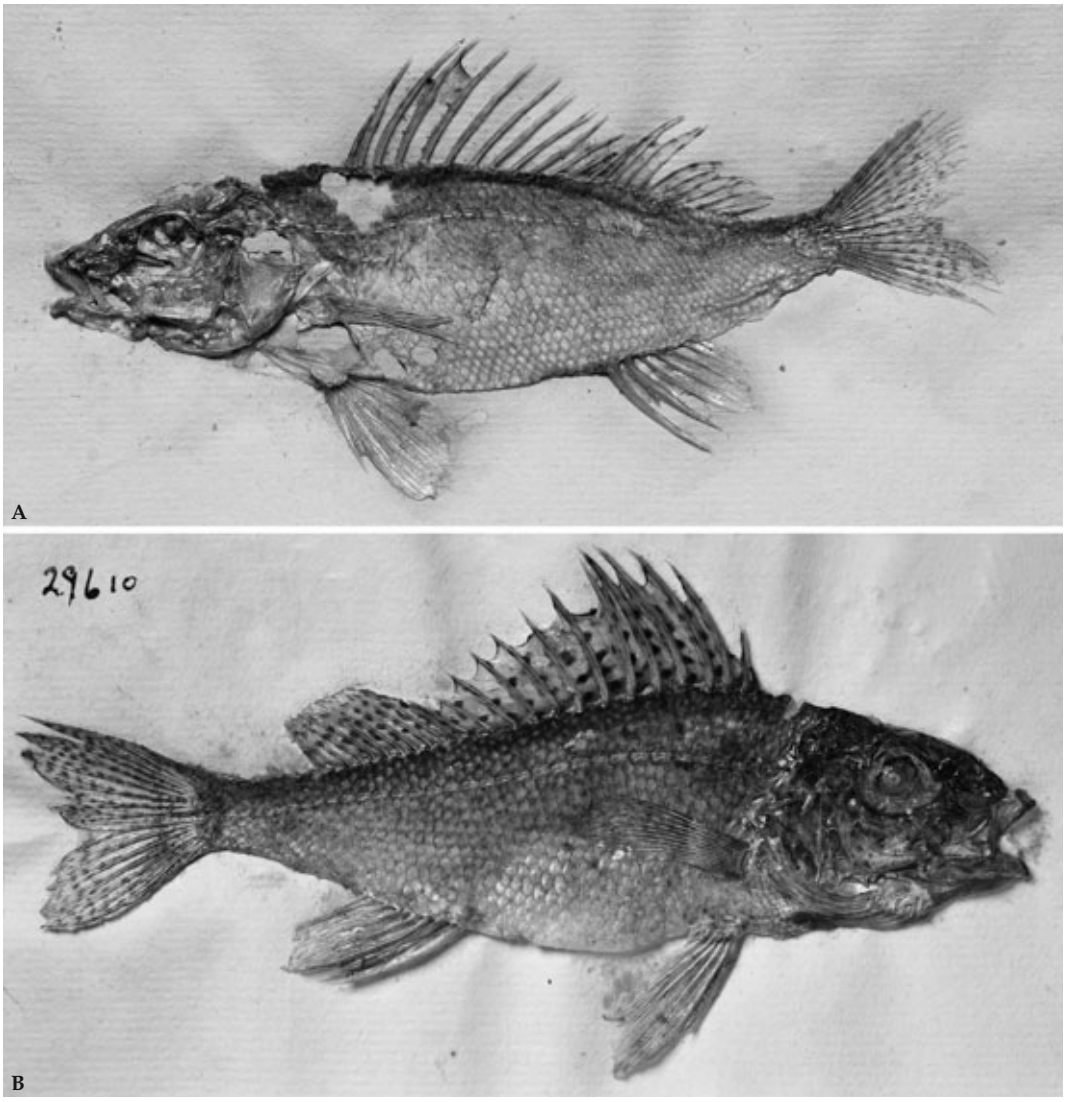

Fig. 1. The two extant of *Perca cernua* Linnaeus, 1758. **A.** Lin.Soc.Lon.2, one of the two syntypes from the Linnaeus Collection (photo courtesy Linnean Society of London). **B.** BMNH 1853.11.12.5, second syntype from the Gronovius fish collection (photo courtesy BMNH).

and Ireland to Eastern Europe and Siberian rivers draining into the Baltic and White Sea and the north eastern Siberian Kolyma River; *G. schraetser* (Linnaeus, 1758) endemic to the Danube basin; *G. baloni* occurring in Danube and Dnepr drainages, and *G. acerina* (Gueldenstaedt, 1774), which is restricted to the Dnepr, Dniester, Kuban, South Bug and Don systems (Oliva 1959; Kovác 1998; Kottelat & Freyhof 2007).

Obviously, when describing a new *Gymnocephalus* species, the question of the geographic origin of the type material of *Perca cernua* Linnaeus, 1758 is of importance. According to Wheeler (1985), two specimens have to be regarded as syntypes, one from Linné's own collection (LS 2, fig. 1a) and one from Gronovius' collection (BMNH 1853.11.12.5, fig. 1b). For the latter specimen, the single available hint about the type locality is indirect through a note by Gronovius himself, who stated "Inhabit magna fatis copia apud Nos in fluminibus" [it lives

in great numbers in our rivers] (Gronovius 1754, p. 41). As Linné based his work partially on that of Gronovius, this implies that Linné got at least part of the material either from Belgium, as Gronovius came from Belgium, or from the Netherlands as Gronovius and his father, who had built up the majority of the Gronovius collection, had later worked in Leiden (Wheeler 1958). Surprisingly however, Linné states in his original work (1758): "Habitat in Europae lacubus" [lives in European lakes], thus contradicting Gronovius' statement by referring to ruffes from lakes and not from rivers. The solution to this contradiction may lie in the likelihood that Linné referred to the second syntype, a specimen possibly from a Swedish lake. This is deduced from Wheeler (1985), who writes "*Perca cernua* of Linnaeus (1758) was based on three earlier literary references, to Linnaeus (1746), Artedi (1738), and Gronovius (1754). There are several other cases of common Swedish fishes which are referred to in the Fauna Svecica (Linnaeus 1746) which are also present in the collection. It is therefore very probable that these specimens were referred to in any description and should therefore be accorded type status. I therefore regard this as part of the type series of *Perca cernua*." Wheeler concludes that Linné must have acquired this specimen on one of his travels in Sweden. As Linné refers to ruffes from lakes it is plausible that he described a specimen that he obtained from a lake in Sweden. For the purpose of describing a new *Gymnocephalus* from the Danube drainage in Bavaria, we can deduce with regard to the type locality of *Perca cernua*, that it is most likely not from the Danube drainage. The same is true for type localities of all taxonomically available synonyma of *Gymnocephalus cernua*, which are according to Kottelat (1997) or original descriptions: *Cernua fluviatilis* Fleming, 1828 ("rivers in England"), *Acerina fischeri* Eichwald, 1871 ("dans quelques lacs du gouvernement de Temsk"), *Acerina czekanowskii* Dybowski, 1874 ("Der Fluss Angara in seinem mittleren und unteren Laufe") *Acerina cernua essipovi* Burmakin, 1941 (Gyda Bay basin, river Yuribei, Siberia).

We morphometrically and genetically compared the ruffe of Lake Ammersee with *G. cernua* and *G. baloni* material from a wide variety of habitats (freshwater lentic and lotic habitats as well as from brackish water) and drainages (Danube, Rhine, Elbe, Odra, Dniestr, Dnepr, Volga, Baltic, Ob). In combination, these comparisons revealed that ruffe from Lake Ammersee is distinct and represents an undescribed species.

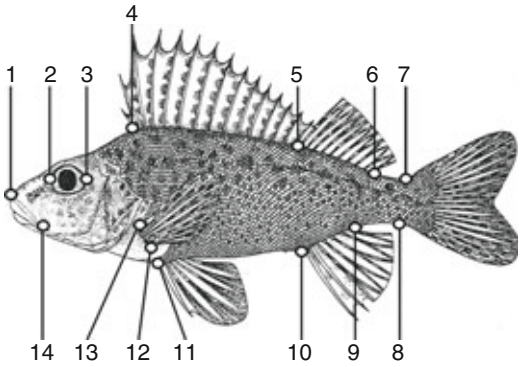

Fig. 2. Drawing of *Gymnocephalus cernua*, showing the locations of the 14 anatomical landmarks (numbered points). Modified from Holčík & Hensel 1974.

Material and methods

28 measurements and 9 meristics were taken from 124 specimens as described in Holčík & Hensel (1974) and Holčík et al. (1989) except for: head width was taken at the ventral base of the largest opercular spine; head length is the distance from the tip of the snout to the ventral base of the largest opercular spine. Measurements are point-to-point using a dial caliper to the nearest 0.01 mm and taken from the left side of specimens; counts follow Holčík (Holčík et al. 1989). In addition, a landmark-based geometric morphometric approach (e.g. Rohlf & Marcus 1993) was applied to investigate body shape differences between 29 specimens of Lake Ammersee ruffe, 31 specimens of the phenetically and genetically closely related *G. baloni* as well as between Lake Ammersee ruffe and three other lacustrine populations of *G. cernua* (Lake Constance, n=26; Lake Mueggelsee, n=23; Lake Stechlinsee, n=20). 14 landmarks were positioned on digital images of carefully preserved fish-bodies (Fig. 2). For morphometric data acquisition the TPS software package (Rohlf & Marcus 1993; Rohlf 2006a,b) was used. Principal components analysis (PCA) based on the partial warp scores was applied to examine variation in body shape among individuals. PCA is part of the IMP package (Sheets 2003), and was used after removing non-shape variation via a "Generalised least squares Procrustes superimposition" (GLS). Procrustes superimposition scales specimens to a unit size, translates them to a common location and rotates them to their corresponding landmarks line up as closely as possible, thus removing artificial variation (non-shape variation) between specimens based on differences in size and position on the picture. For a more comprehensive description of geometric morphometrics see Zelditch et al. (2004) and the literature aforementioned.

According to methodological requirements, different specimens had to be used for different analyses, albeit with a great overlap of used specimens analysed with different methods: For the geometric morphomet-

ric analysis using landmarks only well preserved individuals of minimum size 70 mm SL were used, i. e. only those with a straight body and a natural positioning of jaws and gill covers (not expanded or distorted). Measurements were taken from adult individuals of minimum 70 mm SL. As the only two extant syntypes of *G. cernua* consist of dried half skins (Fig. 1a,b, Wheeler 1958, 1985), head width, body width and interorbital width could not be measured in those specimens. Other measurements taken with uncertainties due to the preservation status of the material have been omitted.

For the following loci DNA sequence characters were determined from a total of 46 individuals of *G. cernua* (n = 24), *G. baloni* (n = 9), *G. ambriaelacus* (n = 10) and *G. schraetser* (n = 3) from different Central European drainages: the nuclear locus LdhA6 (221 bp), the mitochondrial loci 12s and 16s (1127 bp) and the left domain of the mtDNA control region (290 bp). Additionally, we included previously published data (Stepien 1998) as well as data from a preliminary study (Geiger 2006) for the left domain of the mtDNA control region. We focused on the left domain of the control region because of problems amplifying either the whole region or only the right domain. Individuals used in the molecular-genetic analysis are given in the material section with their respective master-DNA Bank accession numbers. Extracted DNA is stored at ZSM as part of DFG funded DNA Bank Network project (www.dnabank-network.org).

PCR product for LdhA6 intron was obtained using primers LdhA6-F1 (5'-TACACTTCCTGGGCSATYGGBATG-3') and LdhA6-R (5'-CGCTSAGGAASACCTCRTCCTTCAC-3'), as originally presented in Quattro & Jones (1999). PCR conditions were slightly modified from those described in Quattro & Jones (1999): 6 min at 94 °C, 45 cycles of 92 °C for 1 min, 55 °C for 1 min, 72 °C for 1.5 min and a final extension of 6 min at 72 °C. We did not include three already published LdhA6 sequences from Stepien et al. (2004 & 2005, GenBank accession numbers AY034781-3) in our analysis because these were 23 bps shorter and differed all in eight nucleotide positions for which all our individuals – irrespective of species – were monomorphic. Partial mitochondrial 12S and 16S rRNA genes were amplified using primers 12s-F1 (5'-TGAAGGAGGATTTAGCAGTAAG-3') and 16s-R1 (5'-AAGTGATTGCGCTACCTTCGCAC-3'). For sequencing, an additional primer 12s-F2 (5'-TCTCTGTGGCAAAAGAGT-3') was used. PCR conditions followed those published (Rüber et al. 2003), although at higher annealing temperatures: 6 min at 94 °C, 45 cycles of 94 °C for 1 min, 56-58 °C for 1 min, 72 °C for 1.5 min and a final extension of 6 min at 72 °C. Primers for the PCR of the left domain of the mtDNA control region were L15926 (5'-TCAAAGCTTACACCAGTCTTGTAAACC-3') and H16498 (5'-CCTGAAGTAGGAACCAGATG-3'). PCR conditions followed those previously published (Stepien et al. 1998): 2 min at 94 °C, 34 cycles of 92 °C for 40 sec, 52 °C for 20 sec, 72 °C for 1 min and a final elongation of 5 min at 72 °C.

Published D-Loop sequences from Stepien et al. (1998) were retrieved from GenBank (accession numbers AF025355–AF025362).

Sequencing of the fragments was done at the sequencing service of the gene lab of the Ludwig Maximilian University in Munich, using the Big Dye v.3.1 kit. Alignment of sequences was straightforward and conducted in BioEdit version 7.0.5.3 (Hall 1999) using the ClustalW multiple alignment function with default settings (Thompson et al. 1994) and adjusted by eye. The derived median-joining haplotype networks containing all possible shortest least complex phylogenetic trees (all maximum parsimony or MP trees) were constructed using the program NETWORK 4.2 following Bahndelt et al. (1995 & 1999) with default settings (epsilon = 0).

Comparative material was available from the Bavarian State Collection of Zoology in Munich (ZSM), Natural History Museum Senckenberg in Frankfurt (SMF), Natural History Museum Vienna (NMW) and Fish Collection Jörg Freyhof in Berlin (FSJF). The holotype (Fig. 3a) and paratypes of *G. baloni* were examined at the Comenius University and the Slovak National Museum (SNMB), Bratislava, Slovakia.

Results

Ruffe from Lake Ammersee differed from all investigated riverine and lacustrine *Gymnocephalus cernua* specimens (Danube N = 25, Baltic Sea N = 23, Elbe N = 42) by a smaller angle between the posterior dorsal fin margin and the caudal peduncle (90-110° vs. 113-154°), by a larger eye diameter (10.2-12.3 % SL vs. 7.9-10.5 % SL) and by an irregular pattern of large dorsolateral dark blotches vs. a pattern of small dots. Two diagnostic characters were also measurable in the two syntypes that clearly differ between *G. cernua* and the new species: the shorter 1st dorsal-fin base with fewer spines in *G. cernua* and the greater angle between posterior dorsal-fin margin and caudal peduncle in *G. cernua*.

The landmark-based geometric morphometric approach using PCA based on the partial warp scores of three lake populations of *G. cernua* and the new species (Fig. 4) revealed obvious differences between the two species despite similarity of ecological conditions possibly influencing body shape. Multivariate geometric analysis of partial warp scores of *G. baloni* specimens (N = 31, including types) and Lake Ammersee ruffe (N = 29) show that these two differ in shape, despite the fact that they are comparatively similar with respect to single measurements: the minimum polygon clusters show no overlap between *G. baloni* and *G. ambriaelacus* individuals (Fig. 5a). In this analysis principal component 2 explains 27.1 % of the total variance. According to the corresponding deformation grid (Fig. 5b) this variance is mainly associated with (1) differences in the relative position

Fig. 3. *Gymnocephalus baloni*. **A.** SNM-RY 2261, holotype (female), 107.3 mm SL; Slovakia: River Danube near Klizská Nemá; coloration in formaline. **B.** ZSM 33416, female, 108.1 mm SL; Germany: Bavaria: River Danube near Niederalteich; coloration in alcohol.

of the tip of the snout and posterior of maxillary, i.e. reflecting the blunter snout in *G. ambriaelacus*, (2) with the insertion of the pectoral and pelvic fin base origin and (3) with an elongation of the caudal peduncle. Principal component 3 explains 10.6 % of total variance and mainly reflects a (1) dorsal compression, associated with the shorter first dorsal fin base in *G. ambriaelacus*, (2) different position of the tip of the snout, (3) eye enlargement and (4) again an elongation of the caudal peduncle in *G. ambriaelacus* (Fig. 5c). The distinctively larger eye diameter of the new species is visualized in the scatterplot of caudal peduncle depth (in % SL) against eye diameter (in % SL) (Fig. 6).

Three independent DNA datasets enabled a phylogenetic network analysis partially integrating Stepien et al.'s (1998) D-Loop data as well as identifying novel character states by using other sequence stretches from new loci. Maternally inherited mitochondrial DNA from dataset A (1417 bp: combined 12s/16s and D-Loop fragment; see Tab. 1-2 and Fig. 7a), from dataset B (290 bp: D-Loop

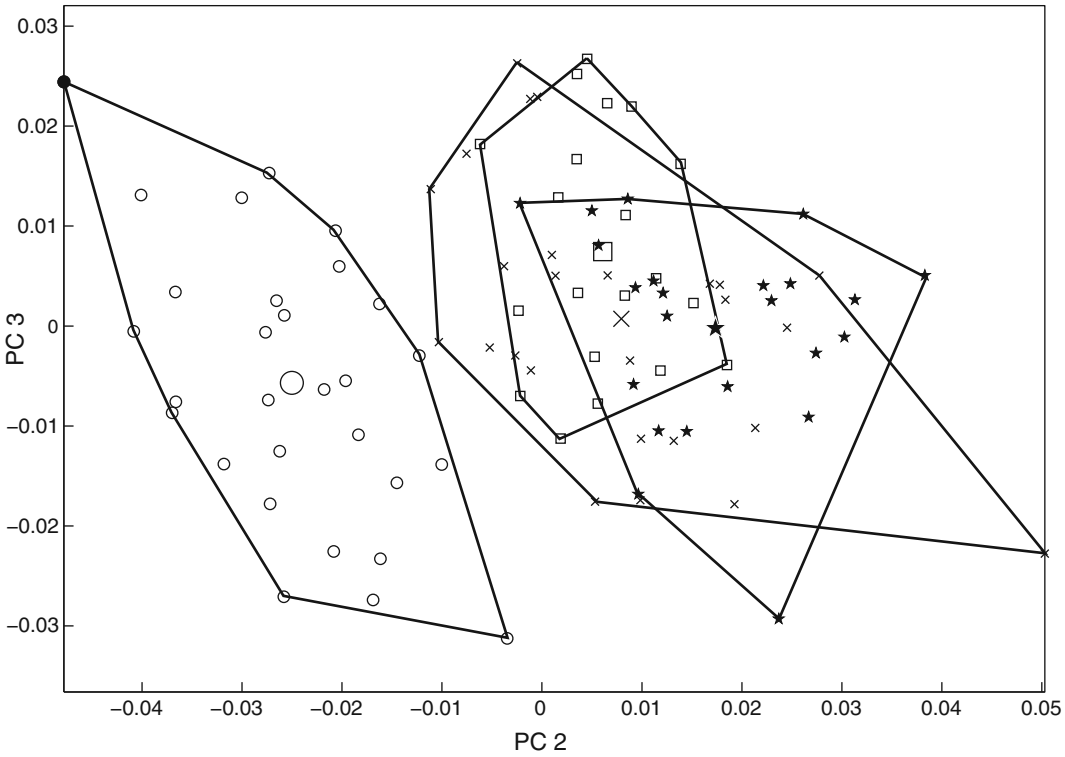

Fig. 4. Scatter plot of PCA of landmark-based geometric morphometric analysis showing scores of PC2 versus PC3 for *Gymnocephalus ambriaelacus* (● holotype, ○ paratypes and other specimens, n = 29) and *G. cernua* from Lake Constance (×, n = 26), Lake Mueggelsee (★, n = 23) and Lake Stechlinsee (□, n = 20). Group mean values are indicated as large symbols.

data only but including data from Stepien et al. 1998; see Tab. 2 and Fig. 7b) as well as from the nuclear DNA dataset C (221 bp: LdhA6, see Tab. 3 and Fig. 7c) clearly show that Ammersee ruffe is more closely related to *G. baloni* than to *G. cernua*. Median joining networks of all three datasets reveal three major clades which correspond to taxonomic clusters within *Gymnocephalus* (Fig. 7). In *G. cernua* there is also evidence for additional geographical substructure: based on dataset A individuals from Russian karst lake Abrau (haplotype number [hn] 4) are close to Baltic Sea haplotype (hn 3) and both are separated from the remaining two *G. cernua* haplogroups (hn 1&2) by at least ten substitutions (Fig. 7a). In the haplotype network based on dataset B (Fig. 7b) there is a distinct cluster of northeastern European and Siberian samples including individuals from Baltic Sea, River Nema and Lake Komsomolskoe ("St. Petersburg" in Tab. 4) and River Ob (all hn 5), as well as one from central – southeastern Europe including samples from Elbe, Odra, Rhine, Danube, Dnieper, Dniester, Bug, Volga drainages (hn 1, 2, 3, 6) and England (hn 4). The haplotype network based on nuclear dataset C (Fig. 7c) indicates only weak additional substructuring in *G. cernua* but again the sample from Lake Abrau (hn 5) is distinct from all other *G. cernua* individuals.

Clearly, our sampling is far from complete, and the three datasets allow only for establishing preliminary phylogeographic patterns. However, based on this, it is highly probable, that Lake Ammersee ruffe is neither conspecific with *G. cernua* nor it is probable that it is close to Siberian mitochondrial lineages which might possibly include *Gymnocephalus* populations that are phylogenetically close to populations that served as a basis for the description of *Acerina fischeri* Eichwald, 1871, *Acerina czeakanowskii* Dybowski, 1874, and *Acerina cernua essipovi* Burmakin, 1941.

The combination of our comparative results using complementary morphometric and genetic datasets clearly differentiates Lake Ammersee ruffe phenetically and phylogenetically from both members of the subgenus *Acerina* and hence can be described as a new species.

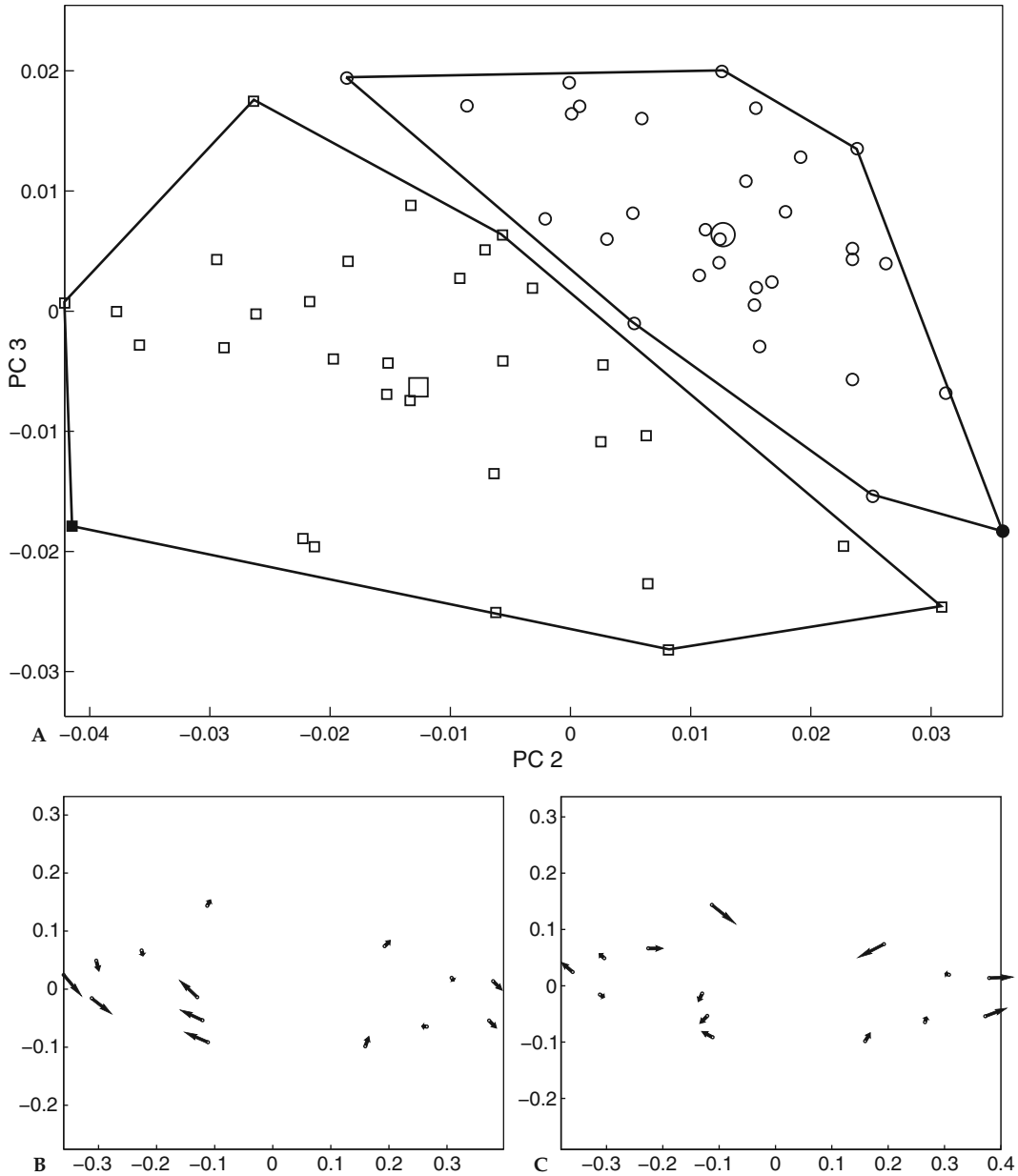

Fig. 5. **A.** Scatter plot of PCA of landmark-based geometric morphometric analysis showing scores of PC2 versus PC3 for *Gymnocephalus ambriaelacus* (● holotype, ○ paratypes and other specimens, n = 29) and *G. baloni* (■ holotype, □ paratypes and other specimens, n = 31). Group mean values are indicated as large symbols. **B.** Deformation grid with vectors of relative displacements of landmarks. The deformation is shown for the mean reference configuration into a hypothetical specimen having a score of +0.1 on PC2 and 0 on every other PC. **C.** Deformation grid with vectors of relative displacements of landmarks. The deformation is shown for the mean reference configuration into a hypothetical specimen having a score of +0.1 on PC3 and 0 on every other PC.

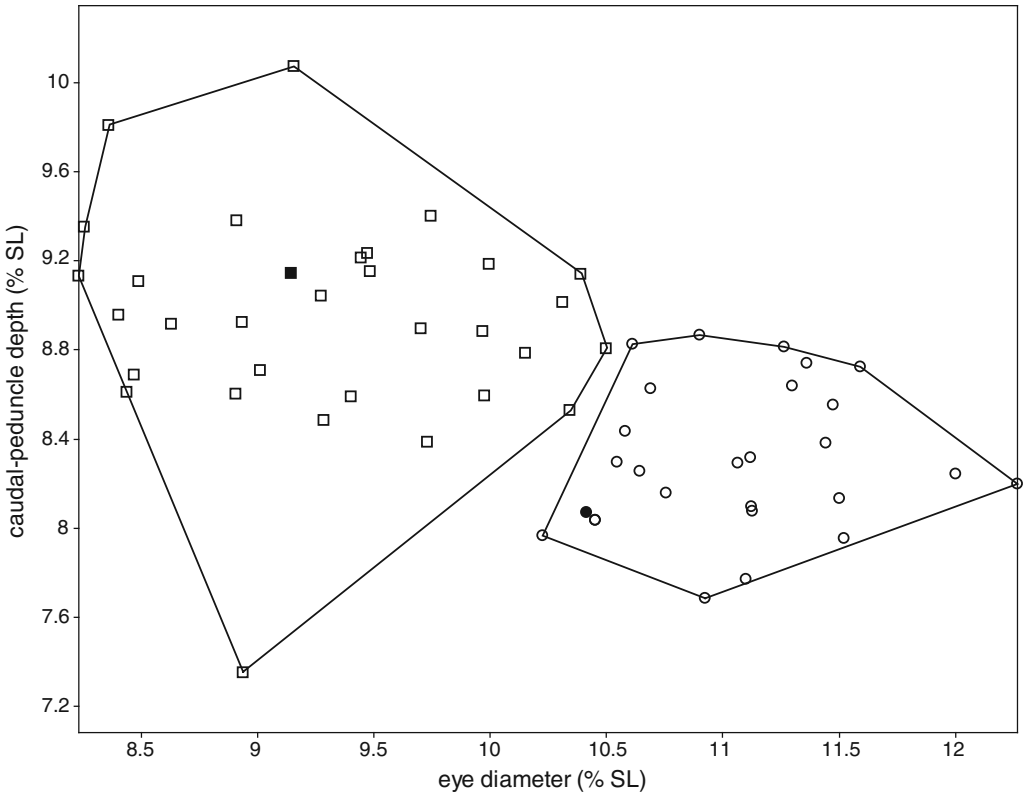

Fig. 6. Scatterplot of caudal peduncle depth (in % SL) against eye diameter (in % SL) for *Gymnocephalus ambriaelacus* (● holotype, ○ paratypes and other specimens, n = 26) and *G. baloni* (■ holotype, □ paratypes and other specimens, n = 32).

Table 1. Variable positions in haplotypes of mtDNA 12s16s sequence data for *Gymnocephalus cernua*, *G. ambriaelacus*, *G. baloni*, and *G. schraetser* with numbers and geographic origin of samples. Numbers in top row correspond to nucleotide position of polymorphisms. H, haplogroup.

	H	24	28	127	130	131	208	256	270	337	348	456	487	518	540
G. cernua															
River Isar (n = 1)	1	A	C	T	G	T	G	T	A	A	A	C	C	G	C
River Danube (n = 9)	1	A	C	T	G	T	G	T	A	A	A	C	C	G	C
River Elbe (n = 2)	2	A	C	T	G	T	G	T	A	A	A	C	C	G	C
River Havel (n = 1)	1	A	C	T	G	T	G	T	A	A	A	C	C	G	C
River Moskva (n = 1)	1	A	C	T	G	T	G	T	A	A	A	C	C	G	C
Odra Estuary (n = 1)	1	A	C	T	G	T	G	T	A	A	A	C	C	G	C
River Bug (n = 1)	2	A	C	T	G	T	G	T	A	A	A	C	C	G	C
Lake Stechlinsee (n = 2)	1	A	C	T	G	T	G	T	A	A	A	C	C	G	C
River Dnepr (n = 1)	1	A	C	T	G	T	G	T	A	A	A	C	C	G	C
River Dniester (n = 1)	2	A	C	T	G	T	G	T	A	A	A	C	C	G	C
Lake Abrau (n = 3)	4	A	C	T	**A**	T	G	**C**	A	A	A	C	C	G	C
Baltic Sea (n = 1)	3	A	C	T	**A**	T	G	**C**	**C**	A	A	C	**T**	G	**T**
G. ambriaelacus (n = 10)	5	**A/G**	**T**	**C**	**A**	**C**	A	T	A	**G**	**T**	**T**	C	**A**	C
G. baloni (n = 9)	6	A	**T**	**C**	**A**	**C**	A	T	A	**G**	**T**	**T**	C	**A**	C
G. schraetser (n = 3)	7	A	C	**C**	**A**	T	G	T	A	A	A	C	C	**A**	C

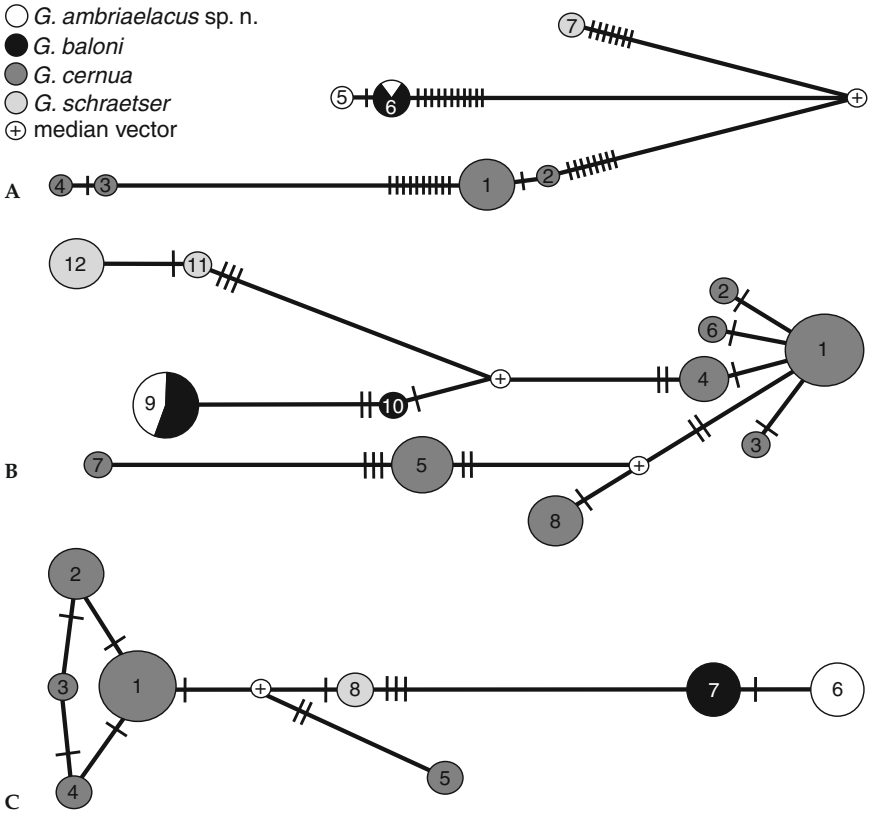

Fig. 7. Median joining haplotype networks based on **A.** two mtDNA loci (12s16s [1127 bp] + control region, left domain [290 bp]); **B.** control region, left domain [290 bp] including data from Stepien et al. (1998) and **C.** nuclear locus LdhA6 (221 bp). See text for haplogroup coding. Circle size corresponds to sample size of sequenced individuals. One bar represents one character state change at a single nucleotide position.

564	603	644	651	711	757	818	819	845	1123
G	T	C	T	C	C	T	C	A	G
G	T	C	T	C	C	T	C	A	G
G	T	C	T	C	C	T	C	A	G
G	T	C	T	C	C	T	C	A	G
G	T	C	T	C	C	T	C	A	G
G	T	C	T	C	C	T	C	A	G
G	T	C	T	C	C	T	C	A	G
G	T	C	T	C	C	T	C	A	G
G	T	C	T	C	C	T	C	A	G
G	T	C	T	C	C	T	C	A	G
A	T	**T**	**A**	**T**	**T**	T	C	A	G
G	T	C	T	**T**	**T**	T	C	A	G
G	**C**	C	T	**T**	**T**	**C**	C	**T**	G
G	**C**	C	T	**T**	**T**	**C**	C	**T**	G
G	**C**	C	T	C	**T**	**C**	**T**	A	**A**

Gymnocephalus ambriaelacus **spec. nov.**
Fig. 8a

Types. Holotype. ZSM 33199, 94 mm SL; Germany: Bavaria: River Isar catchment area: Lake Ammersee east shore near Ried, depth: approx. 5 m; 48°0'21"N 11°8'29"E; W. Ernst, 10 May 2005, (DNA Bank accession number: AB34403544). – Paratypes. ZSM 32824, 4, 112.5-73.6 mm SL; Germany: Bavaria: River Isar catchment area: Lake Ammersee east shore near Ried; 48°0'21"N 11°8'29"E; W. Ernst, Mar 2005, (DNA Bank accession numbers: AB34403545, AB34403560, AB34403575, AB34403566). – ZSM 33314, 10, 106-78.8 mm SL; Germany: Bavaria: River Isar catchment area: Lake Ammersee east shore near Ried; 48°0'21"N 11°8'29"E; W. Ernst, 24 May 2005, (DNA Bank accession numbers: AB34403576, AB34403611, AB34403568). – ZSM 33834, 11, 116.9-76.1 mm SL; same data as holotype. – ZSM 38522, 2, 83.3-79.6 mm SL; same data as holotype, (DNA Bank accession numbers: AB34403594, AB34403552). – ZSM 38781, 8, 93.1-69.6 mm SL; Germany: Bavaria: River Isar catchment area: Lake Ammersee east shore near

Ried; 48°0'20" N 11°8'26" E; W. Ernst, 20 June 2009. SMF 32879, 2, 88.7-79.3 mm SL; Germany: Bavaria: River Isar catchment area: Lake Ammersee east shore near Ried; 48°0'20" N 11°8'26" E; W. Ernst, 20 June 2009.

Additional material. ZSM 30687, 2, 89-86.8 mm SL; Germany: Bavaria: Lake Ammersee between Utting and Schondorf, depth: approx. 50 m; affluent River Amper, tributary to River Isar; W. Ernst, Mar 2003. – ZSM 31966, 1, 85.3 mm SL; Germany: Bavaria: River Isar catchment area: Lake Ammersee east shore near Ried; 48°0'21" N 11°8'29" E; W. Ernst, Oct 2004.

Etymology. The species name is the Latin translation "of the lake of the Ammer region", "*ambriae*" being the genitive of the latinized Celtic word for Ammer region, i. e. *ambro*, and "*lacus*" being the genitive of *lacus*, the Latin word for lake. Lake Ammersee is known historically as "Ambriae Lacus" (Graesse 1909). A noun in apposition.

Diagnosis. A deep-bodied species of *Gymnocephalus* that is distinguished from *G. cernua* by a smaller angle between the posterior dorsal fin margin and the caudal peduncle (90-110° vs. 113-154°), by a larger eye diameter (10.2-12.3 % SL vs. 7.9-10.5 % SL) and by an irregular pattern of large dorsolateral dark blotches vs. a pattern of small dots. It differs from *G. cernua* in being deeper bodied (26.1-33.6 % SL vs. 20.1-30.7 % SL) and having a longer base of the spinous part of the dorsal fin (36.1-41.9 % SL vs. 28.8-39.6 % SL), together with a higher mean and modal number of dorsal fin spines (modal 15 vs 14). It is distinguished from *G. baloni* by the combination of a larger eye diameter (10.2-12.3 % SL vs. 8.2-10.5 % SL), smaller caudal peduncle depth (7.7-8.9 % SL vs. 7.4-10.1 % SL), higher mean and modal number of pectoral fin rays (15 vs. 13) and a steeper convex dorsal profile of the snout.

The nuclear LdhA6 intron haplotype of *G. ambriae-lacus* is unique by having an Adenine (A) at position 16 instead of a Guanine (G) in the alignment of all other examined species (see Table 5).

Description

Based on holotype and all paratypes. See Figure 8a for general appearance and Tables 4 and 5 for morphometric and meristic data of holotype (ZSM 33199), paratypes and other material. A deep bodied *Gymnocephalus* (26.1-33.6 % SL) with large eyes (10.2-12.3 % SL). Head deeper than wide, snout almost rectangular from above and blunt in lateral view with straight ventral profile. Mouth subinferior with lower jaw enclosed in upper jaw. Mandible not reaching to the anterior margin of the eye. Eye diameter greater than maxillary length and equal or smaller than preorbital distance. Dorsal margin of eye contiguous with or projecting beyond contour of predorsal profile. First opercular spine strongly developed, second or third spine weak when present. Preoperculum serrated, 9-15 spineous processes, those on the ventral arch stronger and hooked anteriorwards. Pterygoid with 12-20 thin spines.

Greatest body depth at base of second or third dorsal fin spine 26.1-33.6, mean 30.2 % SL. Head length 28.8-31.8, mean 31.2 % SL. Dorsal body profile slightly convex, almost straight in males and more convex in females. Caudal peduncle slender, longer than deep, its depth 7.7-8.9, mean 8.3% SL.

Dorsal fin with XIV-XVI (mode XV) spines and 10-12 (mode 11) rays. Dorsal-fin spines increasing in length to fourth, decreasing evenly to last spine. Distal margin of dorsal fin almost straight or slightly convex, angle between margin and dorsal profile of caudal peduncle 90-110°. Pectoral fin rounded, insertion anterior to first dorsal-fin spine and pelvic-fin origin, 14-16 rays (mode 15), rays reaching vertically to between 7th and 8th dorsal-fin spine. Pelvic fin with thick spine and 6 rays, second ray longest, origin at height or slightly beyond base of first dorsal-fin spine. Pelvic fin reaching to approximately 10th dorsal-fin spine. Anal fin with 2 strong spines and 5-6 rays, origin at height of last dorsal-fin spine, reaching to the midst of the caudal peduncle. Caudal fin equally bilobed.

Lateral line complete, originating one or two scales posterior to the occipital margin of the operculum, perforating 35-40 scales (mean 36.5) and reaching beyond the hypural.

Coloration. Ground colour in alcohol light beige with black spots on the whole flank region that may aggregate and form dark blotches. A tendency in some specimens for possessing some dark blotches along the base of the dorsal fin and along the lateral line. Most individuals with dark blotches at the base of the caudal fin and on the caudal peduncle, some of which may continue anteriorly forming some cloudy blotches on the flanks. Dorsal head region dark, with numerous aggregated black spots. All individuals with an accumulation of black spots on the operculum, forming a more or less triangular shaped blotch. Number of black spots decreasing ventrally; belly and ventral side whitish-grey. Head mottled with small black spots on the operculum, preoperculum and orbital series, number of spots decreasing ventrally. Fin membranes light greyish and semitransparent. Dorsal-fin membranes with 3-6 dark blotches composed of small black spots, spines usually but not always free of spots. Blotches arranged in a more or less straight vertical line between spines with small, single black spots irregularly scattered between them. Blotches on soft part of the dorsal fin more common and pronounced

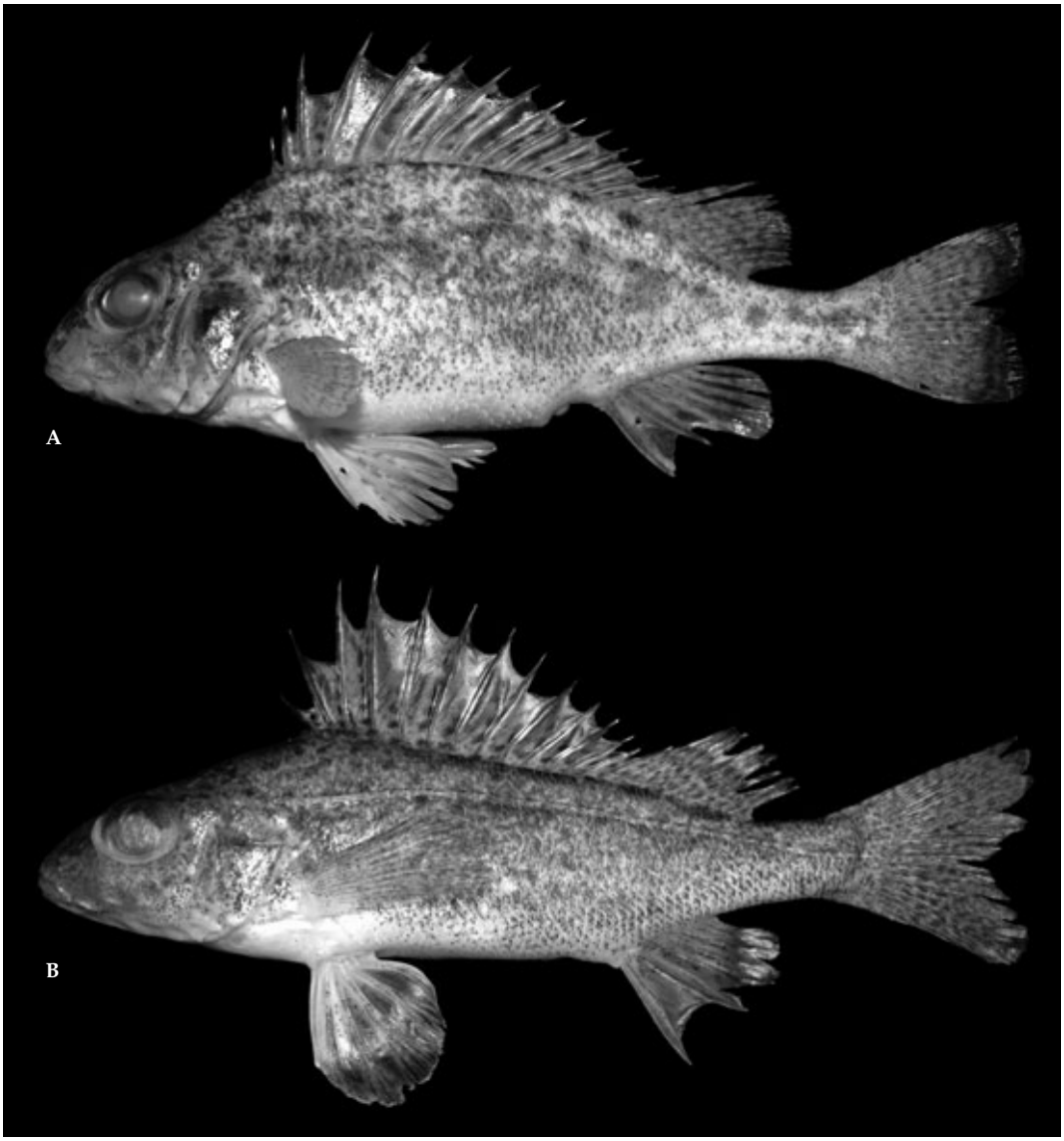

Fig. 8. A. *Gymnocephalus ambriaelacus* sp. n., ZSM 33199, holotype (female), 94 mm SL; Germany: Bavaria: Lake Ammersee at Ried; coloration in alcohol. **B.** *G. cernua*, ZSM 35946, male, 95 mm SL; Germany: Bavaria: Lake Ammersee at Utting, coloration in alcohol.

on the rays, forming distinct bands parallel to the fin margin. Only single small spots on the membranes not aggregating to form blotches. Pectoral fin with small black spots on and in between rays, evenly spread over the whole fin. Pelvic fin with loose small black spots which concentrate on rays. Anal fin with irregular arranged black spots on spines as well as on rays and membranes, more numerous on rays. Caudal fin evenly mottled with numerous small black spots which may form transverse bands.

Life ground-coloration silvery-grey, dark-black blotches aforementioned with a greenish-bronze brilliance. Dorsal fin transparent with spots arranged as aforementioned, tip of spines yellowish and tip of membranes black. Dorsal-fin rays yellowish with black markings. Pectoral fins yellow-whitish transparent with black spots. Pelvic and anal fins whitish and blear, not totally transparent with few

black spots. Caudal fin almost transparent with yellowish rays and black spots as described above.

Distribution. *Gymnocephalus ambriaelacus* is endemic to Lake Ammersee, upper Danube basin, Germany. This dimictic and oligotrophic lake is situated in southern Germany in the State of Bavaria (48° N 11° E, 533 m a.s.l.) and was formed during the last glacial period, the Würm glaciation (139 000-15 000 bp.). The lake basin filled with melted ice about 10 000 years ago (Bayerisches Landesamt für Wasserwirtschaft 2005; Hendl & Liedke 1997) and has a surface area of about 46.6 km^2.

Notes on biology. Ripe females were caught in May in shallow water between 3-5 meters depth and spawned immediately in captivity. Small eggs (~1 mm in diameter) were scattered on the bottom and were only weakly adhesive, some of them even floating. Usually, *G. ambriaelacus* is caught from mid May throughout the summer in large bow nets during the night when fishing for eel (W. Ernst, pers. comm.). According to Wagler (1926) growth in Lake Ammersee ruffe is slower compared to *G. cernua* from Danube and Elbe River and individuals reach only about 4.5 cm after the first and about 8 cm after the second year of life.

Conservation status. *G. ambriaelacus* is not commercially exploited, no catch statistics or records exist from which the conservation status could be estimated.

In October 2005 two *G. cernua* specimens were collected from Lake Ammersee (Fig. 8b), identified by their general morphology, colour pattern and typical obtuse angle between the posterior dorsal-fin margin and caudal peduncle. Both individuals possess the same nuclear LdhA6 haplotype as individuals from Danube River. As no earlier material of *G. cernua* is available from Lake Ammersee, this indicates that this species might have been introduced into Lake Ammersee, as it has been in other German, European and even North American waterbodies, too. It was apparently spread through ballast water to the North American Great Lakes, where it possibly poses a threat to their endemic fish fauna (Gunderson 1998; Newman 1999). Further evidence for occurrence outside of its natural range is accumulating all over Europe, e.g. from Scotland in Lake Lomond in 1982 (Maitland & East 1989),

Table 2. Variable positions in haplotypes of mtDNA control region sequence data for *Gymnocephalus cernua*, *G. ambriaelacus*, *G. baloni*, and *G. schraetser* with numbers and geographic origin of samples including haplotype data from Stepien et al.* (1998). Numbers in top row correspond to nucleotide position of polymorphisms. H, haplogroup.

	H	1	11	14	31	72	77	79	87	107	115	123
G. cernua												
River Isar (n=4)	1	G	A	T	T	A	C	A	A	T	A	G
River Danube (n=9+12*)	1	G	A	T	T	A	C	A	A	T	A	G
Regensburg pond (n=2)	1	G	A	T	T	A	C	A	A	T	A	G
River Lech (n=1)	1	G	A	T	T	A	C	A	A	T	A	G
River Elbe (n=7)	1/3	G	A	T	T	A	C	A	A	T	A	G
Lake Constance (n=1)	2	G	A	T	T	A	C	A	A	T	A	G
River Havel (n=1)	1	G	A	T	T	A	C	A	A	T	A	G
Lake Stechlinsee (n=2)	1	G	A	T	T	A	C	A	A	T	A	G
Odra Estuary (n=1)	1	G	A	T	T	A	C	A	A	T	A	G
River Moskva (n=1)	1	G	A	T	T	A	C	A	A	T	A	G
River Bug (n=2)	1/3	G	A	T	T	A	C	A	A	T	A	G
River Dnepr (n=1)	1	G	A	T	T	A	C	A	A	T	A	G
River Dniester (n=2)	3	G	A	T	T	A	C	A	A	T	A	G
Lake Bassenthwaite (n=11*)	4	G	A	T	**C**	A	C	A	A	T	A	G
St. Petersburg (n=13*)	5	G	A	T	T	A	**A**	**C**	A	T	A	G
Baltic Sea (n=1)	5	G	A	T	T	A	**A**	**C**	A	T	A	G
River Volga (n=3)	1/6/7	G	A	**T/A**	T	A	**A/C**	**A/C**	A	T	A	G
River Ob (n=12*)	5	G	A	T	T	A	**A**	**C**	A	T	A	G
Lake Abrau (n=3)	8	G	A	T	T	A	**A**	**C**	A	**A**	A	G
G. ambriaelacus (n=10)	9	G	**G**	T	T	**T**	C	A	**C**	T	A	**A**
G. baloni (n=9+1*)	9/10	G	**G/A**	T	T	**T**	C	A	**C**	T	A	**A/G**
G. schraetser (n=5*)	11/12	**G/A**	A	T	T	**T**	C	A	**C**	T	**T**	G

Table 3. Complete nuclear LdhA6 intron sequence of *Gymnocephalus ambriaelacus* with marked polymorphic sites and variable positions in haplotypes of nuclear LdhA6 sequence data for *G. cernua*, *G. ambriaelacus*, *G. baloni*, and *G. schraetser* with numbers and geographic origin of samples. Numbers in top row correspond to nucleotide position of polymorphisms. H, haplogroup.

5' CCTGTGTCCACACTG**A**TCCAGGTGAGGAGATTGGGA**G**CAAGCC**A**TACATGTAGCTGTTTGGCA**A**GATCC**T**AC
ATGATGAAATTCATT**A**TATCGAT**A**AGTTCACACA**A**ACACACTGTGCATTCTTCATATGTCATGAAATGACCCACA
ACCCCTGAACCTTGC**G**TTGCTCC**T**TTCCTCTTACAGGGCATGCATGGAGTGAAGGACGAGGTCTTCCTCAGCAA 3'

	H	16	37	44	64	70	88	96	107	163	171
G. cernua											
Lake Ammersee (n = 2)	1	G	G	A	A	C	G	T	G	G	C
River Isar (n = 1)	1	G	G	A	A	C	G	T	G	G	C
River Danube (n = 10)	1/4	G	G	A	A	C	G	T	G	G	C
River Elbe (n = 2)	1	G	G	A	A	C	G	T	G	G	C
River Havel (n = 1)	2	G	G	**G**	A	C	G	T	G	G	C
River Ems (n = 1)	2	G	G	**G**	A	C	G	T	G	G	C
Lake Stechlinsee (n = 2)	2	G	G	**G**	A	C	G	T	G	G	C
Lake Mueggelsee (n = 1)	3	G	G	**G**	**T**	C	G	T	G	G	C
Odra Estuary (n = 1)	2	G	G	**G**	A	C	G	T	G	G	C
River Bug (n = 1)	2	G	G	**G**	A	C	G	T	G	G	C
River Moskva (n = 1)	4	G	G	A	**T**	C	G	T	G	G	C
River Dnepr (n = 1)	2	G	G	**G**	A	C	G	T	G	G	C
River Dniester (n = 1)	2	G	G	**G**	A	C	G	T	G	G	C
Lake Abrau (n = 3)	5	G	**A**	A	A	C	G	T	**A**	**A**	C
Baltic Sea (n = 1)	3	G	G	**G**	**T**	C	G	T	G	G	C
G. ambriaelacus (n = 10)	6	**A**	G	A	A	**T**	**A**	**A**	**A**	G	**T**
G. baloni (n = 9)	7	G	G	A	A	**T**	**A**	**A**	**A**	G	**T**
G. schraetser (n = 3)	8	G	G	A	A	**T**	G	T	**A**	G	**T/C**

124	159	169	172	189	236	243	252	285
G	T	T	A	C	C	T	C	T
G	T	T	A	C	C	T	C	T
G	T	T	A	C	C	T	C	T
G	T	T	A	C	C	T	C	T
G	T	T	A	C	C	**T/C**	C	T
G	T	T	**C**	C	C	T	C	T
G	T	T	A	C	C	T	C	T
G	T	T	A	C	C	T	C	T
G	T	T	A	C	C	T	C	T
G	T	T	A	C	C	T	C	T
G	T	T	A	C	C	**T/C**	C	T
G	T	T	A	C	C	T	C	T
G	T	T	A	C	C	**C**	C	T
G	T	T	A	C	C	T	C	T
G	T	T	A	**T**	C	T	**T**	T
G	T	T	A	**T**	C	T	**T**	T
G	T	**T/A**	A	**C/T**	**C/A**	**T**	**C/T**	**T/A**
G	T	T	A	**T**	C	T	**T**	T
G	T	T	A	C	C	T	C	T
A	T	T	A	C	C	**C**	C	T
A	T	T	A	C	C	**C**	C	T
G	**A**	T	A	**T**	C	**C**	C	T

from England in 1991 in Lake Bassentwhaite and from Germany in Lake Constance in 1987 (Rösch & Schmid 1996; Winfield et al. 1998; Gunderson et al. 1998). More recent reports for introduction are from Italy in Lake S. Croce (Capovilla 2006) and from the Adriatic drainage system of Bosnia and Herzegovina (Dulcic et al. 2005). Additional support for the assumption that *G. cernua* is not an autochthonous element in Lake Ammersee derives from the fact that its occurrence could not be verified from possible founder populations from the lake's in- and affluent, i. e. Ammer River and Amper River respectively (pers. obs.). The nearest neighbour populations of *G. cernua* and *G. baloni* are documented from River Isar which is connected to Lake Ammersee only via its affluent Amper River.

Relationships. According to mitochondrial and nuclear DNA-sequence data *G. ambriaelacus* must have evolved from a *G. baloni* related stock (see Results). This close relationship is reflected in their general phenetic similarity as well (Figs 8a and 3a,b).

Discussion

Only *G. schraetser* and *G. baloni* occur sympatrically with *G. cernua* in the Danubian drainage. Although the similarity between the latter two is striking compared to the very elongate and conspicuously coloured *G. schraetser*, phylogenetic relationships of this trio are discussed controversially. Whereas in the description of *G. baloni* in 1974, Holčík & Hensel propose to place *G. cernua* and *G. baloni* in the subgenus *Acerina* and the remaining two elongated species in the subgenus *Gymnocephalus*

Table 4. Morphometric data for *Gymnocephalus ambriaelacus*, *G. baloni*, *G. cernua* syntypes, and various populations of *G. cernua*. H, holotype; SD, standard deviation.

	G. ambriaelacus			*G. baloni*		
	H	types and others (n = 26)		H	types and others (n = 32)	
		mean	SD		mean	SD
Total length	94.0	109.4	15.1	–	–	–
Standard length	107.3	90.2	12.6	107.3	101.7	14.3
In percent of standard length						
Head length	30.1	31.0	0.7	29.9	29.2	1.2
Head depth	25.8	24.6	0.7	28.9	26.6	1.3
Head width	18.5	17.7	0.9	21.4	19.0	1.3
Body depth	32.9	30.1	1.7	35.7	32.1	1.8
Body width	20.1	17.3	1.8	21.3	19.0	2.4
Caudal peduncle length	20.8	19.1	1.0	18.1	17.9	1.1
Caudal peduncle depth	8.1	8.3	0.3	9.6	8.9	0.5
1st dorsal fin base length	40.7	38.8	1.2	44.6	41.1	1.9
2nd dorsal fin base length	16.1	16.4	0.8	16.9	16.6	1.1
Anal fin base length	12.8	13.4	0.6	15.2	14.6	0.8
Longest pectoral fin ray length	19.6	20.5	0.9	20.7	19.7	1.5
Longest pelvic fin ray length	19.7	20.0	0.9	22.1	20.3	1.6
Predorsal length	36.3	37.8	1.0	37.9	35.4	3.4
Preventral length	35.4	35.5	0.9	41.9	37.0	4.0
Preorbital length	10.2	11.3	0.4	10.0	10.6	1.5
Postorbital length	10.3	10.6	0.3	11.5	11.1	1.3
Eye diameter	10.4	11.1	0.5	9.6	9.5	1.6
Snout length	9.7	10.3	0.4	10.0	9.6	1.6
Interorbital width	6.9	6.7	0.5	6.6	7.1	1.9
Anal fin-anus distance	4.0	5.2	0.8	5.6	5.5	2.4
1st dorsal fin spine length	4.3	5.0	1.2	6.8	6.9	2.2
2nd dorsal fin spine length	7.9	9.3	1.7	12.6	11.9	2.3
3rd dorsal fin spine length	13.4	15.6	1.8	16.2	16.8	1.6
4th dorsal fin spine length	16.8	18.4	1.2	16.7	18.3	1.3
1st anal fin spine length	13.7	14.9	1.1	15.8	14.3	1.5
2nd anal fin spine length	14.3	14.8	1.0	15.8	14.2	1.5
In percent of head length						
Preorbital length	33.9	36.4	1.0	33.4	35.5	2.7
Postorbital length	34.3	34.1	0.8	38.5	37.2	1.4
Eye diameter	34.6	35.8	1.5	32.1	31.8	1.9
Maxillary length	32.2	33.3	1.0	33.4	32.1	2.3
Interorbital distance	23.0	21.7	1.6	22.1	23.0	1.6
Caudal peduncle depth (% of its length)	38.8	43.6	2.7	53.0	50.3	3.6
Eye diameter (% of snout length)	107.7	107.6	5.3	96.0	99.5	8.7
Eye diameter (% of preorbital length)	102.1	98.6	5.6	96.0	90.1	9.8

sensu stricto based on vertebrate counts and some coloration differences, other biologists (Rab et al. 1987; Stepien et al. 1998; Sloss et al. 2004) have suggested a sister-taxon relation between *G. baloni* and *G. schraetser* based on molecular data. According to our genetic data, the phylogenetic position of *G. schraetser* within *Gymnocephalus* cannot be resolved satisfactorily. It seems therefore to be advisable to use a nuclear DNA multi-locus approach to resolve the phylogenetic history in the genus *Gymnocephalus* including also *G. acerina*.

With *Salvelinus evasus*, *Coregonus bavaricus* and *Gymnocephalus ambriaelacus* Lake Ammersee is home to three endemic species from three different families. Compared to other prealpine lakes in that region this elevated degree of endemism is remarkable. At the moment it is only possible to speculate about the reasons and it must remain open, whether this

G. cernua									
syntypes		Baltic Sea		Danube River		Elbe River fresh		Elbe River brackish	
BMNH-	Lin.Soc.-	(n = 23)		(n = 25)		(n = 18)		(n = 24)	
1853.11.12.5	Lon.2	mean	SD	mean	SD	mean	SD	mean	SD
122.1	–	121.7	18.1	122.8	24.8	98.4	9.6	125.0	20.6
101.1	96.8	101.3	15.8	98.9	17,0	80.5	8.1	100.3	16.0
30.6	28.5	28.7	0.7	29.5	0.9	31.3	1.1	33.2	1.1
26.4	25.5	19.9	0.7	22.4	0.8	22.6	0.8	23.7	0.8
–	–	13.6	0.7	16.4	1.0	15.8	0.7	17.0	0.7
35.3	33.0	23.4	1.6	27.0	1.5	26.6	1.1	27.0	1.1
–	–	13.4	0.9	16.3	1.2	14.1	0.8	15.4	0.9
17.9	17.9	23.3	1.1	20.2	1.3	21.2	1.1	20.1	1.2
10.1	9.2	7.5	0.3	8.8	0.3	9.4	0.4	9.2	0.5
40.9	40.9	34.6	1.7	36.0	1.5	34.5	1.8	34.9	1.6
15.8	16.2	17.5	3.6	19.4	1.3	19.5	1.4	18.8	1.2
15.0	14.6	11.4	0.7	12.4	0.8	13.0	0.9	14.7	0.9
21.1	20.9	18.5	1.2	20.1	1.0	20.6	1.1	23.6	1.5
22.0	21.5	18.6	0.9	19.8	1.1	20.4	1.1	22.5	1.0
36.6	33.3	34.2	0.6	35.1	1.0	36.2	1.1	38.3	1.1
39.1	37.2	32.2	2.5	35.2	1.1	35.0	2.3	36.8	2.9
10.4	9.1	10.5	0.4	10.9	0.5	11.1	0.6	12.2	0.8
11.1	10.9	10.1	0.5	10.8	0.8	11.1	0.6	12.3	0.7
9.2	9.5	9.1	0.4	8.7	0.5	9.7	0.5	9.3	0.5
–	10.6	9.1	0.5	8.8	0.4	9.6	0.6	11.4	0.5
–	–	4.8	0.4	5.6	0.4	5.4	0.3	6.2	0.5
–	4.0	3.7	0.6	5.4	0.8	4.8	0.7	4.2	0.5
6.0	3.2	4.4	1.3	6.3	1.7	6.8	1.2	6.9	1.6
11.3	7.3	8.2	1.7	13.2	2.0	12.7	1.7	12.3	2.5
16.5	13.5	13.9	2.0	19.0	1.9	18.6	1.6	17.3	1.9
18.7	17.0	16.8	1.6	20.5	1.3	20.4	1.2	19.1	1.5
13.9	12.0	14.4	1.5	15.7	0.9	16.8	1.7	15.5	3.0
13.8	12.8	12.8	1.3	13.9	0.8	14.9	0.9	16.1	2.4
33.9	31.9	36.6	1.6	37.1	1.4	35.6	1.2	36.9	1.9
36.2	38.2	35.2	1.4	36.7	1.9	35.5	1.5	37.0	2.1
29.9	33.2	31.6	1.3	29.6	1.6	31.1	1.1	28.1	1.2
–	37.0	31.8	1.5	30.0	1.5	30.8	1.1	34.5	1.1
–	–	16.7	1.2	18.8	1.1	17.4	1.0	18.7	1.2
56.3	51.7	32.1	2.0	43.5	3.5	44.5	3.6	45.9	4.6
–	89.8	99.3	5.6	99.0	8.3	101.1	6.1	81.5	4.6
88.2	103.9	86.4	6.0	80.0	5.7	87.4	5.0	76.5	6.1

phenomenon is either due to intrinsic factors favouring speciation in that particular lake, or, if Lake Ammersee has acted for an unknown reason as a reservoir for relict populations, or finally, whether it is simply a sampling artefact.

Results from our morphometric and genetic analyses show that there are probably more species within *G. cernua*. For example ruffes from Baltic Sea drainage are characterised by an elongate and shallow body (body depth 20.9-27.1 % SL) and distinctive genetic characteristics (Fig. 7). Kolomin (1977) pointed to a peculiar ruffe population from Siberian Nadym River, which is close to the type-locality of *A. c. essipovi*. It is characterised by a shallow head, fusiform body and long snout with elongate maxillary. Unfortunately, it is not known were the five syntypes are deposited and we were unable to obtain a copy of the original description by Burmakin (1941). The taxon would be available (Kottelat 1997) but without detailed comparative studies it remains to be studied whether these two forms are conspecific, and distinctive on the species level. The shallow bodied (body depth mean 25 % SL) *Acerina czekanowskii* Dybowski, 1874 from Angara River may also fall into this group, but again no types known.

Comparison material

Gymnocephalus cernua: ZSM 1244-1251, 4 (out of 8), 121.3-80.8 mm SL; Germany: Bavaria: River Danube at Straubing. – ZSM 2449/2453-2459, 7, 118.1-90.4 mm SL; Germany: Bavaria: River Danube at Straubing. – ZSM 18248-18257, 4 (out of 10), 109.7-85.5 mm SL; Germany: Bavaria: River Danube at Straubing. – ZSM 31751, 2, 74.9-74.8 mm SL; Germany: Bavaria: River Danube below Niederalteich. – ZSM 33971, 1, 76.2 mm SL; Germany: Bavaria: River Danube below Niederalteich. – ZSM 31765, 2 (out of 4), 101.7-98.2 mm SL; Germany: Bavaria: River Isar, 600 m above confluence with River Danube at Deggendorf, (DNA Bank accession number: AB34403362). – ZSM 34130, 8 (out of 23), 151.7-86.7 mm SL; Germany: Bavaria: River Isar at "Isar Stau III", approx. 36 km upstream of confluence with River Danube. – ZSM 33857, 23, 140.6-59 mm SL; Germany: Bavaria: River Lech canal in Augsburg, downstream of canoe course. – FSJF 57, 1, 101.7 mm SL; Romania: Tulcea: Danube delta at Bestepe. – FSJF 94, 6, 122-96 mm SL; Germany: Rheinland-Pfalz: River Mosel, reservoir at Müden. – ZSM 33907, 20 (out of 25), 130.5-61 mm SL; Germany: Bavaria: River Main at dam Erlabrunn, NW of Würzburg. – ZSM 31721, 4 (out of 6), 72.5-71.4 mm SL; Germany: Baden-Württemberg: Lake Constance, between Egg, Herrieden and Island of Mainau in shallow water. – ZSM 31769, 2 (out of 6), 80.2-75 mm SL; same data as ZSM 31721. – ZSM 33600, 7 (out of 12), 98.1-70.7 mm SL; same data as ZSM 31721. – ZSM 31969, 2 (out of 6), 81.4-80.2 mm SL; same data as ZSM 31721. – ZSM 31970, 2 (out of 5), 80.5-72.6 mm SL; same data as ZSM 31721. – ZSM 31971, 1 (out of 5), 74.6 mm SL; same data as ZSM 31721; ZSM 31968, 5, 76.3-72.6 mm SL; same data as ZSM 31721. – ZSM 31973, 3 (out of 5), 78.6-75.5 mm SL; same data as ZSM 31721. – ZSM 31578, 4 (out of 13), 106.7-105.6 mm SL; Germany: Lower Saxony: low tide sink-trawl catch, River Elbe at Twielenfleth, lighthouse. – ZSM 31575, 4, 150-126.6 mm SL; same data as ZSM 31578. – ZSM 31574, 2 (out of 8), 76.4-74.6 mm SL; same data as ZSM 31578, (DNA Bank accession number: AB34403376). – ZSM 31577, 3, 173.8-81 mm SL; same data as ZSM 31578. – ZSM 31539, 2 (out of 9), 91.9-85.3 mm SL; same data as ZSM 31578. – ZSM 31573, 6 (out of 9), 107.5-75.7 mm SL; same data as ZSM 31578. – ZSM 31536, 2 (out of 8), 83.8-83.2 mm SL; same data as ZSM 31578. – ZSM 31562, 3 (out of 6), 94.2-84.4 mm SL; same data as ZSM 31578. – ZSM 2298-

Table 5. Meristic data for *Gymnocephalus ambriaelacus*, *G. baloni*, *G. cernua* syntypes, and various populations of *G. cernua*. H, holotype; SD, standard deviation.

	G. ambriaelacus				*G. baloni*			
	H	types and others (n = 26)			H	types and others (n=32)		
		modal	mean	SD		modal	mean	SD
Pectoral fin rays	15	15	14.6	0.6	14	13	13.5	0.8
Pelvic fin rays	6	6	6.0	0	6	6	6.0	0.2
Anal fin spines	2	2	2.0	0	2	2	2.0	0
Anal fin rays	5	5	5.3	0.5	6	6	5.6	0.5
Dorsal fin spines	15	15	14.9	0.5	15	15	15.0	0.6
Dorsal fin rays	12	11	11.3	0.5	11	11	11.4	1.0
Pored lateral line scales	39	37	36.8	1.2	37	36	36.2	1.1
Preopercular spines	13	11	11.3	1.4	8	12	10.8	2.2
Opercular spines	2	1	1.5	0.6	2	2	2.2	0.4
Angle between dorsal fin margin and caudal peduncle	100	–	104	5.4	100	–	98	7.4

2327, 20 (out of 30), 155.7-97.5 mm SL; Germany: State of Hamburg: River Elbe, Elbe harbour area near Hamburg. – ZSM 2328-2358, 13 (out of 28), 130.8-110.2 mm SL same data as ZSM 2298-2327. – ZSM 33717, 18 (out of 27), 109.9-74 mm SL; Germany: Saxony-Anhalt: River Elbe bayou "Priesitzer See" near Pretsch, (DNA Bank accession number: AB34403431). – FSJF 1904, fin sample only, Germany: Brandenburg: River Havel at Rathenow, (DNA Bank accession number: AB34403417). – FSJF 462, 14 (out of 48), 150-80 mm SL; Germany: Brandenburg: Lower River Odra close to Schwedt at river km 685-697, "Unt. Odertal". – FSJF (not catalogued), fin sample only, Germany: Mecklenburg Western Pomerania: Odra Estuary, no exact data available, (DNA Bank accession number: AB34403410). – FSJF 1696, 24, 100.5-80 mm SL; Germany: State of Berlin: Lake Mueggelsee. – FSJF 1697, 20, 100.1-80.2 mm SL; Germany: Brandenburg: Lake Stechlinsee, J. Freyhof, (DNA Bank accession numbers: AB34403550, AB34403538). – FSJF 1818, 23, 150.8-79.3 mm SL; Finland: Baltic Sea, Hailuoto Island, 20 km off shore, (DNA Bank accession number: AB34403432). – FSJF 324, 11, 92–70 mm SL; Ukraine: Dniestr: River Dniester at Khotin (a town), (DNA Bank accession number: AB34403396). – FSJF 362, 4, 84-74 mm SL; Ukraine: Zhitomirskaya Region: Dnepr drainage, River Teterev at Korotyshev (a town), dam lake, backwater and a very small tributary to the dam lake, (DNA Bank accession number: AB34403415). – FSJF (not catalogued), fin sample only, Russia: Moskva Oblast: River Moskva at Zvenigorod, Volga drainage, (DNA Bank accession number: AB34403409). – FSJF (not catalogued), fin sample only, Ukraine: Vistula: River Bug at Bus'k, at the road Bus'k–L'vov, (DNA Bank accession number: AB34403387 & AB34403379).

Gymnocephalus baloni: SNM-RY 2261, holotype, 107.3 mm SL; Slovakia: River Danube near Klizská Nemá, K. Hensel, 25 Oct 1968. – SNM-RY 2262, paratypes, 3 (out of 10), 92.3-118.7 mm SL; same data as holotype. – CU-RY 196, paratypes, 6 (out of 20), 78.7-110.6 mm SL; same data as holotype. – ZSM 32819 (ex FSJF 75), 6 (out of 21), 94.2-79.7 mm SL; Romania: River Danube delta at "Balta Ialomitei". – NMW 42312, 5 (originally determined as *Acerina cernua*), 121.5-96.1 mm SL; Ukraine: Odeska Oblast: River Danube delta at Wilkow (Wylkowe, about 15 km upstream of mouth in Black Sea). – SMF 24051, 1 (originally determined as *Acerina cernua*), 114 mm SL; Serbia: Palanka (most likely from River Danube at Palanka. – ZSM 33416, 1, 108.1 mm SL; Germany: Bavaria: River Danube at Niederalteich. – ZSM 34996, 2, 70.5-65.8 mm SL; Germany: Bavaria: River Danube upstream of Vilshofen, river km 2252-2262, (DNA Bank accession numbers: AB34403540, AB34403562). – ZSM 35002, 1, 108.9 mm SL; same data as ZSM 34996, (DNA Bank accession number: AB34403625). – ZSM 35578, 2, 93.9-89.8 mm SL; same data as ZSM 34996, (DNA Bank accession numbers: AB34403593, AB34403532). – ZSM 35579, 4, 93-65.1 mm SL; same data as ZSM 34996, (DNA Bank accession numbers: AB34403561, AB34403585, AB34403569, AB34403548). – NMW 42294, 1 (originally determined as *Acerina cernua*), 117.4 mm SL; Austria: Petronell (most likely from River Danube E of Vienna). – NMW 42302, 1 (originally determined as *Acerina cernua*), 84.1 mm SL; River Raab, tributary to River Danube. – NMW 81197, 1, 114 mm SL; Austria: Lower Austria: River Danube at river km 1998.6-1999.3, "Stauraum Altenwoerth" E of Krems/Germany. – NMW 81198, 1, 114 mm SL; Austria: Lower Austria: River Danube at River km 2001.5-2000.3, "Stauraum Altenwoerth" E of Krems/Germany. – NMW 81199, 2, 124.4-107.1 mm SL; Austria: Lower Austria: River Danube at "Stauraum Altenwoerth" E of Krems/Germany. – NMW 90714-1, 1 (out of 2), 114.4 mm SL; Austria: Lower Austria: River Danube at Stopfenreuth. – NMW 81144, 1, 120.5 mm SL; Austria: Upper Austria: Innbach stream at mouth in River Danube. – ZSM 1019/48, 1, 104.4 mm SL; Germany: Bavaria: River Paar upstream of intersection with River Danube near Irsching. – ZSM 5008, 1, 93 mm SL; no location available, don. Zool. Inst. Munich, received Mar 1952.

Gymnocephalus schraetser: ZSM 35003, 3 (out of 8), 110.2-93.2 mm SL; Germany: Bavaria: River Danube upstream

G. cernua													
syntypes		Baltic Sea			Danube River			Elbe River fresh			Elbe River brackish		
BMNH-	Lin.Soc.-	(n = 23)			(n = 25)			(n = 18)			(n = 24)		
1853.11.12.5	Lon.2	modal	mean	SD	modal	mean	SD	modal	mean	SD	modal	mean	SD
14	15	14	13.9	0.5	13	13.2	0.6	13	13.1	0.8	14	13.5	0.8
6	6	6	6.0	0	6	6.0	0	6	6.0	0	6	6.0	0
2	2	2	2.0	0	2	2.0	0	2	2.1	0.2	2	2.1	0.3
6	5	5	5.3	0.5	5	5.2	0.4	5	5.3	0.7	6	5.9	0.4
14	13	14	14.2	0.4	14	13.7	0.5	13	13.5	0.6	14	13.6	0.7
12	12	12	12.0	0.5	12	12.4	0.6	13	12.5	0.7	12	12.2	0.6
34	–	37	37.3	1.1	35	35.1	1.1	36	36.3	1.2	37	37.0	1.1
–	8	12	11.2	1.7	9	8.9	0.9	9	9.1	0.9	8	9.4	2.4
1	1	1	1.0	0	1	1.0	0	1	1.0	0	1	1.0	0.3
154	–	–	141	8.6	–	125	7.2	–	121	4.3	–	125	5

of Vilshofen, river km 2257-2262, (DNA Bank accession numbers: AB34403554, AB34403558, AB34403551).

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(Fortsetzung von S. 118)

Auch innerhalb der Kapitel sind die Schwerpunkte heterogen verteilt. In einigen Fällen wie in der "Verbreitung der Chilopoden in Europa" wurde der Titel thematisch passend gewählt. In anderen Fällen, wie im Kapitel "Ökologie" wurde die Beschränkung auf den mitteleuropäischen Raum in einem Unterkapitel fixiert. Teilweise fehlt eine kritische Reflektion der zitierten Befunde. So hätte z. B. auffallen können, dass bei einer zitierten Arbeit über *Lithobius*-Arten in den Alpen (S. 393) die in mitteleuropäischen Wäldern sehr häufige Art *L. mutabilis* ausschließlich oberhalb 1600 m verzeichnet wird. Wenngleich die ausführliche Arbeit zur Trennung von *L. glacialis* erst 2008 erschien, wurde diese hochalpine Art schon 1999 revalidiert und neu für Deutschland nachgewiesen. Dies wird auch korrekt im Kapitel "Verbreitung der Chilopoden in Europa" wiedergegeben. Die Aussage "Echte Hochgebirgstiere … gibt es unter den Chilopoden nicht" auf S. 292 ist damit aber nicht mehr haltbar. Auch auf die vergleichsweise jungen Erkenntnisse über baumbewohnende Chilopoden wird nicht eingegangen, obgleich die betreffende Publikation im Literaturverzeichnis aufgeführt ist.

All diese – angesichts der Fülle an Informationen, die inzwischen zum Thema "Hundertfüßer" existieren, sicher verzeihlichen Fehler – schmälern den Wert des Buches in keiner Weise. Sie wären jedoch durch ein gründlicheres Lektorat vielfach vermeidbar gewesen. Insgesamt muss betont werden, dass hier ein einzigartiges Werk entstanden ist, welches als Nachschlagwerk für diese Tiergruppe sicher über Jahrzehnte Bestand haben wird. Eine englische Übersetzung wird dringend angeraten, um die mühevoll zusammengetragenen Resultate international verfügbar zu machen.

J. Spelda

6. Stock, S. R. 2009. MicroComputed Tomography: Methodology and Applications. – 336 pp. CRC Press, Taylor & Francis Group, Boca Raton, Fl., ISBN 978-1-4200-5876-5.

Microcomputed tomography (microfocus computed tomography, microCT), is a spin off from (diagnostic) medical "CT". By this examination method, individual x-ray projection images of specimens are recorded at successive rotation angles; these serve as base data for subsequent EDV-recalculation of a volumetric data set ("3D grey scale image" of the specimen). In the case of microCT (µCT) machines are customized for small (< ~ 15 cm) samples. It is particularly the increase of computer performance, allowing graphical processing of the often voluminous data sets for "normally" equipped users at the PC level, which triggered a boom in microCT in recent years. MicroCT allows visualization of structures with (relatively) high x-ray absorption. In the research field of biology these are, for example, internal (e. g. vertebrates) or external (e. g. arthropods) skeletal elements etc. Evidently, this can be utilized for systematic research. Indeed, microCT is about to become a standard technique in this field and most major natural history museum/institutions are gathering respective equipment.

With all aspects involved – ranging from technical principles of data acquisition to graphical interpretation – the entire technique is exceedingly complex. Some basic knowledge, however, is a prerequisite for tasks, such as purchasing a microCT scanner or establishing the method at a research institution. The present book is perfectly suited for this purpose. It is the first comprehensive account of microCT and provides a perfect introduction into the entire methodology. In fact, the whole range of aspects, starting with technical basics (beam technology) via specifics of machines until application examples – well structured into many individual chapters –, is addressed. The second part is chiefly a review of studies applying microCT. This stands for the particular strength of the book: assembling all the references must have cost enormous effort. It seems, nearly the entire literature dealing with microCT until 2008 is covered here. This provides a most useful basis for over viewing potentialities perspectives and of the method. Several flaws contrast this all: Reading – particularly for a non-native English speaker – is difficult. Very long (up to six lines – whole matter width) sentences are encountered frequently in the text. In many places, explanations of technical backgrounds and procedures are imprecise and difficult to follow. To give only one example for a confusing explanation, surface rendering by threshold segmentation is described as: "… apply a threshold to a dataset and view the resulting 3D rendering of the voxels more absorbing than the threshold." Definitely, you do not view voxels in this visualization mode and there is no word on the fundamental differences between volume and surface rendering. Something else that could be criticized is the scattered presentation of references. A single comprehensive list at the end of the book might have been better than many separate small ones for chapters.

Nevertheless, this book is a highly valuable resource for a variety of tasks. It is very useful for interpreting results, planning research efficiently or judgement on the feasibility of projects etc. Overall, it can be recommended to beginners at the entry-level just like to experienced users who want to get deeper into the technical background and widen their scope on microCT. It can be used for both, introductory reading and reference book for (fundamental) terms used in microCT. The latter is facilitated by the elaborate index at the end of the book.

Bernhard Ruthensteiner