Supplementary information,

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1. Dissection strategy



Supplementary Figure 1

Schematic depiction of the dissection strategy utilised in this study. Red dotted lines mark the cuts made. The upper and lower oral jaws and the lower pharyngeal jaw constituted the 'lower suspensorium' that was used for RNA-extraction. The dissection included the following tissues: bone, cartilage, teeth, muscle, tendons, fat, and blood vessels.

2. 2D geometric morphometric analysis

Method

A Scanco μ CT 40 (SCANCO Medical AG, Brüttisellen, Switzerland) collected a series of twodimensional micro-computed tomography (micro-CT) images of the head of each fish with a resolution of either 2 or 10 μ m/pixel. We isolated regions of the resulting .tiff images showing the head of the fish, and simultaneously converted them to DICOM images, using custom-written software (Matlab R2011b, The MathWorks, Inc., Natick, MA, USA). From these, the TINA Geometric Morphometrics Toolkit generated three-dimensional reconstructions of the bones in each fish's head (Schunke *et al.* 2012); we down-sampled the 2 μ m/pixel scans fivefold, so that all reconstructions had a voxel size of 10 μ m. Reconstructions were rendered using the surface rendering style shipped with TINA (tmlt_surface_style.txt), with thresholds adjusted as needed to show all jaw bone features. We rotated each reconstruction to show a lateral view of the head, superimposing the left and right otoliths and jaw bones. The dump function of TINA exported a two-dimensional screenshot of the three-dimensional reconstruction as a tiff image, which we converted to bitmap. TpsUtil (ver. 1.64; Rohlf 2015) built a randomized tps file from the bitmap images. We used tpsDig2 (ver. 2.30; Rohlf 2017) to set the scale of each image using the length of the TINA crosshairs as a standardized number of voxels. We placed a set of functionally-relevant landmarks and semi-landmarks on bones of the oral jaws (premaxilla, dentary, and articular) and the lower pharyngeal jaw using tpsDig2 (Suppl. Table 1, Suppl. Figure 2), referring to the corresponding three-dimensional reconstruction in TINA as a guide to accurately place each landmark. Next, we used tpsUtil to restore the original order of the specimens and to designate semi-landmarks by creating a sliders file. From the tps file and sliders file, tpsrelw32 (ver 1.60; Rohlf 2017b) performed a semi-landmark superimposition. We imported the aligned landmark set into MorphoJ (ver. 1.06d; Klingenberg 2011) with the centroid sizes as covariates, performed a Procrustes superimposition, then adjusted for allometry using a pooled within-species regression of Procrustes coordinates on centroid size (Klingenberg 2016). A permutation test using 10,000 permutations indicated a significant effect of specimen size on shape (p=0.0007), so we performed our final principle component analysis on the regression residuals to determine the shape changes responsible for variability in our specimens.

Supplementary Table 1

Landmarks and semi-landmarks used for geometric morphometrics of oral and pharyngeal jaw bones. Semi-landmarks are indicated with a superscript ^{*}. Terminology as in (Barel & van Oijen 1976). Landmarks are based on those in (Fujimura & Okada 2008; Kalt 2017; Powder *et al.* 2015).

Premaxilla

- 1 Dorsal tip of ascending arm
- 2 Anterior tip (base of tooth)
- 3 Posterior end of dentiginous area (base of tooth)
- 4 Posterior tip of dentiginous arm
- ^{*}5 Curve between dentiginous arm and ascending arm

Dentary

- 6 Posterior tip of coronoid (dentary) process
- 7 Posterior end of dentiginous area (base of tooth)
- 8 Anterior tip (base of tooth)
- 9 Anterior ventral corner of chin
- 10 Posterior ventral tip
- *11 Reentrant angle

Articular

- 12 Dorsal tip of primordial (articular) process
- *13 Posterior ventral border of dorsal obturated foramen

- 14 Anterior tip of articular excurvation
- 15 Anterior process of coulter area
- 16 Ventral tip of retroarticular process
- 17 Postarticulation process of coulter area

Lower pharyngeal

- 18 Posterior end of horn
- 19 Posterior end of dentiginous area (base of tooth)
- 20 Anterior end of dentiginous area (base of tooth)
- 21 Anterior tip of keel
- *22 Center of ventral-most point





Supplementary Figure 2

Landmarks and semilandmarks for geometric morphometrics, shown schematically (left) and on a two-dimensional image of a three-dimensional reconstruction (right). Semilandmarks are denoted with crosshairs in the schematic image (left). See Supplementary Table 2 for landmark locations.

Results

Increasing PC1 loading was associated with the oral jaws closing and the mouth becoming more superior and upward-pointing; the premaxilla having a decreased angle between its ascending and dentiginous arms, and a shorter dentiginous area; the dorsal obturated foramen having a more acute angle at its posteroventral border (between the primordial process and articular excurvation); and the lower pharyngeal jaw having a shorter keel (Suppl. Figure 3b). Increasing PC2 loading was

associated with the premaxilla having a longer dentiginous arm; the dentary having a longer dentiginous area; the articular having a longer anteroventral portion and anterior-posteriorly wider coulter area; and the lower pharyngeal jaw having a longer dentiginous area, shorter keel, and more horizontal orientation (Suppl. Figure 3c). Increasing PC3 loading was associated with the premaxilla having a longer dentiginous arm; the dentary having a longer dentiginous area and longer coronoid process; the dorsal obturated foramen having a more obtuse angle at its posteroventral border; the articular having a anterior-posteriorly narrower coulter area and more vertical alignment; and the lower pharyngeal jaw having longer, more dorsally-pointing, horns and more horizontal orientation (Suppl. Figure 3d).



Supplementary Figure 3

Results of the principle component analysis on the landmarks of oral and pharyngeal jaw bones. (a) Plotting the first and second principle components (PC1 and PC2) shows individuals of the same species grouped together, with the two species that are algae browsing herbivores and one omnivorous species having negative PC1 loadings while the other omnivore and the two carnivorous species have positive PC2 loadings. (b)—(d) Deformation grids and wireframes for PC1—PC3, respectively, with the left column of plots having a scale factor of -0.1 and the right column having a scale factor of 0.1. Solid grey areas indicate the average (consensus) landmark configuration, while black lines indicate the deformed configuration and black filled circles indicate landmarks.

Discussion

Our morphometric analysis proved the morphological features of juvenile cichlids are similar to those previously described in adults – for example, the mouths of the carnivorous juveniles were less blunt and angled more superiorly compared to herbivores, as is seen in the external morphology of adults of the same species and other Great Lake cichlids (Cooper *et al.* 2010; Wanek & Sturmbauer 2015). This suggests that individuals have already acquired their species-specific adaptive features upon completion of larval development (stage 26). The oral jaw bones show pronounced differences between species, reflecting the diversity of methods employed to acquire food – species that bite off algae have shorter, more robust oral jaws to produce higher scraping forces than species that use suction to capture their prey (Albertson & Kocher 2001). The lower pharyngeal jaw showed the most noticeable differences between carnivorous species, likely reflecting the different hardnesses of their prey (Hulsey *et al.* 2006; Muschick *et al.* 2012). Our observed separation of species according to differences in prey capture and prey processing supports the idea that the oral and pharyngeal jaws specialise for different tasks (Liem 1973).

3. Gene Ontology analysis

Supplementary Table 2

Candidate genes that are alternatively spliced with "pharyngeal jaw system" GO term annotation.

O.niloticus gene ID	Ensemble ID	Gene name	Gene description
			PR domain containing 1,
on.gene.LG11.793	ENSTNIG0000003926	PRDM1	with ZNF domain
on.gene.LG12.131	ENSGACG00000013057	TBX1	T-box 1
			PBX/knotted 1 homeobox
on.gene.LG16-21.21	ENSGACG0000001456	PKNOX1	1
on.gene.LG16-21.422	ENSORLG00000017372	dlx2a	dlx2a protein
			wingless-type MMTV
			integration site family,
on.gene.LG18.504	ENSTNIG0000008486	WNT9A	member 9A
			secreted protein, acidic,
on.gene.LG2.11	ENSGACG0000016847	SPARC	cysteine-rich (osteonectin)
			Retinoic acid receptor
on.gene.LG20.704	ENSORLG0000007861	A5JL88_ORYLA	gamma 1
			Fas (TNFRSF6)
on.gene.LG23.458	ENSORLG00000017140	FAF1	associated factor 1
on.gene.LG5.47	ENSGACG00000011231	BARX1	BARX homeobox 1
			fibroblast growth factor 8
on.gene.UNK45.28	ENSTNIG0000006362	FGF8 (1 of 2)	(androgen-induced)

4. RNA-seq analysis



Supplementary Figure 4

Venn diagram of overlap between differentially expressed (DE) genes and alternatively spliced (AS) genes.

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