**Supplementary Methods S1. Ultra-conserved element (UCE) sequence generation and phylogenetic analyses**

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To generate the UCE sequences, we first extracted DNA using Qiagen DNEasy kits. For each extaction, we quantified the DNA concentration, equilibrated them to 10 ng/uL, and then sonicated the DNA to generate sequence products of 300-500 bp.Following this protocol, we quantified and then prepared samples using a PCR reaction mix consisting of 15-20 uL DNA. After this PCR step, we purified libraries, rehydrated them, combined them into pools of equimolar ratios (~500 ng per pool), and subsequently enriched them for UCEs using methods implemented previously (18, 28). After qPCR-quantification of the enriched, double-indexed pools, we created an equimolar solution of all individuals and sequenced libraries using the Illumina NextSeq PE150 platform.

After sequencing, we trimmed adapters, low quality bases, and sequences containing ambiguous base calls. Then, we assembled reads on a species-by-species basis into contigs using the program Trinity (1). Following assembly, we used the PHYLUCE software package (2) to align species-specific contigs to the UCE probes. Contigs that matched no UCEs and contigs that also matched multiple loci were removed. Using the remaining set of contigs, we generated a matrix including only UCE loci that were recovered from 95% of the species examined. Then, we aligned contigs with MAFFT across the selected taxa prior to phylogenetic analyses (3).

To reconstruct bifurcating phylogenetic trees for the UCE loci to use in the comparative analyses, we utilized a de novo SNP calling approach by aligning all raw reads against the sample with the highest coverage across all UCE loci. This method integrates BWA v. 0.7.7-1 and PICARD v. 1.106 (http://picard.sourceforge.net/) to output alignments in BAM format, repair any formatting violations, add read group header information, and mark duplicates in each BAM. We then merged all resulting BAMs into one file, realigned the data and called SNPs and indels using GATK v. 3.5. To ensure high-quality SNPs in downstream analyses, the data was hierarchically filtered according to stringent quality and validation parameters, excluding SNPs with QUAL scores under 25, low variant confidence, and poor validation. The resulting data was filtered further using VCFTOOLS v.0.1.14 (4) to remove all loci that missed SNP calls for over 25% of the species. To account for linkage disequilibrium of SNPs in the same UCE locus, the filtered VCF file was also manually pared down to the highest quality SNP per locus, resulting in 1027 SNPs.

**Supplementary Methods S2. Models of Malawi-wide convergence at multiple levels**

The four evolutionary models (BM1, BMS, OU1, OUM) were fitted individually to the two functional abilities (protrusion distance and protrusion angle), both mechanical properties (KT and αN), and all morphological traits (the four link lengths in the four-bar linkage). For all SIMMAP trait reconstructions, we recorded the AIC score for each model and the model-averaged peak locations across the 100 trees. Model averages were calculated from each model's peak location weighted according to the relative support of the model. The differences in AIC scores (the models with lowest AIC score) were used to select the best-supported model for each trait. We inferred a ∆AIC of less than 2.0 to suggest similar support for competing models while a ∆AIC of greater than 2.0 was taken as greater support for a more parameter-rich model. We further used kernel density estimation (KDE) from the KS library (62) to calculate the confidence intervals for peak locations.

**References**

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**Supplementary Table S1. Feeding guild adaptive optima.** Support for four models of trait evolution including single (BM1) and multiple (BMS) rate Brownian motion as well as single (OU1) and multiple peak (OUM) Ornstein-Uhlenbeck models. These models were examined for each trait independently across the three levels of organization (function, mechanics, morphology). Best-supported models appear in bold. Average ∆AIC (± standard error) values are given for each best model (highlighted in bold) relative to the next best of the other three models examined based on SIMMAP trait histories reconstructed for 100 trees. In general, the performance and mechanical traits showed evidence of different optima for convergent Malawi feeding guilds while the four-bar linkage morphology did not exhibit clear optima.

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| --- | --- | --- | --- | --- |
| organizational | trait | Brownian | Ornstein- Uhlenbeck | ∆AIC |
| level |
| function | distance | **BMS** | OUM | 1.2±2.5 |
|  | angle | BM1 | **OU1** | **4.8±3.5** |
| mechanics | KT | BM1 | **OUM** | **4.7±1.7** |
|  | αN | BM1 | **OUM** | **9.8±2.1** |
| morphology | fixed | **BM1** | OUM | 1.2±6.1 |
|  | nasal | **BMS** | OUM | 1.8±2.3 |
|  | maxilla | **BM1** | OUM | 0.7±1.6 |
|  | lower jaw | **BM1** | OUM | 0.6±5.1 |