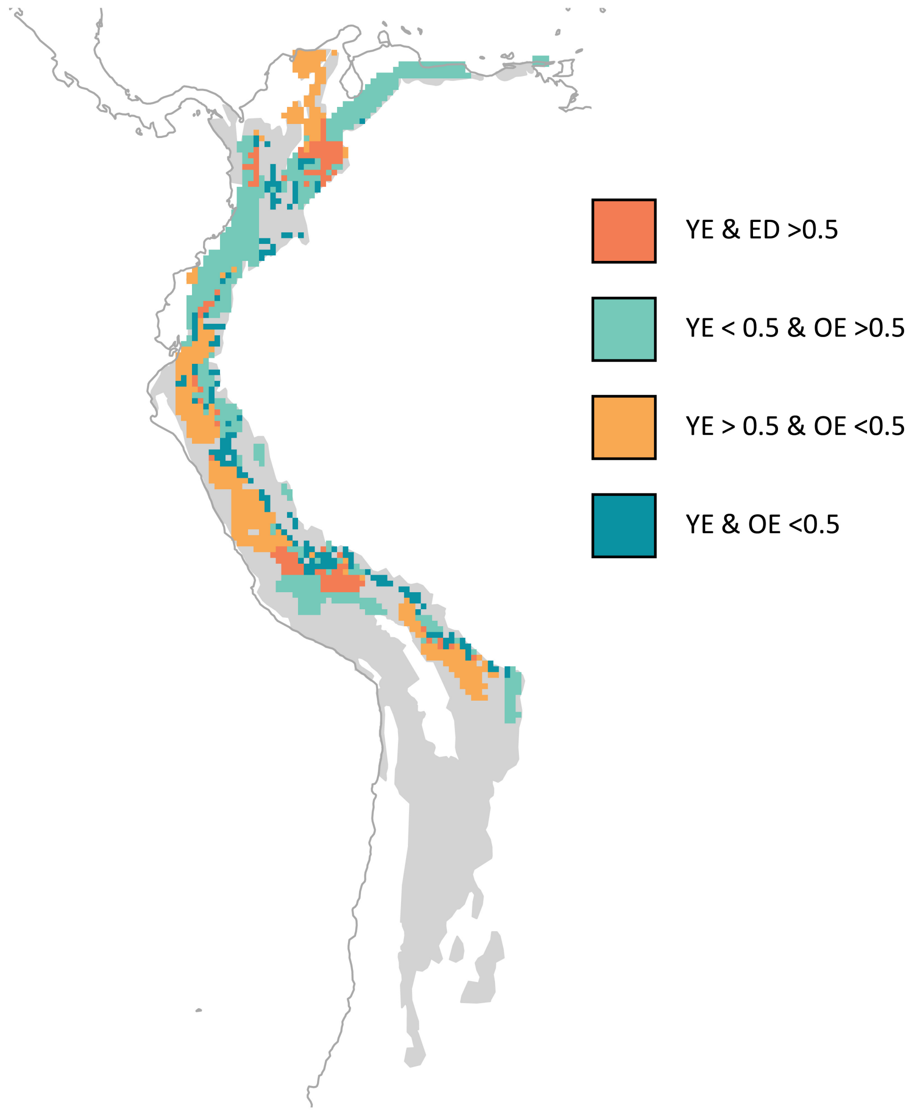
Supplementary Information

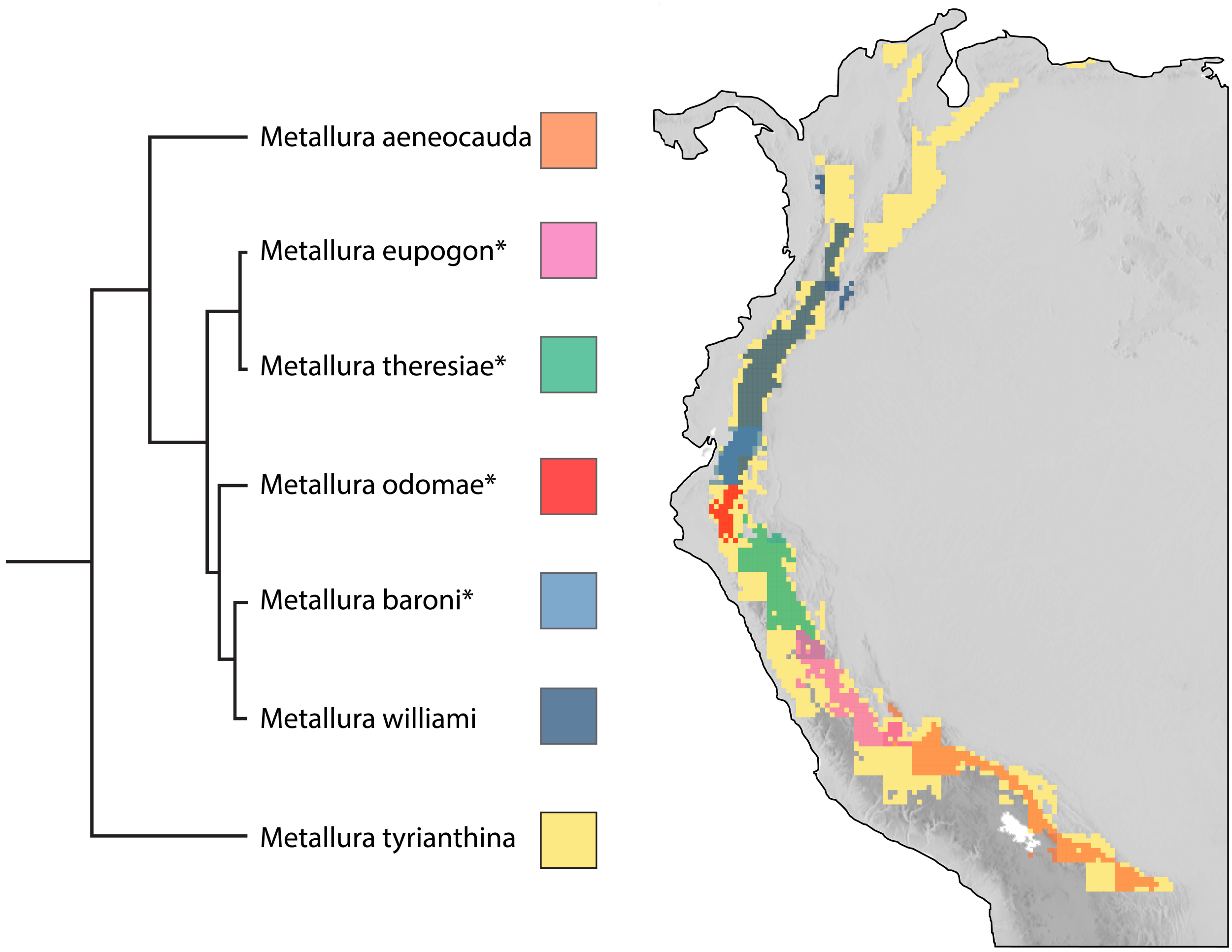
Supplementary Table S1a. Applying a one-way Chi-squared test to examine if aggregations of young endemic species are geographically separate from aggregations of old endemic species. The analysis includes all grid cells housing at least one of the two age classes (Supplementary Fig. S1b). Let *YE* and *OE* denote the standardised richness of young and old endemic species, respectively. Then, Let z denote the frequency of grid cells with a *YE* exceeding 0.5, and q denote the frequency of grid cells with *OE* exceeding 0.5 (Fig. 2). A value of standardised richness exceeding 0.5 means that the majority of null model iterations sampled fewer Young or old endemic species than observed in the grid cell. The contingency table below shows the observed and expected frequencies for each grid cell category. The observed frequency of grid cells with YE & OE > 0.5 were half the expected ($\chi^2 = 156.53$, $p < 0.001$).

	YE & OE <0.5	YE > 0.5 & OE <0.5	YE < 0.5 & OE >0.5	YE & OE >0.5
observed	174	289	377	108
expected (formula)	(1-z)*(1-z)	p*(1-q)	(1-z)*q	z*q
expected (frequencies)	269	194	282	203

Supplementary Fig. S1b: The distribution of young and old endemic species in the North & Central Andes. Let YE and OE denote the standardised richness of young and old endemic species, respectively. A value of standardised richness exceeding 0.5 means that the majority of null model iterations sampled fewer young or old endemic species than observed in the grid cell. As such, red grid cells mean an overrepresentation of both age classes; Blue grid cells mean an underrepresentation of both age classes. Green colour means that only old endemic species are overrepresented; yellow means that only young endemic species are overrepresented. Grey areas mark areas in the North and Central Andes where both age classes are absent



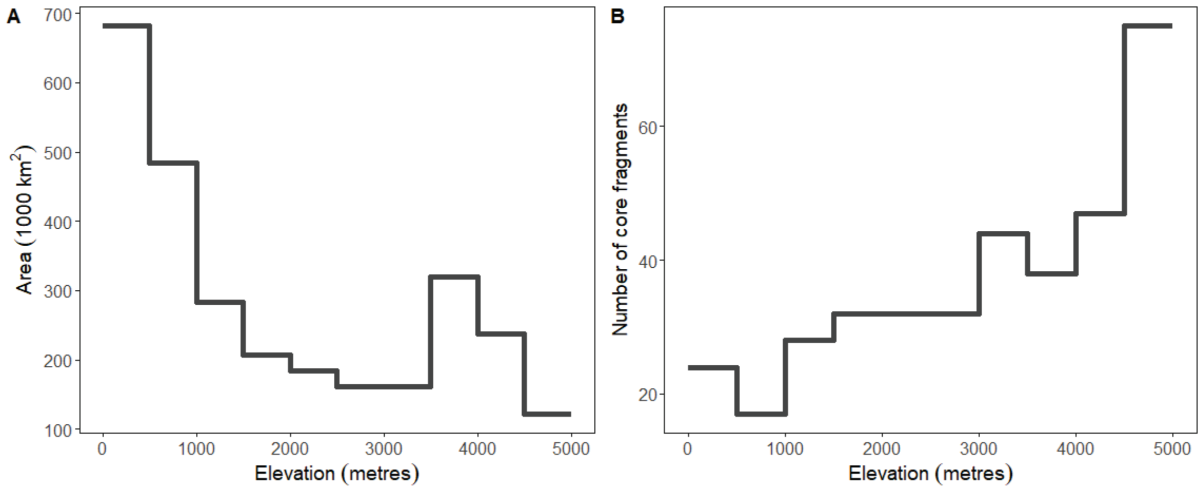
Supplementary Fig. S2: Maps showing the distribution of seven *Metallura* hummingbirds. Note that young endemic species (marked with stars) are dispersed between mountain tops with little or no geographic overlap [1].



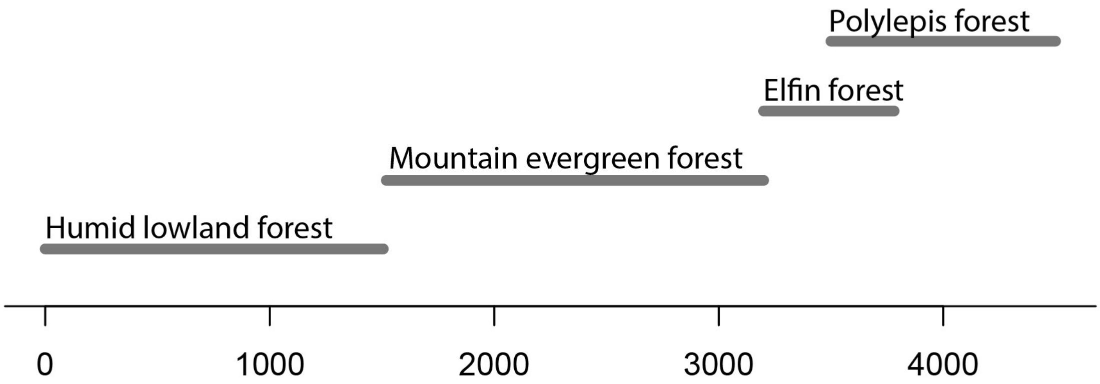
Supplementary Table S3: Applying Fisher's exact test to examine if young and old endemic species have different habitat preferences. The Contingency table below shows the number of species occurring in each habitat. Fisher's exact p states the probability that young and old endemic species occupy the same habitats.

	Humid lowland	Cloud forest	Humid highland	Paramo/ Puna	Arid shrubland
Young endemic species	4	3	9	2	0
Old endemic species	5	12	3	1	1
p = 0.026					

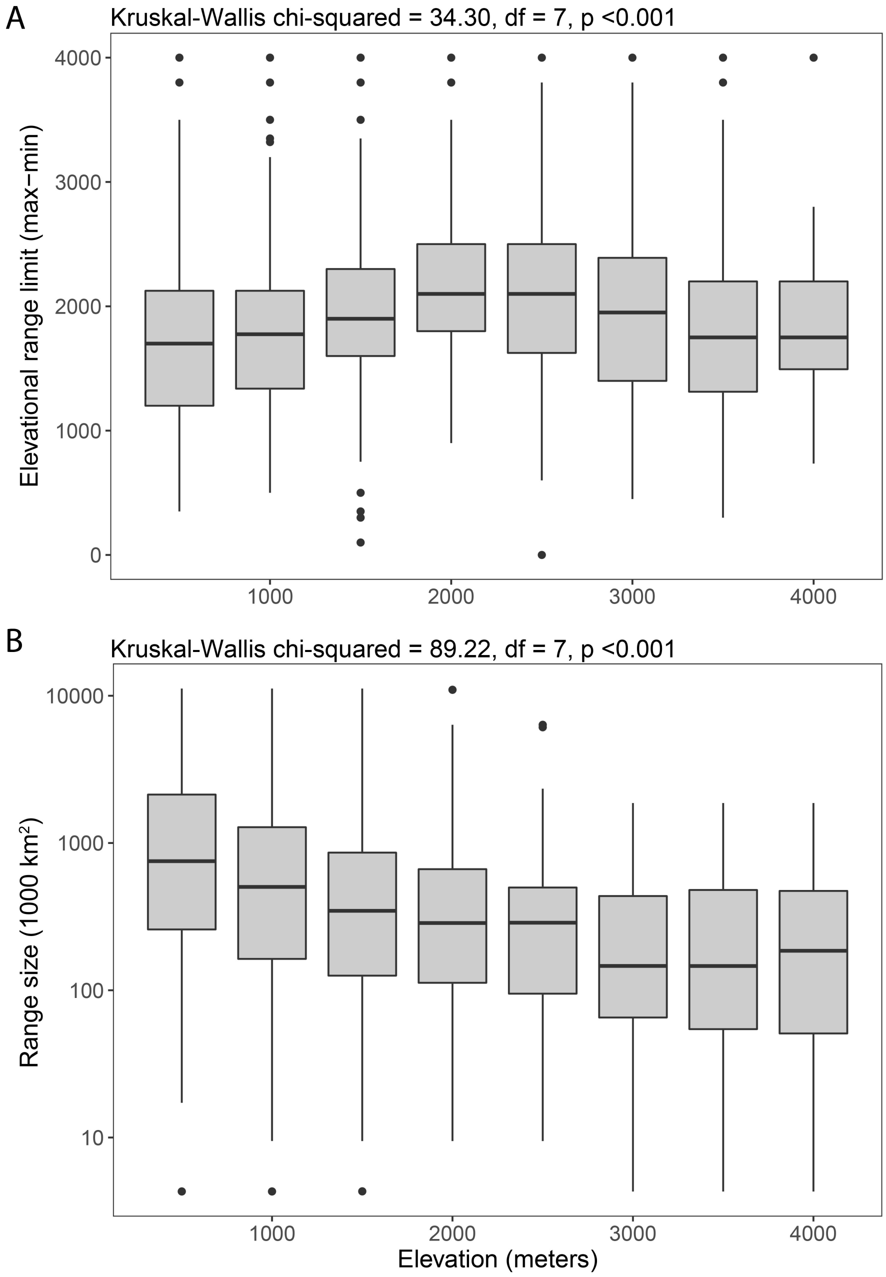
Supplementary Fig. S4: Landscape area and fragmentation, respectively, along the Andean elevational gradient in intervals of 500 meters above sea level. The landscape's area was measured in units of 1000 km^2 (A), and fragmentation was measured as the number of isolated landscape fragments (B). To avoid oversampling small neighbouring fragments, we merged fragments with less than 20 km distance.



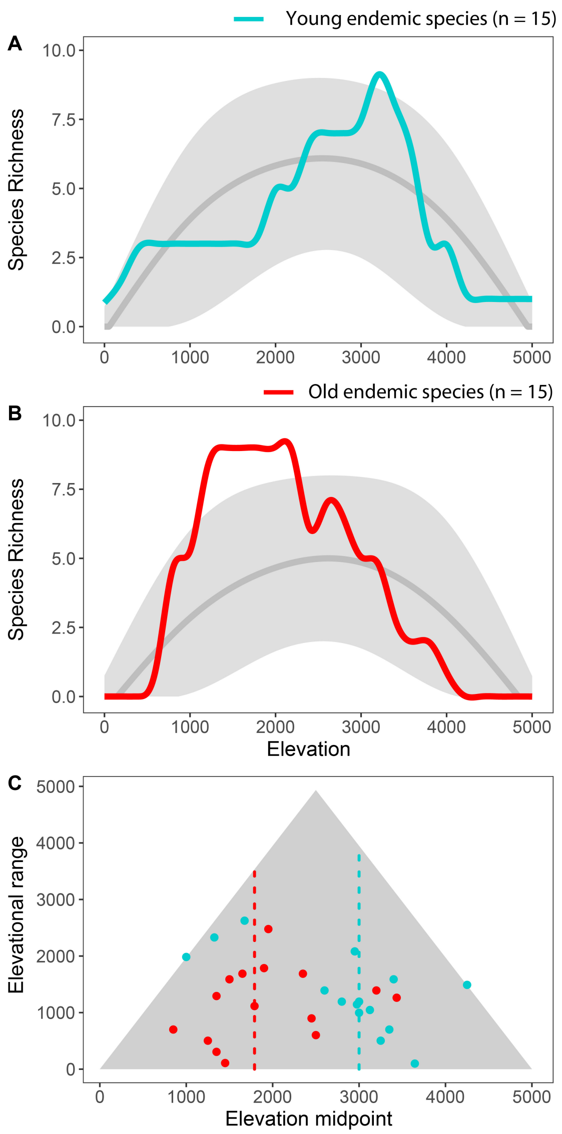
Supplementary Table S5: Elevational zonation of humid forest habitats in the Andes following Stotz, Fitzpatrick [2]



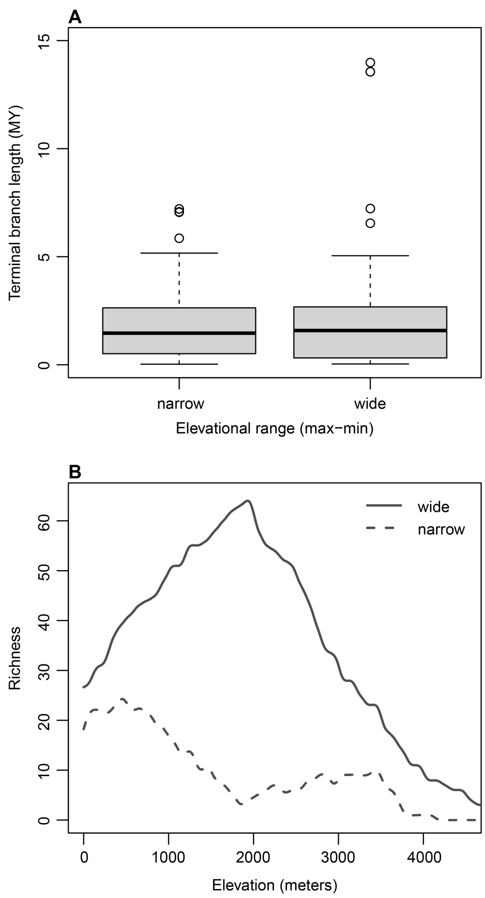
Supplementary Fig. S6: Elevational gradients in the elevational range limits (max-min elevation) of species and their geographic range size (1000 km^2). Species tend to have the broadest elevational ranges at mid-elevation: ca. 2000-2500 metres (A), whereas geographic range size decreases with elevation up to 3000 metres (B). Both plots comprise all species with geographical distributions overlapping with the Andean mountains polygons shown in Fig. 1 (n = 229).



Supplementary Fig. S7: comparing the elevational pattern in young and old endemic species against a mid-domain effect. (A-B) We modelled the mid-domain effect by randomly shuffling young and old endemic species along the gradient while maintaining their elevational range coherency using the empirical range frequency distribution following the guidelines by Colwell, Rahbek and Gotelli [3]. The grey lines show the median, and the shaded area shows the 95% confidence interval for 1000 null model repetitions. (C) The species' elevational range is plotted against their elevational midpoint. Dashed lines mark the median elevational midpoint of young and old endemic species. The Grey triangle outlines the midpoint limits for a given elevational range. The results show that the elevational distribution of young and old endemic species does not reflect a mid-domain effect as a stand-alone hypothesis. The young endemic species are more species-rich at ~3000 metres than the null model predicts. Vice versa, the old endemic species are more species-rich at ~1500 metres than expected.



Supplementary Fig. S8: Comparative analyses of species with narrow and wide elevational range limits (defined by the 25% and 75% quartiles, respectively). Panel A compares the terminal branch length for these two groups. The results show that the terminal branch length is similar between species with narrow and wide elevational distributions. Panel B shows the elevational pattern in the species richness of each group. It appears that species with narrow elevational ranges are least species-rich at 1500-2000 metres. 12 additional species were added to the phylogeny for conducting these analyses (See Supplementary Table S10d)



Supplementary Table S9a: Sources of hummingbird elevational distributions

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Supplementary Table S9b. Elevational range limits for all 229 extant hummingbird species occurring within the Central and Northern Andes. Units are metres above sea level.

Species_name	Min elevation	Max elevation
Adelomyia melanogenys	900	2900
Aglaeactis aliciae	3000	4300
Aglaeactis castelnaudii	2600	4200
Aglaeactis cupripennis	2500	4600
Aglaeactis pamela	3000	3500
Aglaiocercus berlepschi	1450	1800
Aglaiocercus coelestis	800	2300
Aglaiocercus kingii	900	3000
Amazilia amabilis	0	1400
Amazilia amazilia	0	2700
Amazilia brevirostris	0	500
Amazilia castaneiventris	150	2500
Amazilia chionogaster	0	3500
Amazilia cyanifrons	400	2200
Amazilia edward	0	1800
Amazilia fimbriata	0	1740
Amazilia franciae	300	2750
Amazilia lactea	0	2300
Amazilia leucogaster	0	250
Amazilia rosenbergi	0	800
Amazilia saucerottei	0	2000
Amazilia tobaci	0	2500
Amazilia tzacatl	0	2000
Amazilia versicolor	0	950
Amazilia viridicauda	900	2800
Amazilia viridigaster	0	2100
Androdon aequatorialis	300	2400
Anthocephala berlepschi	1200	2300
Anthocephala floriceps	600	2300
Anthracothorax nigricollis	0	2100
Anthracothorax prevostii	0	1100
Anthracothorax viridigula	0	500
Avocettula recurvirostris	0	1200
Boissonneaua flavescens	1400	3600
Boissonneaua jardini	350	2200
Boissonneaua matthewsii	1200	3300
Calliphlox amethystina	0	1500
Calliphlox mitchellii	450	2400
Campylopterus ensipennis	700	2000
Campylopterus falcatus	400	3000
Campylopterus largipennis	0	1500
Campylopterus phainopeplus	1200	3500

Campylopterus villaviscensio	800	1700
Chaetocercus astreans	350	3000
Chaetocercus berlepschi	0	2000
Chaetocercus bombus	0	2700
Chaetocercus heliodor	1000	3000
Chaetocercus jourdanii	900	3000
Chaetocercus mulsant	800	3500
Chalcostigma herrani	2450	4000
Chalcostigma heteropogon	2800	4075
Chalcostigma olivaceum	3150	4700
Chalcostigma ruficeps	1400	3300
Chalcostigma stanleyi	2800	4500
Chalybura buffonii	0	2000
Chalybura urochrysia	0	1700
Chlorestes notata	0	1000
Chlorostilbon alice	750	1800
Chlorostilbon assimilis	0	1500
Chlorostilbon gibsoni	0	2300
Chlorostilbon lucidus	0	2500
Chlorostilbon melanorhynchus	600	2700
Chlorostilbon mellisugus	0	2600
Chlorostilbon poortmani	600	2800
Chlorostilbon russatus	250	2600
Chlorostilbon stenurus	1000	3000
Chrysolampis mosquitus	0	1750
Chrysuronia oenone	0	1700
Coeligena bonapartei	1400	3200
Coeligena coeligena	400	2650
Coeligena helianthea	1900	3300
Coeligena iris	1500	3500
Coeligena lutetiae	2600	3750
Coeligena orina	2500	3500
Coeligena phalerata	1200	3700
Coeligena prunellei	1000	2800
Coeligena torquata	1500	3500
Coeligena violifer	2500	3900
Coeligena wilsoni	800	2300
Colibri coruscans	500	4500
Colibri delphinae	0	2800
Colibri serrirostris	0	2100
Colibri thalassinus	479	3800
Discosura conversii	250	1600
Discosura langsdorffi	0	1200
Discosura popelairii	500	1800
Doryfera johannae	280	1800
Doryfera ludovicae	100	3200
Ensifera ensifera	2200	3600

Eriocnemis aline	1000	2800
Eriocnemis cupreoventris	1950	3200
Eriocnemis derbyi	300	3650
Eriocnemis glaucopoides	1900	2900
Eriocnemis luciani	2400	4800
Eriocnemis mirabilis	2200	2800
Eriocnemis mosquera	2500	3600
Eriocnemis nigrivestis	2400	3600
Eriocnemis vestita	2250	4200
Eulidia yarrellii	110	700
Eupetomena macroura	0	1800
Eutoxeres aquila	0	2400
Eutoxeres condamini	0	2800
Florisuga mellivora	0	1600
Glaucis aeneus	0	1500
Glaucis hirsutus	0	1300
Goethalsia bella	500	1800
Goldmania violiceps	500	1300
Haplophaedia assimilis	1500	2500
Haplophaedia aureliae	900	2500
Haplophaedia lugens	1100	2500
Heliangelus amethysticollis	1600	3700
Heliangelus clarisse	1800	3600
Heliangelus exortis	1600	3400
Heliangelus mavors	1500	3200
Heliangelus micraster	2200	3400
Heliangelus regalis	1230	2350
Heliangelus spencei	2500	2500
Heliangelus strophianus	700	3200
Heliangelus viola	1000	3300
Heliodoxa aurescens	0	1500
Heliodoxa branickii	650	1700
Heliodoxa gularis	300	1320
Heliodoxa imperatrix	700	2300
Heliodoxa jacula	300	2200
Heliodoxa leadbeateri	500	2400
Heliodoxa rubinoides	1100	2650
Heliodoxa schreibersii	0	1500
Heliomaster furcifer	0	1000
Heliomaster longirostris	0	1829
Heliothryx auritus	0	1300
Heliothryx barroti	0	1800
Hylocharis chrysura	0	1100
Hylocharis cyanus	0	1250
Hylocharis eliciae	0	1235
Hylocharis grayi	0	2600
Hylocharis humboldtii	0	500

Hylocharis sapphirina	20	500
Hylonympha macrocerca	500	1200
Juliamyia julie	0	1750
Klais guimeti	0	1900
Lafresnaya lafresnayi	1600	3990
Lepidopyga coeruleogularis	0	700
Lepidopyga goudoti	0	1600
Lepidopyga lilliae	0	100
Lesbia nuna	1700	3800
Lesbia victoriae	2300	4100
Leucippus baeri	0	1300
Leucippus chlorocercus	0	450
Leucippus fallax	0	800
Leucippus taczanowskii	100	2800
Loddigesia mirabilis	2000	2900
Lophornis delattrei	0	2200
Lophornis ornatus	0	950
Lophornis stictolophus	400	1300
Lophornis verreauxii	450	800
Metallura aeneocauda	2800	3750
Metallura baroni	1900	4000
Metallura eupogon	3000	3700
Metallura iracunda	1850	3800
Metallura odomae	2600	3650
Metallura phoebe	2500	4400
Metallura theresiae	2400	3550
Metallura tyrianthina	1700	4200
Metallura williami	2700	4000
Microstilbon burmeisteri	0	2000
Myrmia micrura	5	800
Myrtis fanny	0	3200
Ocreatus addae	1400	1500
Ocreatus peruanus	1200	1500
Ocreatus underwoodii	850	2600
Opisthoprora euryptera	2400	3600
Oreonympha nobilis	2500	3900
Oreotrochilus adela	2550	4000
Oreotrochilus chimborazo	3500	5000
Oreotrochilus cyanolaemus	3648	3648
Oreotrochilus estella	3250	4600
Oreotrochilus leucopleurus	1200	4000
Oreotrochilus melanogaster	3100	4800
Oreotrochilus stolzmanni	3200	3500
Oxypogon cyanolaemus	3000	4800
Oxypogon guerinii	3000	5200
Oxypogon lindenii	3000	5200
Oxypogon stuebelii	3400	4135

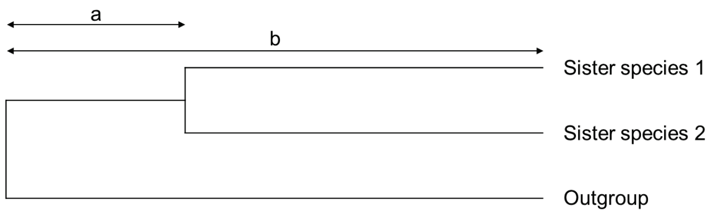
Patagona gigas	1800	4300
Phaeochroa cuvierii	0	1300
Phaethornis anthophilus	0	1200
Phaethornis atrimentalis	100	1600
Phaethornis augusti	0	2500
Phaethornis bourcieri	0	1600
Phaethornis griseogularis	300	2200
Phaethornis guy	300	2700
Phaethornis hispidus	80	1200
Phaethornis koepckeae	500	1300
Phaethornis longirostris	0	1600
Phaethornis longuemareus	0	1200
Phaethornis malaris	0	1200
Phaethornis philippii	12	500
Phaethornis pretrei	0	1900
Phaethornis ruber	0	1100
Phaethornis striigularis	0	1800
Phaethornis stuarti	350	1400
Phaethornis subochraceus	0	700
Phaethornis syrmatophorus	900	2500
Phaethornis yaruqui	0	1700
Phlogophilus harterti	750	1500
Phlogophilus hemileucurus	400	2000
Polyonymus caroli	1500	3400
Polytmus guainumbi	0	1500
Pterophanes cyanopterus	2600	4075
Ramphomicron dorsale	2000	4500
Ramphomicron microrhynchum	2500	4075
Rhodopis vesper	0	3800
Sappho sparganurus	2000	3600
Schistes albogularis	600	2200
Schistes geoffroyi	100	2500
Sephanoides sephaniodes	0	2000
Sternoclyta cyanopectus	700	2000
Taphrolesbia griseiventris	2750	3200
Taphrospilus hypostictus	500	1600
Thalurania colombica	0	2000
Thalurania furcata	0	1900
Thaumastura cora	0	3000
Threnetes leucurus	0	1600
Threnetes ruckeri	0	1300
Topaza pyra	30	500
Urochroa bougueri	800	2500
Urochroa leucura	1000	1500
Urosticte benjamini	700	2200
Urosticte ruficrissa	1000	2450

Supplementary material S9c: Reduction in species range size caused by the elevational filtering of geographic ranges.

Species group	Percentage reduction in range size from 1 to 0.25-degree resolution (mean; sd)
All hummingbird species in the Andean mountain polygon (n = 229)	0.45;0.31
Endemic species (n = 58)	0.75;0.18
Young endemic species	0.69;0.27
Old endemic species	0.77;0.15

Supplementary Methods S10: Protocol for adding missing species to the hummingbird phylogeny

Supplementary Table S10a. Listing all sister species sampled in the phylogeny that are also represented by terminal branches. For each pair of sister species, we determine the stem branch's length (in Million years; MY) leading to the speciation event (a) and the total branch length (MY) since the most recent common ancestor (b). Dividing the stem branch length with the total branch length gives the relative stem length leading to the speciation event (a/b). Subtracting this ratio from one gives the terminal branch length ratio (*R*), which is directly proportional to the terminal branch length of a missing species in the phylogeny. See the example in Supplementary Methods S10b.



Sister species pair		**Stem branch length (a)**	**Total branch length (b)**	**Terminal branch Ratio (R=1-a/b)**
Abeillia abeillei	*Klais guimeti*	0.3468	6.7098	0.9483
Amazilia amabilis	*Amazilia decora*	0.1538	1.9088	0.9194
Amazilia beryllina	*Amazilia cyanura*	0.2249	0.6019	0.6263
Amazilia brevirostris	*Amazilia leucogaster*	0.3768	0.4760	0.2084
Amazilia chionogaster	*Amazilia viridicauda*	1.6470	3.4230	0.5188
Anthracothorax prevostii	*Anthracothorax veraguensis*	1.0100	1.3761	0.2660
Archilochus alexandri	*Archilochus colubris*	2.3250	3.3320	0.3022
Boissonneaua matthewsii	*Boissonneaua flavescens*	1.0430	3.7200	0.7196
Calliphlox mitchellii	*Calliphlox bryantae*	0.2653	1.3943	0.8097
Calypte costae	*Calypte anna*	0.8100	2.4450	0.6687
Campylopterus duidae	*Campylopterus hyperythrus*	4.6400	4.9510	0.0628
Chalcostigma ruficeps	*Chalcostigma olivaceum*	0.2453	4.7383	0.9482
Chalybura buffonii	*Chalybura urochrysia*	1.3300	5.0610	0.7372
Chlorostilbon maugaeus	*Chlorostilbon swainsonii*	1.4760	4.9020	0.6989
Chlorostilbon melanorhynchus	*Chlorostilbon assimilis*	1.5420	2.8648	0.4617
Coeligena coeligena	*Coeligena wilsoni*	0.6087	5.0107	0.8785
Coeligena lutetiae	*Coeligena orina*	0.2604	0.8517	0.6943
Discosura langsdorffi	*Discosura popelairii*	2.4990	2.9263	0.1460
Doricha enicura	*Calothorax lucifer*	2.3910	4.2010	0.4308
Doryfera Ludovicae	*Doryfera johannae*	1.1220	6.6910	0.8323
Elvira chionura	*Elvira cupreiceps*	0.2642	0.7172	0.6316
Eriocnemis cupreoventris	*Eriocnemis derbyi*	0.4968	3.7918	0.8690

Eulampis holosericeus	*Eulampis jugularis*	1.4880	2.5550	0.4176
Eupherusa cyanophrys	*Eupherusa poliocerca*	0.7095	1.6103	0.5594
Eupherusa nigriventris	*Eupherusa eximia*	0.3815	1.6105	0.7631
Eutoxeres aquila	*Eutoxeres condamini*	6.0200	19.5800	0.6925
Florisuga mellivora	*Florisuga fusca*	13.8100	18.8070	0.2657
Goethalsia bella	*Goldmania violiceps*	0.8676	3.2566	0.7336
Heliodoxa aurescens	*Clytolaema rubricauda*	1.5850	9.2440	0.8285
Heliodoxa gularis	*Heliodoxa branickii*	4.0110	6.6400	0.3959
Heliodoxa jacula	*Heliodoxa leadbeateri*	2.1870	5.0530	0.5672
Heliomaster furcifer	*Heliomaster squamosus*	2.2100	4.6730	0.5271
Heliothryx aurita	*Heliothryx barroti*	12.2600	13.9960	0.1240
Hylocharis xantusii	*Hylocharis leucotis*	5.0230	7.5820	0.3375
Lampornis calolaemus	*Lampornis castaneoventris*	0.0574	0.0923	0.3781
Lampornis viridipallens	*Lampornis sybillae*	0.3990	2.7620	0.8555
Lesbia nuna	*Lesbia victoriae*	1.3590	4.8500	0.7198
Metallura eupogon	*Metallura theresiae*	0.8247	1.0108	0.1841
Metallura williami	*Metallura baroni*	0.4102	0.7276	0.4362
Myrtis fanny	*Rhodopis vesper*	0.1763	1.6393	0.8925
Phaethornis guy	*Phaethornis yaruqui*	0.7433	4.5163	0.8354
Phaethornis hispidus	*Phaethornis bourcieri*	3.1180	3.3030	0.0560
Phaethornis longuemareus	*Phaethornis nattereri*	0.0892	0.7860	0.8865
Phaethornis malaris	*Phaethornis superciliosus*	0.7682	4.5169	0.8299
Phaethornis philippii	*Phaethornis koepckeae*	1.2470	3.3027	0.6224
Phaethornis rupurumii	*Phaethornis squalidus*	0.6180	0.7860	0.2137
Phaethornis striigularis	*Phaethornis griseogularis*	0.6322	2.4866	0.7458
Phlogophilus harterti	*Phlogophilus hemileucurus*	10.8900	13.2450	0.1778
Polytmus milleri	*Polytmus theresiae*	3.3300	6.8000	0.5103
Sephanoides fernandensis	*Sephanoides sephanoides*	10.2700	13.4200	0.2347
Thaumastura cora	*Myrmia micrura*	0.6077	1.6397	0.6294
Topaza pella	*Topaza pyra*	15.8600	18.8026	0.1565
Trochilus polytmus	*Trochilus scitulus*	0.5600	0.6500	0.1385
Urosticte benjamini	*Urosticte ruficrissa*	6.0840	6.2595	0.0280

Supplementary Methods S10b. Example: Adding *Anthocephala berlepschi* to the phylogeny: Adding the sister species to *A. floriceps*, which, in the McGuire et al. phylogeny [4], has a terminal length of 4.78 MY. From the pool of sister species pairs, we randomly sample a ratio *R* given as the stem branch length divided relative to the total branch length (Supplementary Table S10a; *1-length a/ length b*). The resulting terminal branch length of *A. berlepschi/floriceps* then becomes 0.47**R*.

Supplementary Table S10c. List of the 58 hummingbird species classified as range-restricted (endemic species) and their sampling status in the phylogeny [4]. *Status*: stating whether a species has been sampled in the phylogeny or added based on prior taxonomical information. The number of added species was 26 (44.84% of the 58 endemic species). *Taxonomical prior*: Taxonomical knowledge used to add species to the phylogeny and check the sampling status of a focal species' closest extant relatives. *Status of closet relatives:* Stating whether the taxonomical closest relatives have been sampled in the phylogeny. Species added to the phylogeny include all missing endemics and missing close relatives to the sampled endemics. *Terminal branch length* is determined after all species have been added to the phylogeny. The branch lengths for added species are written as a range corresponding to the 95% confidence interval within a population of 1000 trees in units of million years (MY). Species added as polytomies with sampled species had constrained placements in the phylogeny, and thus, their branch lengths were invariant across the 1000 trees. The average percentage of added species in a random sample of endemic species was 45.06 ±11.31SD.

Species	**Status**	**Taxonomical prior**	**Status of closet relatives**	**Terminal branch length (MY)**	**Number of subspecies**
Aglaeactis aliciae	added	*Aglaeactis spp.*	all sampled	1.3	Monotypic
Aglaeactis castelnaudii	sampled	*Aglaeactis spp.*	all sampled exept *A. aliciae*	0.31	2
Aglaeactis pamela	sampled	*Aglaeactis spp.*	all sampled exept *A. aliciae*	0.51	Monotypic
Aglaiocercus berlepschi	added	*A. coelestis & kingii*	both sampled	2.64	Monotypic
Amazilia castaneiventris	sampled	*A. tzacatl*	sampled	0.34	Monotypic
Amazilia viridicauda	sampled	*A. chionogaster*	sampled	1.776	Monotypic
Anthocephala berlepschi	added	*A. floriceps*	sampled	0.27-4.51	Monotypic
Anthocephala floriceps	sampled	*A. berlepschi*	added	0.27-4.51	Monotypic
Campylopterus ensipennis	sampled	*C. falcatus & C. phainopeplus*	Sampled exept *C. phainopeplus*	3.3	Monotypic
Campylopterus phainopeplus	added	*C. falcatus & C. ensipennis*	both samped	3.3	Monotypic
Chaetocercus astreans	added	*C. heliodor[5]*	*C. heliodor added to C. bombus[6]*	0.01-0.59	Monotypic
Chaetocercus berlepschi	added	*C. bombus[6].*	sampled	0.01-0.59	Monotypic
Chalcostigma heteropogon	added	*C. herrani, C. olivaceum, C. ruficeps & C. stanleyi*	all sampled	4.74	Monotypic

Chlorostilbon alice	added	*C. poortmani*	sampled	0.16-2.69	Monotypic
Chlorostilbon russatus	added	*C. poortmani*	sampled	0.16-2.69	Monotypic
Chlorostilbon stenurus	added	*C. poortmani*	sampled	0.16-2.69	2
Coeligena helianthea	sampled	*C. lutetiae, C. orina & C. violifer*	all sampled	0.1	2
Coeligena orina	sampled	*C. helianthea, C. lutetiae & C. violifer*	all sampled	0.59	Monotypic
Coeligena phalerata	sampled	*Coeligena spp.*	all sampled	2.32	Monotypic
Coeligena prunellei	sampled	*C. coeligena & C. wilsoni*	both sampled	5.01	Monotypic
Eriocnemis cupreoventris	sampled	*E. derbyi, E. luciani*	both sampled	3.3	Monotypic
Eriocnemis mirabilis	added	*E. aline*	sampled	0.4-6.73	Monotypic
Eriocnemis nigrivestis	sampled	*E. derbyi & E. vestita*	both sampled	0.97	Monotypic
Eulidia yarrellii	sampled	monotypic genus		1.59	Monotypic
Goethalsia bella	sampled	monotypic genus		2.39	Monotypic
Goldmania violiceps	sampled	monotypic genus		2.39	Monotypic
Haplophaedia lugens	sampled	*H. aureliae*	sampled	1.28	Monotypic
Heliangelus clarisse	added	*H. amethysticollis*	sampled	0.2-3.4	Monotypic
Heliangelus mavors	added	*Heliangelus spp.[7]*	all sampled	7.08	Monotypic
Heliangelus micraster	sampled	*H. exortis*	sampled	0.22	2
Heliangelus regalis	sampled	*Heliangelus spp.;* monotypic		7.08	2
Heliangelus spencei	added	*H. amethysticollis*	sampled	0.2-3.4	Monotypic
Heliangelus strophianus	sampled	*H. amethysticollis*	sampled	4.3	Monotypic
Heliodoxa imperatrix	sampled	*Heliodoxa spp.;* monotypic		4.58	Monotypic
Hylonympha macrocerca	added	*Eugenes fulgens[8]*	sampled	0.46-7.69	Monotypic
Lepidopyga lilliae	added	*L. coeruleogularis*	sampled	0.1-1.62	Monotypic
Leucippus baeri	sampled	*Leucippus spp.*	all sampled	1.54	Monotypic
Loddigesia mirabilis	sampled	*monotypic genus*		5.1	Monotypic
Metallura baroni	sampled	*M. williami, M. aeneocauda, M. odomae, M. theresiae and M. eupogon*	all sampled	0.32	Monotypic
Metallura eupogon	sampled	*M. williami, M. baroni, M. odomae, M. theresiae & M. aeneocauda*	all sampled	0.19	Monotypic
Metallura iracunda	added	*M. tyrianthina*	sampled	0.22-3.8	Monotypic
Metallura odomae	sampled	*M. aeneocauda, M. baroni, M. iracunda, M. theresiae & M. williami*	all sampled	0.73	Monotypic

Metallura theresiae	sampled	*M. aeneocauda, M. baroni, M. iracunda, M. odomae & M. williami*	all sampled	0.19	2
Ocreatus addae	added	*O. underwoodii*	sampled	0.35-5.88	2
Ocreatus peruanus	added	*O. underwoodii*	sampled	0.35-5.88	Monotypic
Oreonympha nobilis	sampled	monotypic genus		4.3	2
Oreotrochilus chimborazo	sampled	*O. stolzmanni, O. cyanolaemus & O. melanogaster*	all sampled	0.5	2
Oreotrochilus cyanolaemus	added	*O. melanogaster[9]*	sampled	0.01-0.04	Monotypic
Oxypogon cyanolaemus	added	*Oxypogon spp.*	*Oxypogon guerinii* sampled	0.2-3.36	Monotypic
Oxypogon guerinii	sampled	*O. cyanolaemus, O. lindenii & O. stuebelii*	all added	0.2-3.36	Monotypic
Oxypogon lindenii	added	*Oxypogon spp.*	*Oxypogon guerinii* sampled	0.2-3.36	Monotypic
Oxypogon stuebelii	added	*Oxypogon spp.*	*Oxypogon guerinii* sampled	0.2-3.36	Monotypic
Phlogophilus harterti	sampled	*P. hemileucurus*	sampled	2.36	Monotypic
Ramphomicron dorsale	added	*R. microrhynchum*	sampled	0.27-4.56	Monotypic
Sternoclyta cyanopectus	added	*Eugenes fulgens & Hylonympha macrocerca[8]*	*Eugenes fulgens* sampled	8.19	Monotypic
Taphrolesbia griseiventris	sampled	monotypic genus		3.22	Monotypic
Urochroa bougueri	sampled	*Urochroa leucura*	added	0.32-10.65	Monotypic
Urochroa leucura	added	*Urochroa bougueri*	sampled	0.32-10.65	Monotypic
% added species				**44.84**	

Supplementary Table S10d: Additional species added to the phylogeny for producing Supplementary Fig. S8. *Status*: stating whether a species has been sampled in the phylogeny or added based on prior taxonomical information. *Taxonomical prior*: The taxonomical knowledge used to add species to the phylogeny and check the sampling status of a focal species' closest extant relatives. *Status of closet relatives:* Stating whether the taxonomical closest relatives have been sampled in the phylogeny. Species added to the phylogeny include all missing endemics and missing close relatives to the sampled endemics. *Terminal branch length* is determined after all species have been added to the phylogeny. The branch lengths for added species are written as a range corresponding to the 95% confidence interval within a population of 1000 trees in units of million years (MY). Species added as polytomies with sampled species had constrained placements in the phylogeny, and thus, their branch lengths were invariant across the 1000 trees.

Species	**Status**	**Taxonomical prior**	**Status of closet relatives**	**Terminal branch length (MY)**	**Number of subspecies**
Amazilia cyanifrons	added	*Amazilia saucerottei*	sampled	0.03-0.53	Monotypic
Chaetocercus jourdanii	added	Outgroup to *Eulidia yarrellii, Chaetocercus spp. [6]*	sampled	1.59-1.74	3
Chlorostilbon gibsoni	added	*Chlorostilbon mellisugus*	sampled	0.11-1.78	2
Haplophaedia assimilis	added	*Haplophaedia aureliae*	sampled	0.07-1.2	2
Hylocharis humboldtii	added	*Hylocharis grayi*	sampled	0.06-1.05	Monotypic
Lophornis ornatus	Not added	Poor taxonomic prior information. elationships within *Lophornis* have not been determined	NA	NA	Monotypic
Lophornis stictolophus	added	*Lophornis delattrei*	sampled	0.13-2.15	Monotypic
Lophornis verreauxii	added	*Lophornis chalybeus*	sampled		2
Oreotrochilus leucopleurus	added	*Oreotrochilus estella*	sampled	0.07-1.12	Monotypic
Oreotrochilus adela	added	Outgroup to *Oreotrochilus spp.*	*O. Chimborazo, O. estella, O. melanogaster* & *O. Stolzmani* sampled	1.19	Monotypic
Phaethornis stuarti	added	*Phaethornis ruber*	sampled	0.09-1.45	Monotypic
Phaethornis subochraceus	added	*Phaethornis pretrei*	sampled	0.09-1.49	Monotypic
Schistes albogularis	added	*Schistes geoffroyi*	sampled	0.73-10.91	Monotypic

Supplementary Table S10e: List of endemic species classified as young and old across 1000 generated trees. In each tree, species unsampled by McGuire [4] were added to their sampled sister lineages (Supplementary Table S10c) using randomly sampled *R* values (Supplementary Table S10a). The numbers represent the percentage of trees in which a focal species was sampled as young or old (respectively 1st and 4th branch length quartile). The dashed line represents the quartile boundaries selecting the consensus composition of young and old endemic species. The table also includes sensitivity analyses using a 'late-burst model', where unsampled species were added towards the tip of the sampled sister lineage; secondly, an 'early burst model' where missing species were added towards the base of the sampled sister lineage. For this procedure, we repeated the existing protocol by subsetting R values to the 75% quantile (late-burst: $0.72 < R < 0.97$) and the 25% quantile (early-burst: $0.03 < R < 0.24$ in Table S10a).

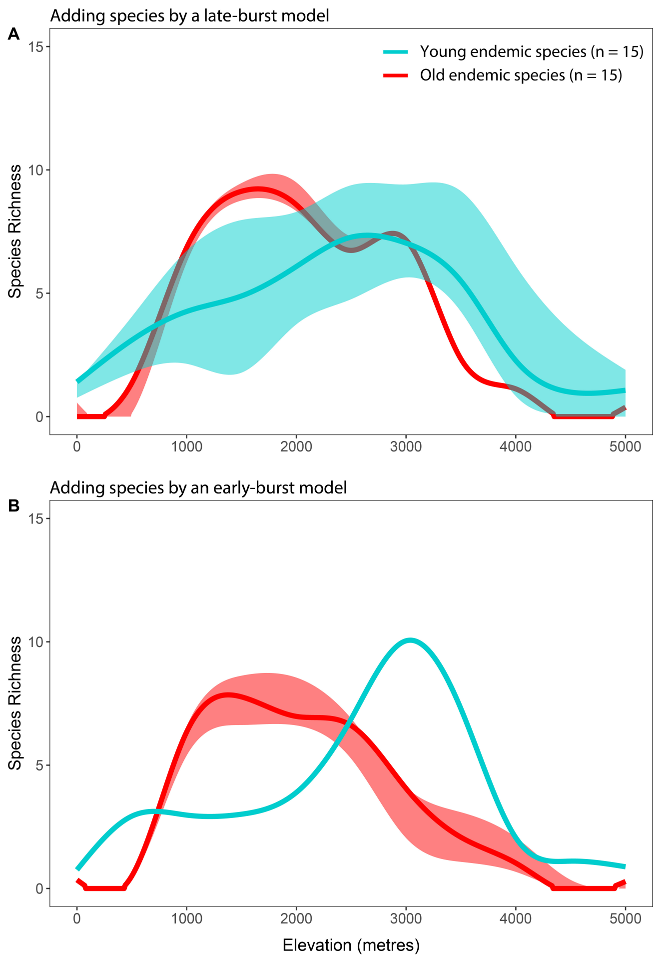
Young endemic species

All R values (0.05 < R < 0.97)		Early burst model (0.05 < R < 0.24)		late burst model (0.73 < R < 0.97)	
Species	Frequency (%)	Species	Frequency (%)	Species	Frequency (%)
Aglaeactis castelnaudii	100	Aglaeactis castelnaudii	100	Chaetocercus astreans	100
Coeligena helianthea	100	Aglaeactis pamela	100	Chaetocercus berlepschi	100
Heliangelus micraster	100	Amazilia castaneiventris	100	Coeligena helianthea	100
Metallura eupogon	100	Chaetocercus astreans	100	Metallura eupogon	100
Metallura theresiae	100	Chaetocercus berlepschi	100	Metallura theresiae	100
Oreotrochilus cyanolaemus	100	Coeligena helianthea	100	Oreotrochilus cyanolaemus	100
Metallura baroni	99.7	Coeligena orina	100	Heliangelus micraster	98.8
Amazilia castaneiventris	98.9	Eriocnemis nigrivestis	100	Aglaeactis castelnaudii	91.9
Oreotrochilus chimborazo	95.1	Heliangelus micraster	100	Metallura baroni	85.2
Chaetocercus astreans	89.5	Metallura baroni	100	Lepidopyga lilliae	80.7
Chaetocercus berlepschi	89.5	Metallura eupogon	100	Amazilia castaneiventris	74.5
Aglaeactis pamela	89.4	Metallura odomae	100	Chlorostilbon alice	40.1
Coeligena orina	70.8	Metallura theresiae	100	Chlorostilbon russatus	40.1
Metallura odomae	38.6	Oreotrochilus chimborazo	100	Chlorostilbon stenurus	40.1
Lepidopyga lilliae	31	Oreotrochilus cyanolaemus	100	Oreotrochilus chimborazo	34.6
Chlorostilbon alice	21.2			Oxypogon guerinii	28
Chlorostilbon russatus	21.2			Oxypogon cyanolaemus	28

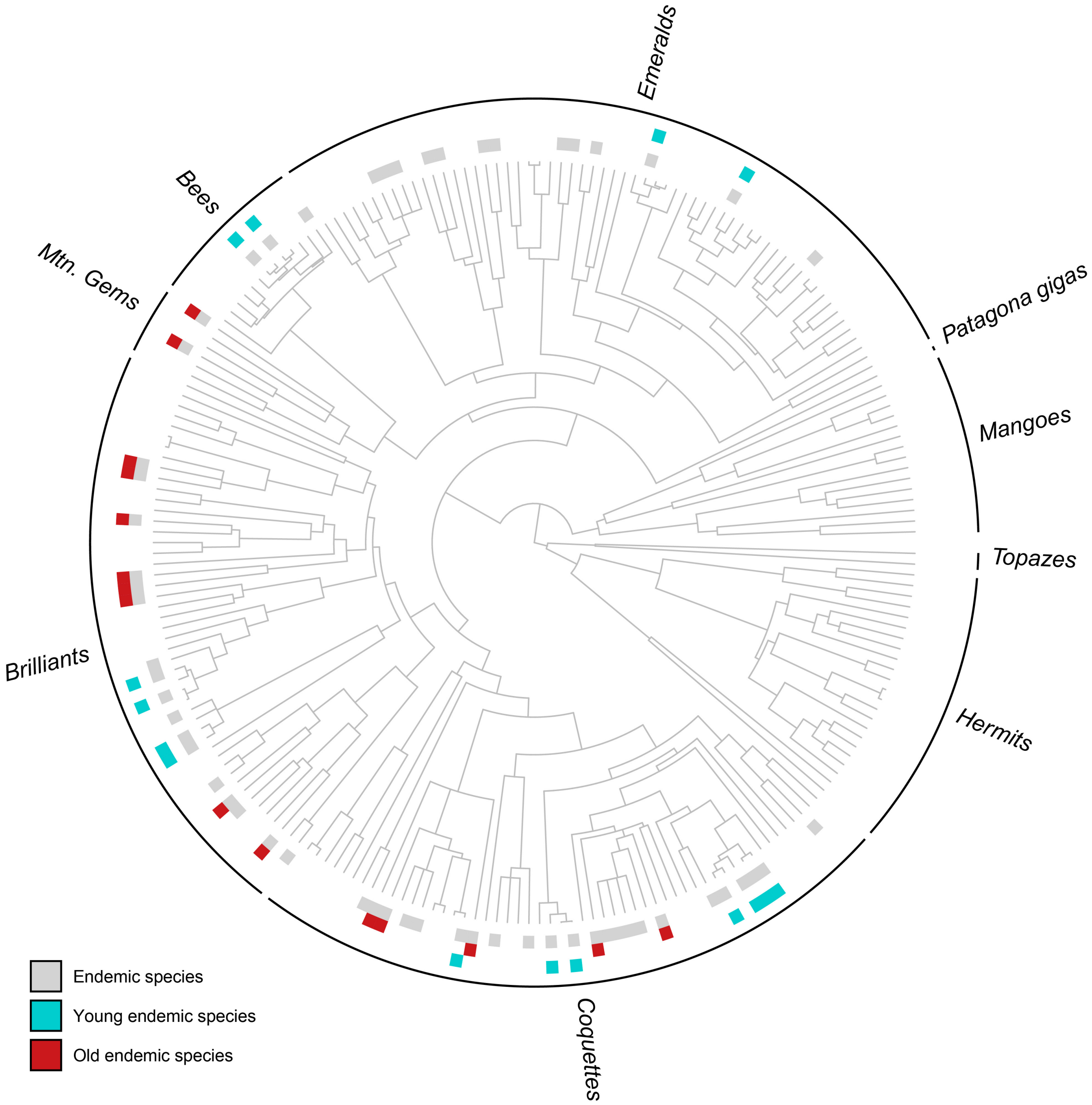
Chlorostilbon stenurus	21.2			Oxypogon lindenii	28
Oxypogon guerinii	16.1			Oxypogon stuebelii	28
Oxypogon cyanolaemus	16.1			Heliangelus clarisse	26.6
Oxypogon lindenii	16.1			Heliangelus spencei	26.6
Oxypogon stuebelii	16.1			Metallura iracunda	23.9
Heliangelus clarisse	13.6			Anthocephala floriceps	23.6
Heliangelus spencei	13.6			Anthocephala berlepschi	23.6
Metallura iracunda	13			Ramphomicron dorsale	20.4
Anthocephala floriceps	10.1			Aglaeactis pamela	18.2
Anthocephala berlepschi	10.1			Ocreatus addae	16
Eriocnemis nigrivestis	8.5			Ocreatus peruanus	16
Ocreatus addae	7.4			Eriocnemis mirabilis	13.8
Ocreatus peruanus	7.4			Hylonympha macrocerca	10.6
Ramphomicron dorsale	6.7			Urochroa bougueri	5.8
Hylonympha macrocerca	6.2			Urochroa leucura	5.8
Eriocnemis mirabilis	5.8			Coeligena orina	5.2
Urochroa bougueri	4.1			Metallura odomae	0.1
Urochroa leucura	4.1				
Old endemic species					
All R values (0.05 < R < 0.97)		Early burst model (0.05 < R < 0.24)		late burst model (0.73 < R < 0.97)	
Species	Frequency (%)	Species	Frequency (%)	Species	Frequency (%)
Chalcostigma heteropogon	100	Chalcostigma heteropogon	100	Campylopterus ensipennis	100
Coeligena prunellei	100	Coeligena prunellei	100	Campylopterus phainopeplus	100
Heliangelus regalis	100	Eriocnemis mirabilis	100	Chalcostigma heteropogon	100
Heliodoxa imperatrix	100	Heliangelus regalis	100	Coeligena prunellei	100
Loddigesia mirabilis	100	Heliodoxa imperatrix	100	Eriocnemis cupreoventris	100
Sternoclyta cyanopectus	100	Hylonympha macrocerca	100	Heliangelus regalis	100
Oreonympha nobilis	99.9	Loddigesia mirabilis	100	Heliangelus strophianus	100
Heliangelus strophianus	99.7	Ocreatus_addae	100	Heliangelus mavors	100
Heliangelus mavors	99.7	Heliangelus mavors	100	Heliodoxa imperatrix	100
Urochroa bougueri	73.8	Ocreatus_peruanus	100	Loddigesia mirabilis	100
Urochroa leucura	73.8	Sternoclyta cyanopectus	100	Oreonympha nobilis	100
Hylonympha macrocerca	65.9	Urochroa bougueri	100	Sternoclyta cyanopectus	100
Eriocnemis mirabilis	58.9	Urochroa_leucura	100	Taphrolesbia griseiventris	100
Ocreatus addae	55.8	Oreonympha nobilis	94.5	Aglaiocercus berlepschi	71.6

Ocreatus peruanus	55.8	Heliangelus strophianus	79.1	Goethalsia bella	67.4
Campylopterus ensipennis	49.5	Ramphomicron dorsale	26.9	Goldmania violiceps	67.4
Campylopterus phainopeplus	49.5	Anthocephala floriceps	20.9	Urochroa bougueri	32.6
Anthocephala floriceps	35.5	Anthocephala berlepschi	20.9	Urochroa leucura	32.6
Anthocephala berlepschi	35.5				
Ramphomicron dorsale	34.3				
Eriocnemis cupreoventris	13.4				
Metallura iracunda	13.4				
Taphrolesbia griseiventris	5.1				
Heliangelus clarisse	3.1				
Heliangelus spencei	3.1				
Oxypogon guerinii	2.9				
Oxypogon cyanolaemus	2.9				
Oxypogon lindenii	2.9				
Oxypogon stuebelii	2.9				
Aglaiocercus berlepschi	0.1				
Chlorostilbon alice	0.1				
Chlorostilbon russatus	0.1				
Chlorostilbon stenurus	0.1				

Supplementary Fig. S10f: Elevational segregation between young and old endemic species using two rules to add unsampled species to the phylogeny. (A) Using a 'late-burst model', we added missing species towards the tip of the sampled sister lineage. For this procedure, we repeated the existing protocol (Supplementary Tables S10a-c) by subsetting R values to the 75% quantile ($0.73 < R < 0.97$). (B) Using an 'early-burst model', we added missing species towards the base of the sampled sister lineage. Here, we used R values belong to the 25% quantile ($0.05 < R < 0.24$). The procedure of adding missing species to the phylogeny caused uncertainties in the composition of young and old endemic species (Supplementary Table S10d), represented here as the 95% confidence intervals (shaded areas).



Supplementary Fig. S11: The phylogenetic distribution of endemic hummingbirds. The phylogeny [4] comprises 220 of the 229 hummingbirds occurring within the Central and Northern Andes. Young (n=15) and old species (n=15) represent consensus quartiles of the regional pool of endemic hummingbirds (n=58; Supplementary Table S10d). 26 endemic species were added to the phylogeny based on prior taxonomical information (Supplementary Table S10c). In this example, their branch lengths were determined using the median Ratio value across all sister species comparisons (*R*= 0.41).



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