The genomic basis of similarity in the cichlid fishes of the Lake Victoria Region Superflock

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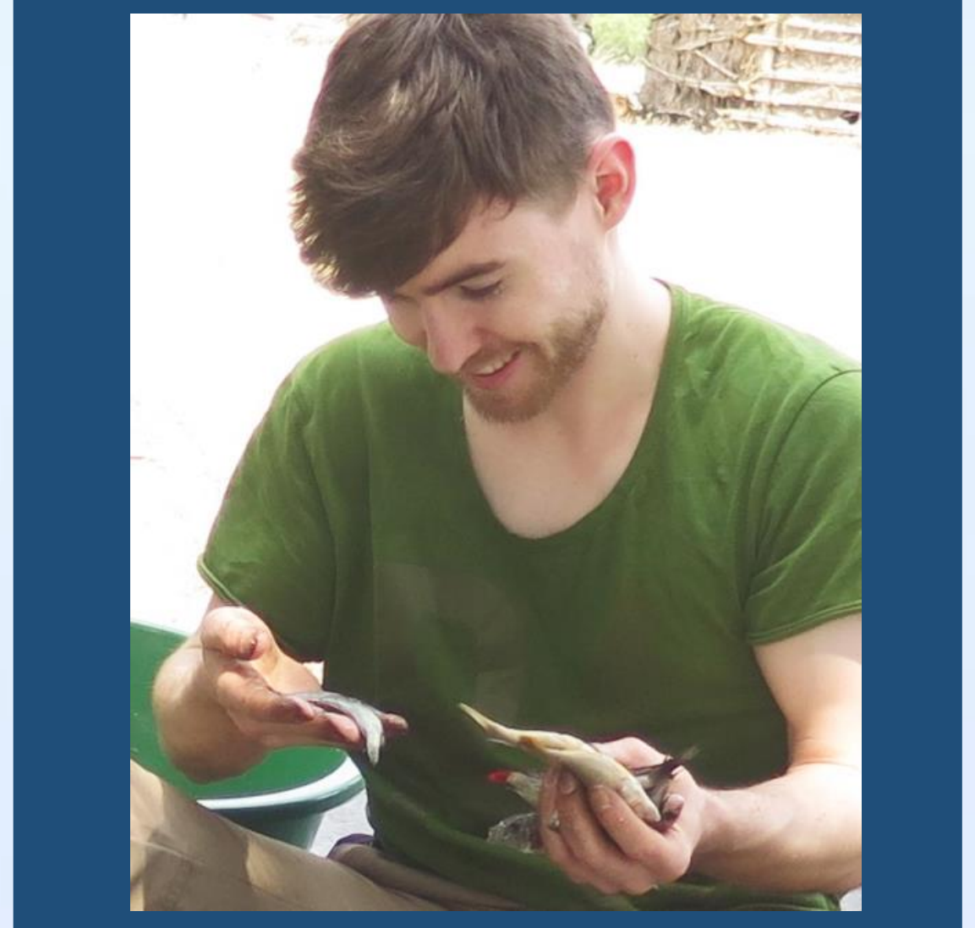

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Introduction

Haplochromis is a genus of East African cichlids that is known for its large adaptive capabilities and species richness. This genus radiated within Lakes Albert, Edward, Kivu, and Victoria (Fig. 1). They exploited the ecological opportunities within these lakes and gave rise to the Lake Victoria Region Superflock. Each lake is inhabited by its endemic assemblage of *Haplochromis* species that shows a large variation in eco-morphological adaptations.

The species diversity of most lakes was quite well understood, except for that of Lake Edward. Therefore, we started the project by performing a revision of all Lake Edward *Haplochromis* species.

We whole genome sequenced nearly all species from Lakes Albert, Edward, and Kivu, and some representatives from Lake Victoria to investigate the genomic basis of the eco-morphological similarities between species from different lakes.

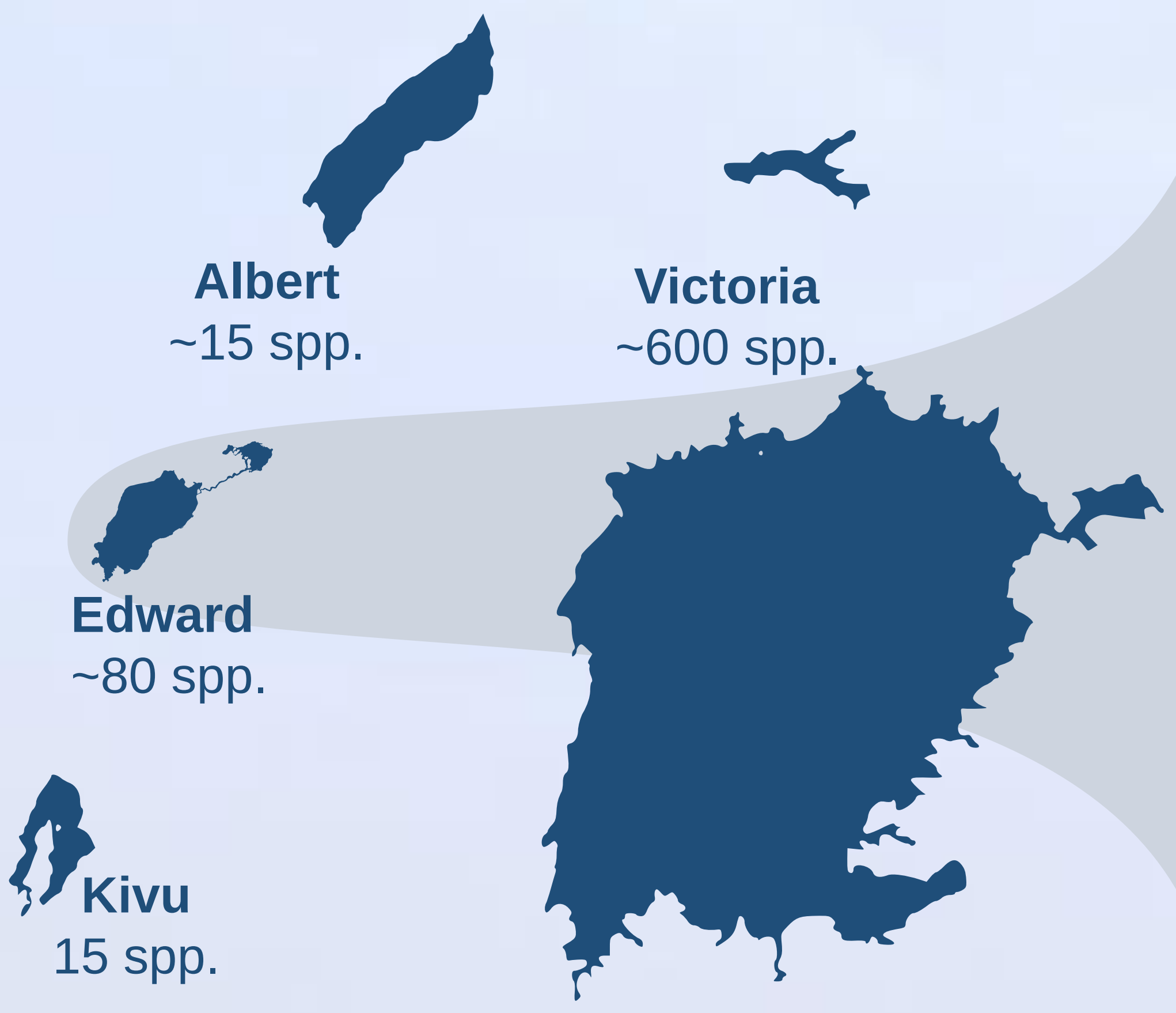
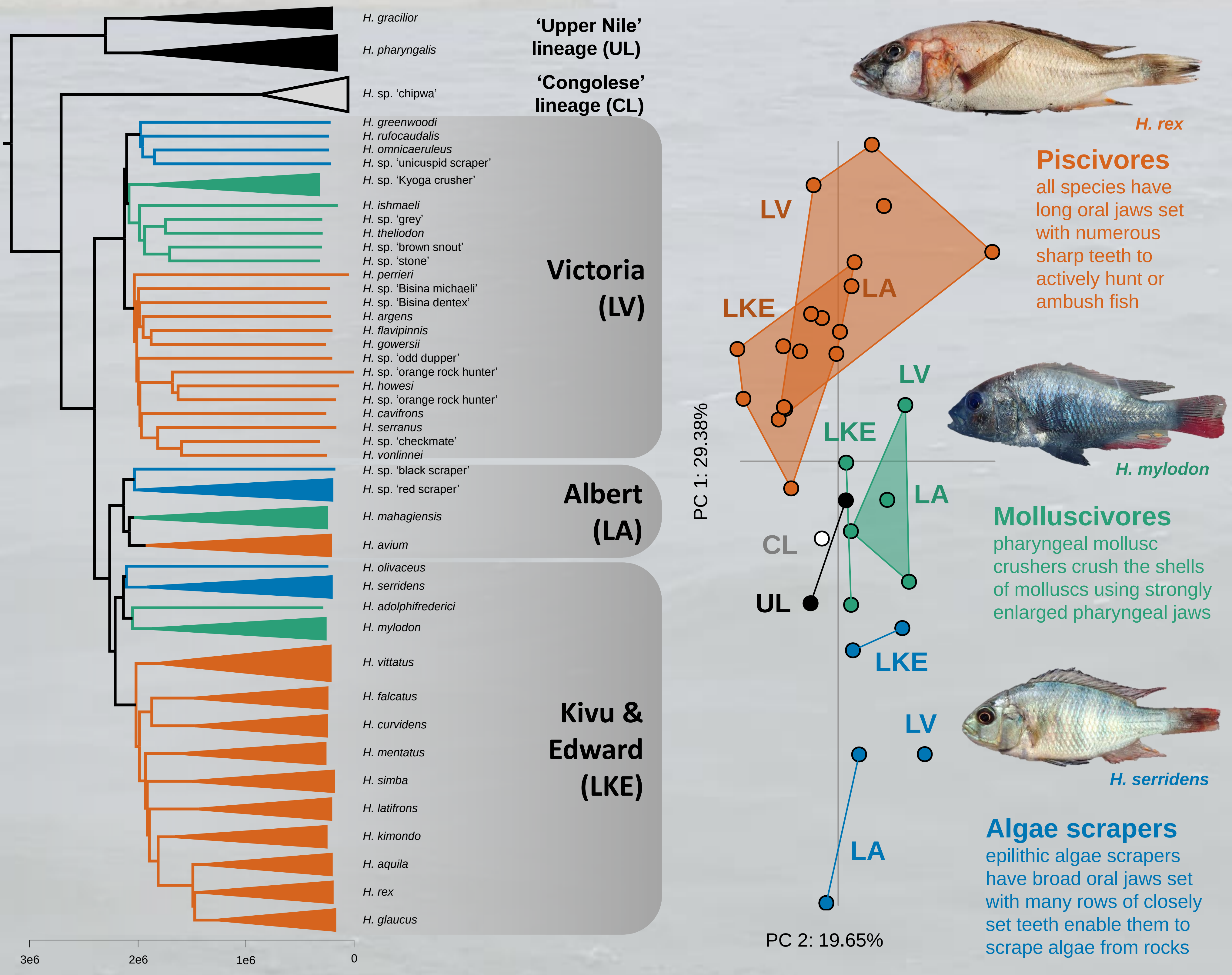


Fig. 1. Lake Victoria region
inhabited by ~700 spp. of *Haplochromis*, which radiated rapidly over the last 150 ka

Genomically different, eco-morphologically similar

We selected several piscivores, molluscivores, and epilithic algae scrapers from each of the four lakes in the Lake Victoria region. Our NJ tree (Fig. 2) supports that the Lake Victoria Region Superflock is monophyletic and consists out of three radiations. All species from Lakes Victoria and Albert form two separate radiations, while those of Lakes Kivu and Edward form a single radiation. In morphospace, the selected species cluster by eco-morphological group instead of by radiation, showing a strong degree of similarity across radiations.



Piscivores
all species have long oral jaws set with numerous sharp teeth to actively hunt or ambush fish

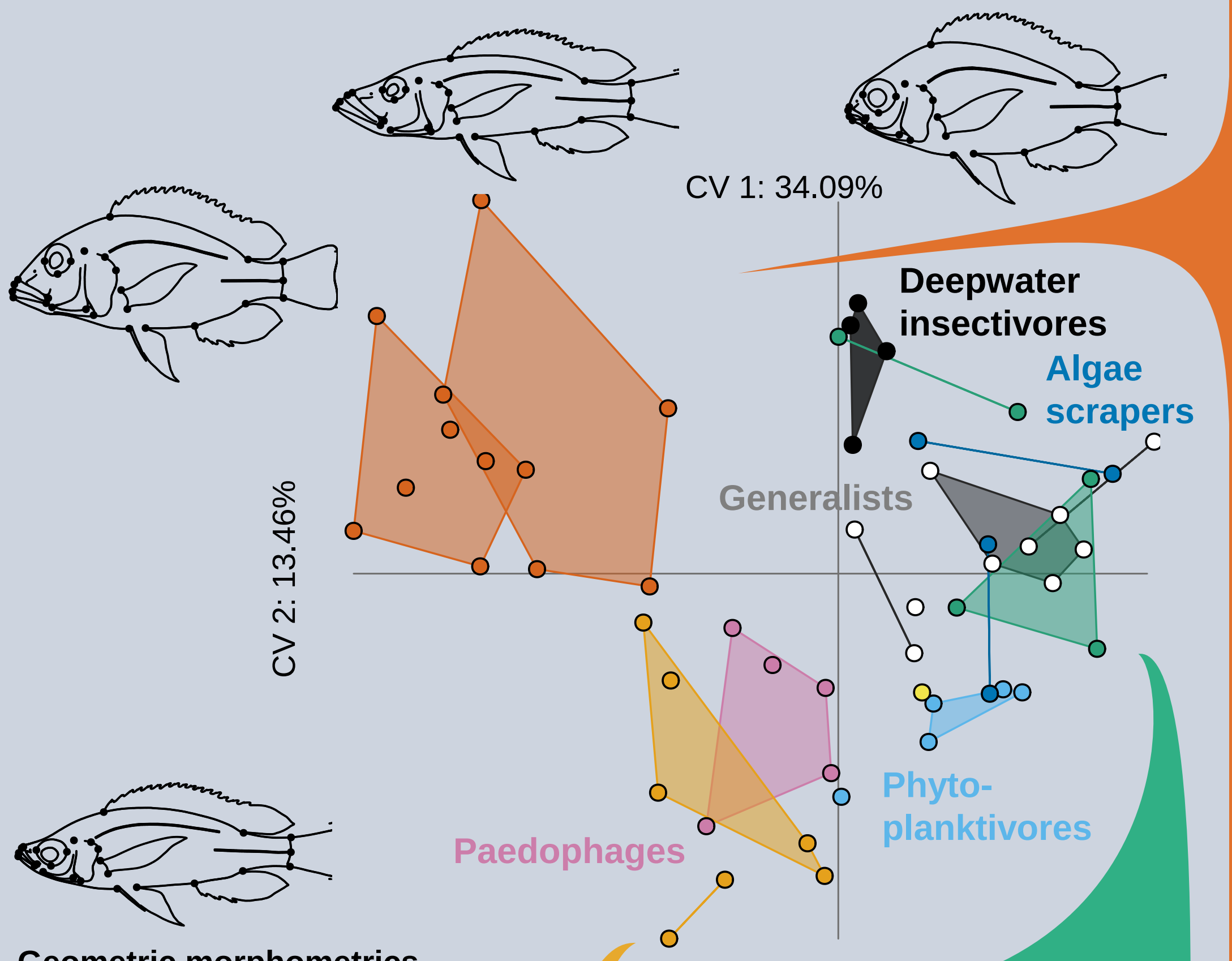
Molluscivores
pharyngeal mollusc crushers crush the shells of molluscs using strongly enlarged pharyngeal jaws

Algae scrapers
epilithic algae scrapers have broad oral jaws set with many rows of closely set teeth enable them to scrape algae from rocks

Fig. 2. Neighbour joining tree based on WGS data and geometric morphometrics.
Several piscivores, pharyngeal mollusc crushers, and epilithic algae scrapers from each of four lakes and representatives of the ancestral 'Congolese' and 'Upper Nile' lineages were selected. A neighbour joining tree (left) and a PCA on body landmarks of the same species (right) are shown. In the PCA, only means of species are plotted and *a posteriori* grouped by eco-morphological group and lineage.

Revision of Lake Edward haplochromines

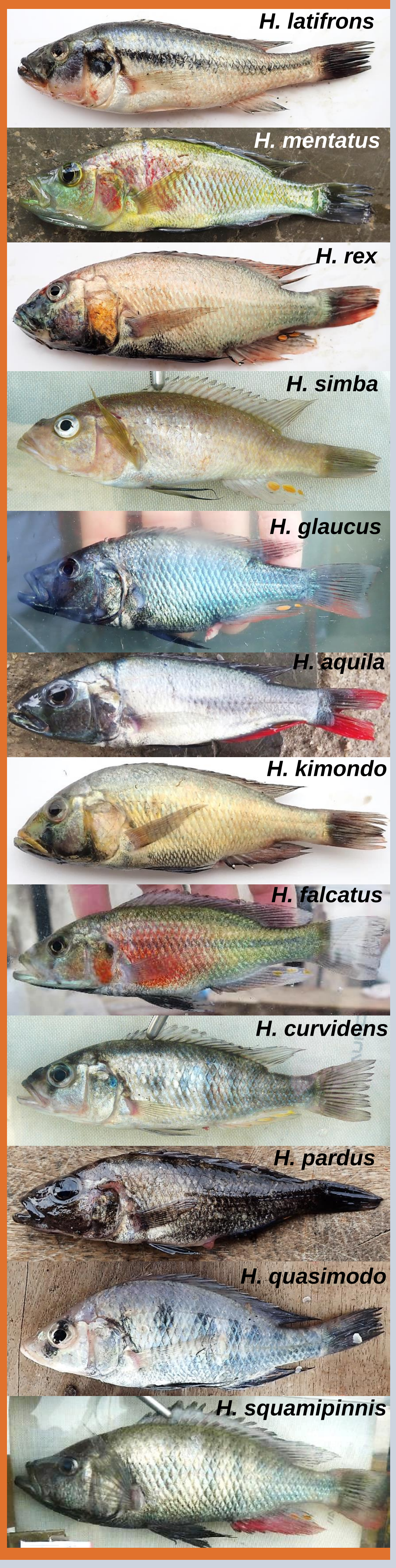
52 species inhabit Lakes Edward and George, of which 29 are newly discovered species. All species belong to nine major eco-morphological groups that mostly differ in their trophic morphologies (dentitions and head shapes), diets, and habitat preferences.



Geometric morphometrics.
CVA on 52 *Haplochromis* species from Lake Edward (n=552).
Only means of species are shown and *a posteriori* grouped by eco-morphological group.

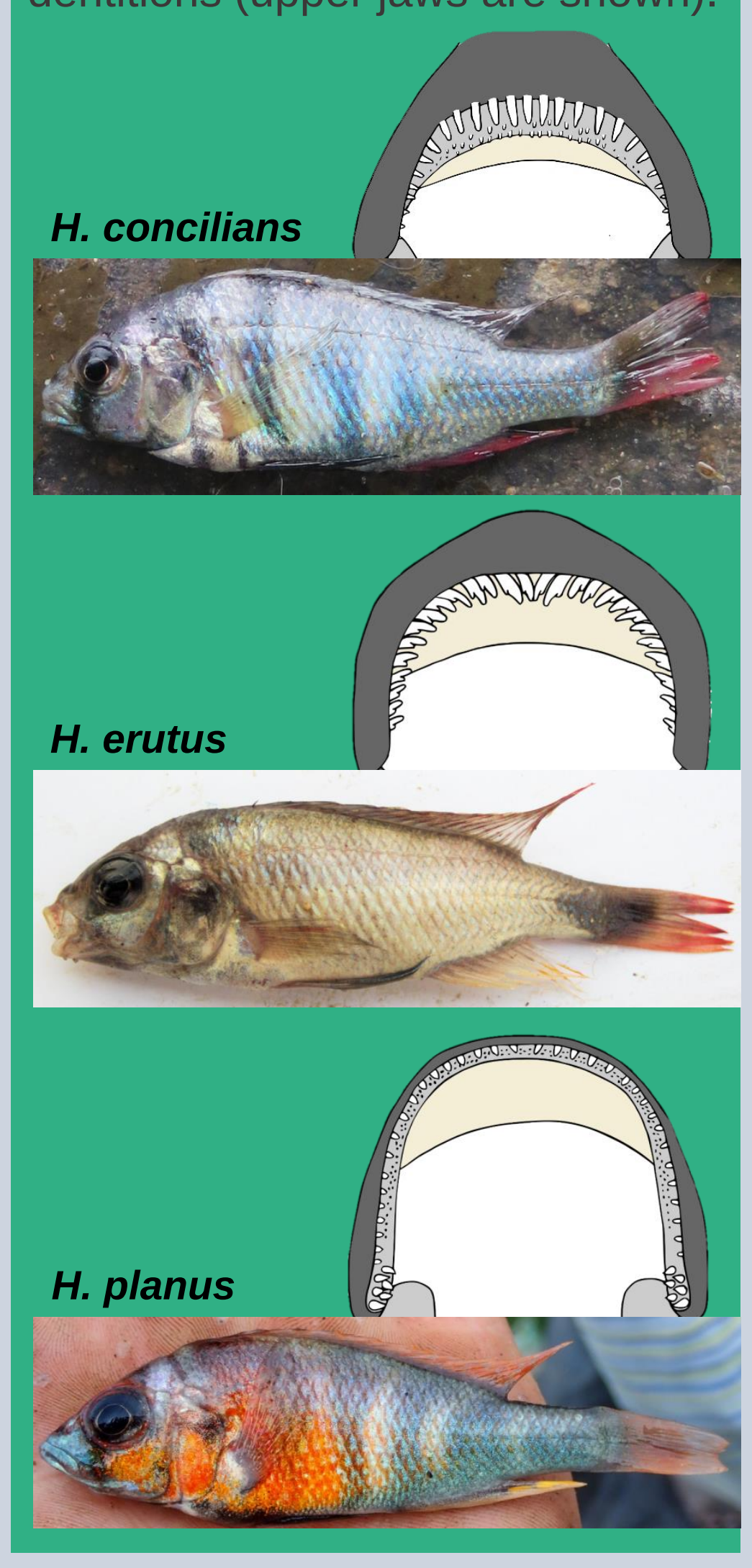
Piscivores

12 species, 10 newly described



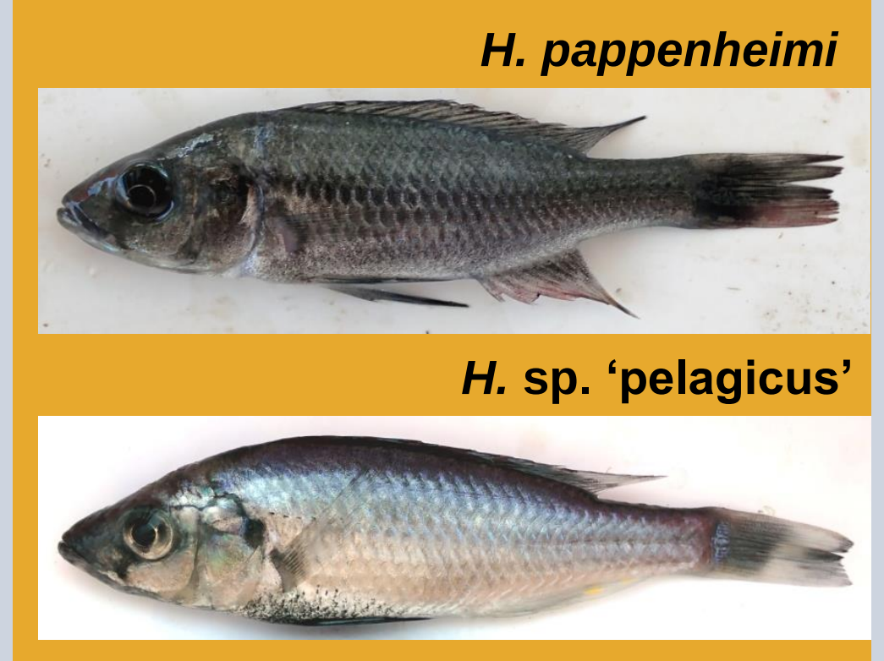
Molluscivores

3 newly described species of oral mollusc shellers with very different dentitions (upper jaws are shown).



Pelagic species

2 species of deepwater zooplanktivores, one of which is new to science.



1 newly discovered pelagic species, presumed to be an insecti-piscivorous species

Fig. 3. Local gene tree
Local gene tree for piscivores, molluscivores, and algae scrapers is shown (chr2: 13271493-13272363; fAstCal1.2 reference genome).

Similarity evolved partially because different species share the same genes

Several regions in the DNA were found to be associated with strong phenotypic similarities (using a GWA mapping approach, not shown). These genes were found in cichlid species from different lakes and show that many of the strong similarities evolved partially because they share the same genes (*e.g.*, see Fig. 3). They inherited most of these genes from the common ancestor of the Lake Victoria Region Superflock, while they acquired some others from distantly related species through hybridization (crossbreeding between different species). Because these cichlids retain and inherit candidate adaptive genes from distantly related species, species can significantly change many of their external features over just a few generations. We show that many genes across their genome contribute to the evolution of a large diversity of external features in species that evolved independently from each other. These results might also prove important for effective fisheries management and conservation efforts.