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Sarah-sophie Weil, Laure Gallien, Sébastien Lavergne, Luca Börger, Gabriel W Hassler, Michaël P J Nicolai, William L Allen

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ECOGRAPHY

Research

0 Chameleon biogeographic dispersal associated with extreme life history strategies 61

5 Sarah-Sophie Weil, Laure Gallien*, Sébastien Lavergne, Luca Börger, Gabriel Hassler, Michaël P. J. Nicolai and William L. Allen* 65
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Q2 S.-S. Weil (<https://orcid.org/0000-0003-2280-9612>) ✉ (sarah-sophie.weil@gmx.de), L. Gallien and S. Lavergne, Univ. Grenoble Alpes, Univ. Savoie Mont Blanc, CNRS, LECA (Laboratoire d'Ecologie Alpine), Grenoble, France. – S.-S.W, L. Börger and W. L. Allen, Dept of Biosciences, Swansea Univ., Singleton Park, Swansea, Wales, UK. – G. Hassler, Dept of Computational Medicine, Univ. of California, Los Angeles, CA, USA. – M. P. J. Nicolai (<https://orcid.org/0000-0002-9570-0311>), Biology Dept, Evolution and Optics of Nanostructures Group, Ghent Univ., Ghent, Belgium. 75

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Understanding the role of traits in dispersal is necessary to improve our knowledge of historical biogeography, community assembly processes and predictions of species' future movements. Here we aimed to determine the relationship between three traits (coastal distribution, body size, position on the fast/slow life history continuum) and past dispersal probability on an evolutionary timescale in chameleons (Chamaeleonidae). Using species' distribution data we identified the nine most important biogeographic regions for all included chameleons (181/217 species). We compiled life history trait data and used phylogenetic factor analysis to infer independent body size and fast/slow life history trait axes. Finally, we tested whether traits and trait combinations related to biogeographic dispersal success in the past, using trait-dependent biogeographic models. All three traits were associated with past biogeographical movements. Lineages having coastal distributions and those with large bodies had higher dispersal probabilities. Interestingly, chameleons with either a very fast or very slow life history were more successful dispersers than species with an intermediate strategy. Together, the three traits 'coastal, large-bodied and extreme life history' form a dispersal syndrome. Traits have played an important role in the biogeographic history of chameleons. While only fast traits have been linked to present-day invasion success in reptiles, both extremes of the life history spectrum were likely advantageous for dispersal and establishment during past biogeographic movements. Fast-living species may be less susceptible to stochastic extinction in the first phases of a colonization (due to rapid population growth), and slow-living species may be less vulnerable to environmental stochasticity (due to low demographic variability). Our results call for broader analyses testing the general influence of life history strategy in biogeographic dispersal success, which would help explain species distribution patterns on Earth.

Keywords: biogeography, Chamaeleonidae, dispersal, life history continuum, species' traits, trait-dependent biogeography

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0 Introduction

Species' traits can impact biogeographic processes such as dispersal, extinction and cladogenesis and likely play a part in shaping the distribution of life on Earth (Ronce and Clobert 2012, Zamudio et al. 2016, Chichorro et al. 2019). While associations between traits and short-distance dispersal at the level of individuals and populations have been studied extensively (Whitmee and Orme 2013), the role of traits in broad-scale historical biogeographic dispersal outcomes at the species level is only just beginning to be formally investigated (Sukumaran and Knowles 2018, Klaus and Matzke 2020). Integrating dispersal events and species' trait evolution on evolutionary timescales offers potential insight into the role of traits in species' biogeographic movements. This will advance our understanding of processes in historical biogeography and community assembly, which may enable better predictions of species' movements in the future (Lowe and McPeck 2014, Estrada et al. 2016).

To colonize a distant location, species must succeed at three sequential stages of dispersal: emigration, movement (or 'passage' if referring to passive dispersal) and establishment (Nathan 2001). Different types of traits might be linked to successfully overcoming each stage (Estrada et al. 2016). The emigration stage in biogeographic dispersal is strongly influenced by species' geographic distributions; coastal species, for example, are more likely to be moved from their native range by storms and cyclones than species living far away from the coast (Blom et al. 2019). In the movement and establishment stages, larger animals might have a survival advantage since their relative metabolic rate (relative to body size) is lower than that of smaller species (Andrews and Pough 1985, White et al. 2019), which improves their resistance to stress (including long periods of food and water shortage; Van Bocxlaer et al. 2010). On the other hand, transoceanic, cyclone-driven rafting dispersal of small organisms has long been reported (Ozgo et al. 2016, Lindo 2020). Establishment at a new location depends first and foremost upon the arrival of a reproductively viable founding population, which is determined by population size and species' life history traits (Safriel and Ritte 1980). While some traits are likely linked to specific stages of the dispersal process (e.g. coastal distribution to emigration), other traits may be related to several dispersal stages at the same time (such as body size). In addition, traits may have multiplicative effects, i.e. a species holding several dispersal traits may have a much higher probability of dispersal success than could be expected based on estimations from the individual traits. It is therefore important to consider combinations of traits that might form a successful disperser phenotype (Van Bocxlaer et al. 2010).

Further clues to understanding how traits influenced biogeographic movements in the past can be found in today's biological invasions. In some groups, invasive species belong to lineages with particularly frequent historical biogeographical movements (e.g. in pines: Gallien et al. 2016; and in Australian acacias and eucalypts: Gallien et al. 2019). Furthermore, in both processes taxon-specific barriers need

to be overcome for a successful range expansion (e.g. large water bodies). While some barriers may be very different in the two processes (e.g. those related to emigration), others may be comparable (e.g. those related to establishment) and the traits associated with overcoming them may be similar.

In today's biological invasions, a species' position on the fast/slow life history continuum has been linked to its invasion success (Sol et al. 2012, Capellini et al. 2015, Allen et al. 2017). The fast/slow life history continuum (Dobson and Oli 2007, Jeschke and Kokko 2009) is a descriptive analogue of the mechanistic r/K selection theory of life history evolution (MacArthur and Wilson 1967, Pianka 1970). Life history traits of fast species can be equated to those of r-strategists (e.g. early reproduction, big litters/clutches), and life history traits of slow species to those of K-strategists (e.g. low fecundity, long lifespan). Birds with traits associated with slow life history and bet-hedging strategies, such as large brains and iteroparous reproduction, are more successful invaders (Sol et al. 2012). Slow and bet-hedging species may have the resources (and lifespans) to wait for favourable environmental conditions to produce offspring (Cáceres 1997), and they exhibit less demographic variability over the years, which buffers the effects of environmental stochasticity (Sæther and Bakke 2000, Jeppsson and Forslund 2012). On the other hand, in mammals, amphibians and (non-avian) reptiles, the opposite pattern has been found: species with fast life histories are more successful throughout the invasion pathway than slow species (Capellini et al. 2015, Allen et al. 2017). Fast species are able to quickly establish sizable populations, hence they may be able to quickly overcome the period in which founder populations are particularly vulnerable to stochastic extinction (Caswell et al. 2003, Blackburn et al. 2015). The relationship between life history strategy and present-day biological invasions and species' movements has inspired us to investigate the role these strategies have played as drivers of global biogeography in the past.

Here, we use recently developed trait-dependent biogeographic models (Klaus and Matzke 2020) to test the effect of three binary traits (coastal distribution, body size and life history strategy) and their combination in dispersal outcomes on an evolutionary timescale. We investigate these traits in the family of chameleons (Chamaeleonidae) which comprises 217 species in 12 genera (according to <www.reptile-database.org>, accessed 20 May 2021). Most species occur in Madagascar and Africa, but some species can be found in southern Europe, the Middle East, India and Indian Ocean islands (IUCN 2019). Chameleons are situated within the squamate clade of Acrodonta, and are hypothesized to have diverged from their sister clade Agamidae ca 90 million years ago (mya) (Townsend et al. 2011, Tolley et al. 2013). Chameleon phylogeography suggests an African origin with multiple oceanic dispersal events to Madagascar, the Comoros Islands, Arabia, the Seychelles, India and Europe (Raxworthy et al. 2002, Townsend et al. 2011, Tolley et al. 2013), which makes the group well-suited for investigating how traits relate to dispersal patterns.

0 First, we analysed whether chameleon distributions (coastal versus non-coastal) and body size (and associated life history trait covariation) are related to past dispersal outcomes, two traits identified as affecting historical dispersal in other reptile clades (Blom et al. 2019, Nicolai and Matzke 2019). Body size is known to evolve under different selective pressures from life history (e.g. temperature; Tinkle et al. 1970), but through allometric constraints selection pressures on body size can indirectly influence traits that are related to the fast/slow life history spectrum (Bauwens and Díaz-Uriarte 1997, Bakewell et al. 2020, Meiri et al. 2021). We therefore placed species on a body size-independent fast/slow life history continuum using phylogenetic factor analysis. We then evaluated the relationship between this body size-independent life history strategy and past dispersal outcomes, which has not been done in the context of historical biogeographic dispersal before. Finally, we combined all three traits (coastal distribution, body size and life history strategy) and investigated the possibility of a successful dispersal syndrome. We used trait-dependent biogeographic models to test the following hypotheses:

- 1) Coastal lineages and large-bodied lineages were better dispersers than non-coastal and small-bodied lineages, respectively, in the past, as demonstrated in other reptile clades.
- 2) Chameleon lineages with fast life histories were better biogeographic dispersers than lineages with slow traits in the past, following patterns in invasive reptiles.
- 3) Chameleon lineages holding all traits hypothesized to favour dispersal (coastal distribution, large body and fast life history strategy) were better dispersers than lineages holding only one of these traits.

Material and methods

To assess whether, and how, three traits (coastal distribution, body size and body size-independent life history strategy) have influenced past dispersal success of chameleons we built and compared trait-independent and trait-dependent biogeographical models (Fig. 1). Biogeographical models estimate ancestral ranges of species

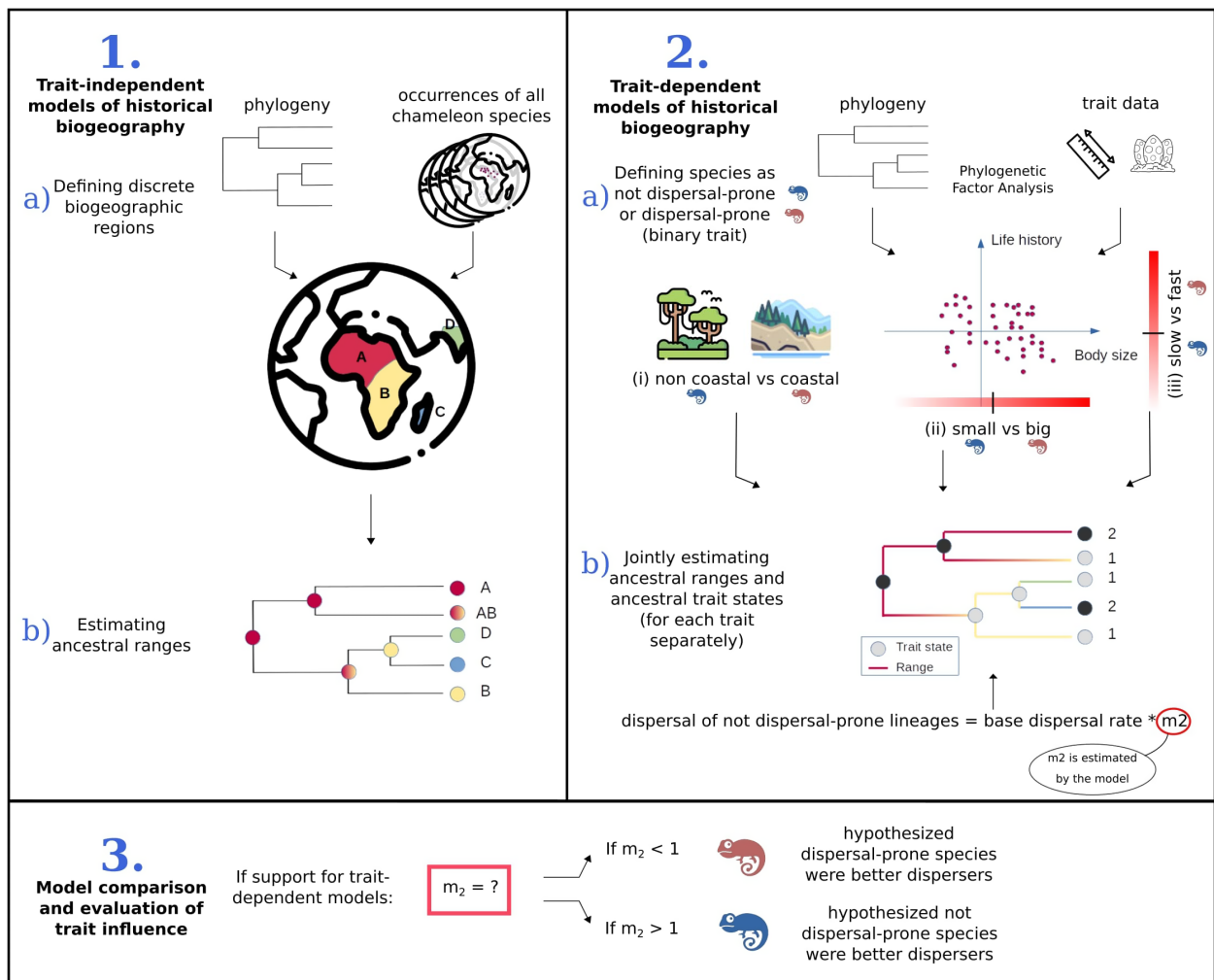


Figure 1. Schematic presentation of analysis workflow. Icons: Flaticon.com.

0 based on species' extant distributions and allow us to
estimate past movements between discrete biogeographic
regions (see 'Chamaeleonidae biogeographic regions'
5 In trait-dependent biogeographical models, a binary trait can
influence dispersal rates of lineages. To define this binary
trait and classify species according to body size and body
size-independent life history strategy we used phylogenetic
factor analysis (see 'Trait data and phylogenetic factor
10 analysis' section for details). Comparison between trait-
dependent and trait-independent models reveals whether a
given trait had an influence on dispersal success in the past.
If this is the case, the direction of the relationship between
a given trait and dispersal success will be investigated (with
15 the estimated parameter m_2 ; see 'Trait-dependent dispersal:
'BioGeoBEARS'' section for details). All analyses were
performed using R ver. 3.6.3 (<www.r-project.org>) unless
otherwise specified.

20 Chamaeleonidae phylogeny and distribution

We focused only on chameleon species for which genetic
data were available (181/217 species, ca 83%), using a subset
25 of the Tonini et al. (2017) squamate consensus tree. To
quantify the effect of phylogenetic uncertainty in results we
repeated the analyses on a set of 100 uniformly sampled trees
from a sample of the posterior distribution of Tonini et al.
(2017) (Supporting information). Species' distribution
30 data were obtained from IUCN (2019). We kept records
where presence was defined as extant and origin as native.
We transformed the data into rasters in cylindrical equal
area projection (Behrmann with standard parallels at 30° to
35 avoid distortion of area at higher latitudes, which allows for
a better comparison between different raster cells at different
latitudes) with a resolution of ca 93×93 km.

40 Chamaeleonidae biogeographic regions

To estimate species' movements in the past, the first step
is to identify the most important biogeographic regions
specific to chameleon species. We did so with a data-
driven approach using extant species' distribution data.
45 After evaluating alternative bioregionalization methods
(Supporting information) we chose to use a clustering
algorithm (unweighted pair group with arithmetic mean,
Kreft and Jetz 2010) on between-site phylogenetic distances
(modified Simpson's phylogenetic beta-diversity index
50 (Lennon et al. 2001 after Simpson 1943); Eq. 1). This
method calculates the phylogenetic distance between raster
cells based on extant species' distribution data and their
phylogenetic relationships, and then groups raster cells
together according to the amount of evolutionary history
55 they share. Hence, this method identifies barriers that have
acted as actual barriers to gene flow over evolutionary time,
and dispersal that is estimated between regions can be
considered biogeographic dispersal (Kreft and Jetz 2010)
60 (Eq. 1):

$$\text{Simpson} = \frac{\min(b,c)}{\min(b,c) + a} \quad (1)$$

where a =length of shared branches on the phylogenetic tree
65 between two different raster cells, and b and c =length of
unique branches in two different raster cells.

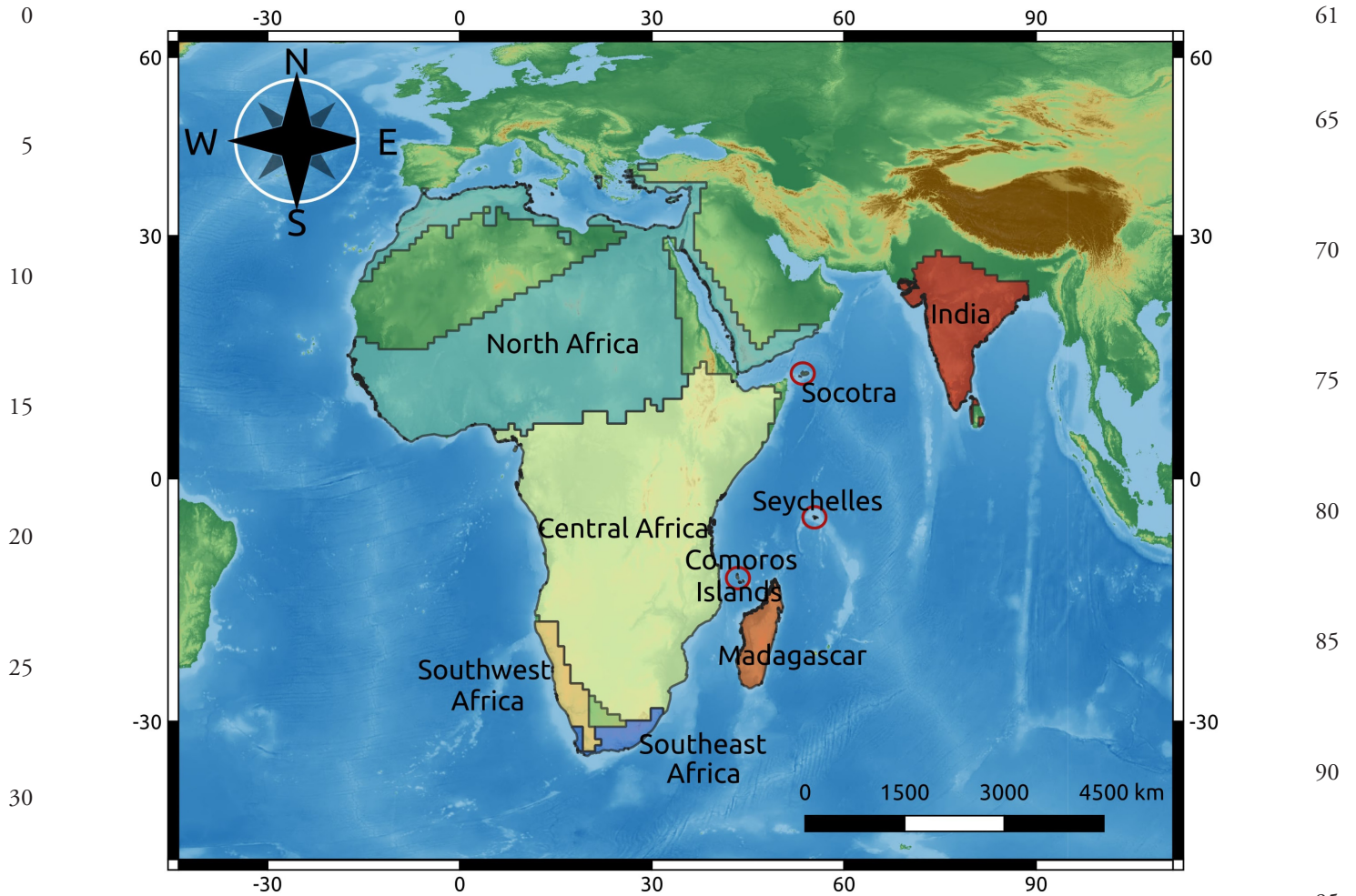
The phylogenetic beta-diversity matrix was weighted by
a geographical distance matrix (great-circle distances on
70 latitude/longitude coordinates). Non-contiguous regions
were separated manually. In this way, we identified nine
biogeographic regions: north Africa and Arabia, central
Africa, southeast Africa, southwest Africa, India, Socotra,
Madagascar, the Comoros Islands and the Seychelles
(Fig. 2). Extant species occupy three biogeographical regions
at maximum. We therefore allowed ancestral distributions
to extend to a maximum of three regions (Supporting
information).

80 Trait data and phylogenetic factor analysis

Trait-dependent biogeographic models can presently only
take binary traits into account (see 'Trait-dependent disper-
85 sal: 'BioGeoBEARS'' section). We hence defined four binary
trait datasets, based on three focal traits and their combina-
tion: 1) coastal distribution: coastal species (species living
within 10 km of the coast) versus non-coastal species; 2) body
size and associated life history trait covariation: large-bodied
species versus small-bodied species; 3) body size-independent
90 life history: fast versus slow life history; and 4) dispersal syn-
drome: species holding all three hypothesized dispersal traits
(coastal distribution + large bodied + fast life history) versus
species that do not have all three traits.

We identified species as coastal if they lived less than 10 km
away from the sea (74 coastal species, ca 41%) using QGIS
(QGIS Development Team 2020) and a global terrain model
for ocean and land (GEBCO Compilation Group 2021). To
100 assess sensitivity to the 10 km threshold, we analysed three
additional classifications where we defined species as coastal
if they lived less than 2, 15 or 25 km away from the sea. To
rank species according to body sizes and life history strategies,
we compiled a dataset of life history traits and identified the
main axes of variation with a phylogenetic factor analysis
105 (PFA, Tolkoﬀ et al. 2018). The trait data included: snout-
vent-length (SVL, 100% coverage) as a proxy for body size,
clutch size (67% coverage), number of clutches per year
(24% coverage), age at sexual maturity (29% coverage),
gestation time (28% coverage) and reproductive lifespan
110 (18% coverage; Nečas 1999, Glaw and Vences 2007, Tilbury
2010, Allen et al. 2017, Meiri 2018, Hughes and Blackburn
2020).

We performed PFA using the Julia package
PhylogeneticFactorAnalysis.jl ver. 0.1.4 (Hassler et al.
2021) which relies on a development version of BEAST
(Suchard et al. 2018) to be released with BEAST ver. 1.10.5.
Missing data were handled in PFA through integrating out
115 missing values in likelihood calculations, allowing inclusion
of species with incomplete trait data, while avoiding biases
121



35 Figure 2. The nine biogeographic regions for Chamaeleonidae, identified through UPGMA clustering on a modified Simpson's phylogenetic beta-diversity distance matrix.

30 associated with data imputation (Supporting information).
 40 To identify a size-specific fast/slow continuum (cf. Jeschke and Kokko 2009) independent from allometric constraints, we structured the PFA so that body size (as captured by SVL) loaded only onto the first factor while all other traits loaded onto all factors. This forced life history trait variation associated with body size onto the first factor with any additional factors capturing size-independent patterns of life history covariation (Supporting information). The first factor capturing size-dependent relationships was defined by positive loadings on SVL and clutch size (Fig. 3). The second factor was associated with size-independent fast/slow strategies and defined by gestation time and sexual maturity, with fast species of early sexual maturity and short gestation time on one side, and species with opposing traits on the other. Altogether, 32% of trait variance was attributable to the first factor and 16% to the second.

50 We used the first factor of the PFA to assess the role of body size and associated allometric relationships by median-splitting the species along this factor (i.e. using the median to assign species as small or large). We used the second factor as

a representation of the fast/slow spectrum and median-split species along this factor to differentiate fast from slow species and obtain the life history trait dataset. We further tested alternative splitting thresholds (see 'Life history strategy' section in Results; Supporting information): 1) the fastest 25% of species versus the rest; 2) the fastest 75% versus the rest; and 3) the fastest 25% and slowest 25% ('extreme' life history) versus the rest. According to the results of these splits our definition of the dispersal syndrome changed (see 'Dispersal syndrome' section in Results). Finally, we assessed the sensitivity of our main results to the binarization of the continuous traits by moving the cutoff 10% in either direction.

Trait-dependent dispersal: 'BioGeoBEARS'

To assess the effect of traits on dispersal outcomes in the biogeographic history of chameleons, we used three biogeographic models that estimate ancestral ranges implemented in the R package 'BioGeoBEARS' ver. 1.1.2 (Matzke 2013, 2014): 1) dispersal-extinction-cladogenesis

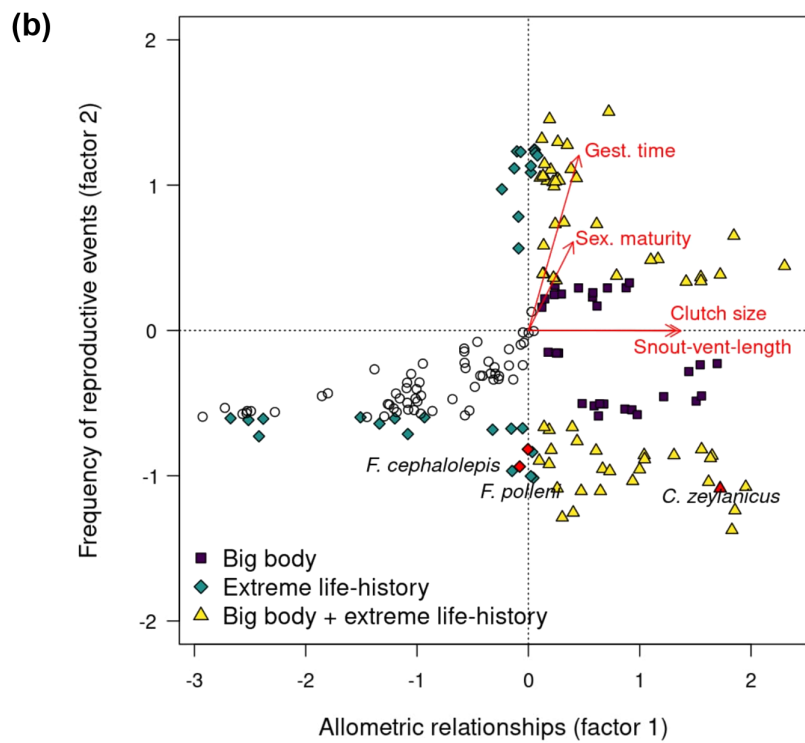
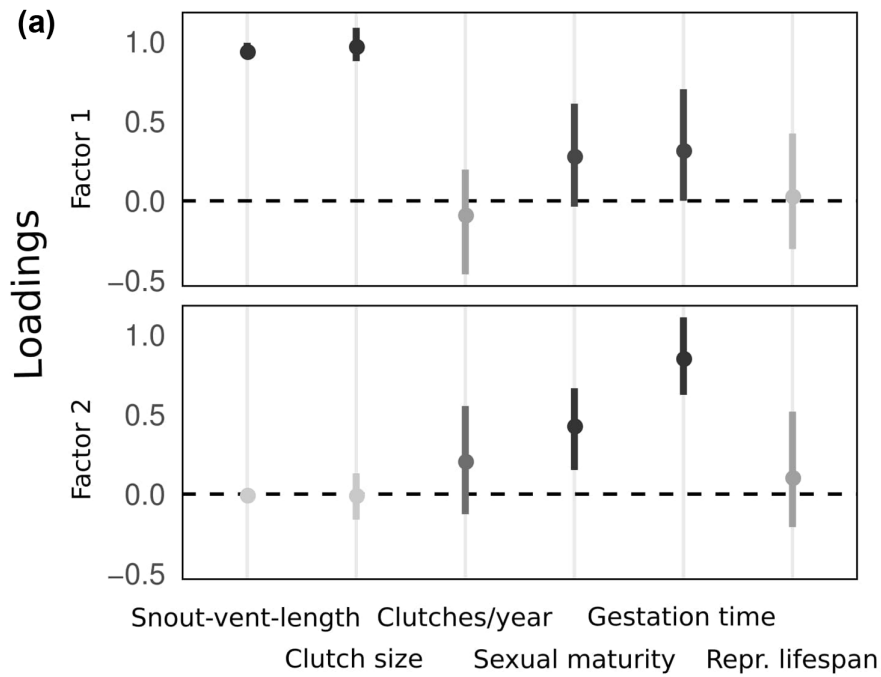


Figure 3. Results of the phylogenetic factor analysis. The estimates for the loadings of the body size and life history variables onto the two identified factors are given in panel 2a. Points represent the posterior mean while error bars represent the 95% highest posterior density interval. Shading indicates the posterior probability p that loadings are of the same sign as their posterior means. The light end of the spectrum corresponds to $p=0.5$ (i.e. the loadings value has equal probability of being positive or negative), while the dark end corresponds to $p=1$ (i.e. the parameter's sign is certain). In panel 2b, chameleon species are plotted in the factor space with different symbols depending on whether the species were classified as large-bodied (square), having an extreme life history strategy (diamond) or as being both large-bodied and having an extreme life history strategy (triangle). Small-bodied species with an intermediate life history strategy are indicated by simple dots. The original variables that loaded most strongly on the two identified factors are represented by red symbols. The three species that are associated with recent oceanic dispersal are labelled and indicated by red symbols.

0 (DEC; Ree et al. 2005, Ree and Smith 2008); 2) DIVA-
like (a likelihood implementation of DIVA; Ronquist
1997); and 3) BAYAREA-like (a likelihood implementation
of BayArea; Landis et al. 2013). In the 'BioGeoBEARS'
5 implementation of these models, biogeographical
movements (i.e. anagenetic and cladogenetic dispersal rates)
can be influenced by lineages' trait values. These models go
beyond investigating correlations between traits and species'
distributions to allow quantitative estimations of the
10 importance of traits in dispersal processes at large temporal
and spatial scales (Sukumaran and Knowles 2018, Klaus
and Matzke 2020). At present the trait can take only two
states (i.e. it is a binary trait) and it is itself evolving on the
phylogeny, i.e. ancestral trait states and ranges are jointly
15 estimated on the phylogeny. All models are implemented
in a common likelihood framework which allows for model
comparison.

The influence of trait states on dispersal rates is implemented
via dispersal multipliers m_1 and m_2 . If a lineage is in trait
state 1 (e.g. large body size), the base dispersal rate d is
multiplied by m_1 , and if a lineage is in trait state 2 (e.g. small
body size), d is multiplied by m_2 (Klaus and Matzke 2020
and <<http://phylo.wikidot.com/biogeobears>>). In practice,
25 m_1 is fixed to 1, and only m_2 is inferred: $m_2 > 1$ indicates
that lineages in trait state 2 (e.g. small-bodied) were more
successful dispersers than lineages in trait state 1, and $m_2 < 1$
indicates the inverse. The transition rates from one trait state
to the other, t_{12} and t_{21} , are inferred as well. To compare
30 trait-independent models to trait-dependent '+ m_2 ' models,
the log-likelihood from the independent trait evolution
on the tree is combined with the log-likelihood from the
independent geographic data. Therefore, we ran just the trait
data under binary discrete character models as implemented
35 in the 'BioGeoBEARS' package to independently estimate
the parameters t_{12} and t_{21} (Klaus and Matzke 2020). The
log-likelihood of the trait-independent models was then the
sum of the log-likelihood of these independent trait data and
the log-likelihood of the geographic data (i.e. log-likelihood
40 from 'BioGeoBEARS' runs without parameters m_2 , t_{12} and
 t_{21}). The log-likelihood reflects whether incorporating the
trait (e.g. body size) improves model fit and m_2 indicates
which trait state the dispersal is associated with (e.g. large
45 body size).

Plate tectonics and island uplift influenced species' past
movements between biogeographic regions. We therefore
implemented a time-stratified analysis and defined manual
dispersal multiplier matrices (MDMMs) to account for
50 islands uplifts and differences in the ease of continental
versus oceanic-with-currents versus oceanic-against-currents
dispersal (Supporting information). We also took changing
geography into account by modifying dispersal probabilities
between any two areas depending on the distance between
55 them (+ x model variant). Based on GPlates (Müller et al.
2018) and the global plate and rotation model of
Matthews et al. (2016), we accounted for changing distances
between regions by recalculating the distances for every time
60 slice (Supporting information). We further introduced a

root constraint in central Africa to reflect findings from the
literature (Tolley et al. 2013; Supporting information). 61

In summary, we first evaluated 30 trait-independent
models: three types of biogeographical models (DEC, DIVA
and BAYAREA) \times two types of influence of geographic
65 distances (base model and + x -variant) \times five different
MDMMs. We compared these 30 models with the corrected
Akaike information criterion (AICc), and identified the best
base model: DEC with MDMM distinguishing continental
70 versus oceanic barriers and paleo-current directions
(Supporting information). Second, for each of the traits
(coastal distribution, body size, four life history strategies,
dispersal syndrome) we ran the two trait-dependent
biogeographic models (+ m_2 and + m_2x) using the previously
75 selected best base model. Third, for each trait, we used AICc
to compare the four final models (two trait-independent
models: base, base+ x and two trait-dependent models:
base+ m_2 , base+ m_2x). In addition, we ran founder event
80 models (+ j) for two traits (body size and extreme life history
strategy) but, since they did not affect the m_2 parameter
estimates significantly (Supporting information) and a
critique of Ree and Sanmartín (2018) highlighted conceptual
85 problems, we did not pursue this avenue further to reduce
computation time.

To assess phylogenetic uncertainty, we reran the trait-
dependent model for every trait (coastal distribution,
body size, life history strategy and dispersal syndrome) for
every tree across the set of 100 trees from the posterior (see
90 'Chamaeleonidae phylogeny and distribution' section).
Each new run included a new phylogenetic factor analysis
to reclassify species as large versus small, to reclassify the life
history strategies and to recalculate the dispersal phenotype
95 (Supporting information).

All 'BioGeoBEARS' analyses were performed on R
ver. 3.6.2 (<www.r-project.org>) using the GRICAD
infrastructure (<<https://gricad.univ-grenoble-alpes.fr>>). The
biogeographical analyses amounted to more than 44 600 h \times
100 cores of computation time.

Results 105

Trait-dependent biogeographic models

Coastal distribution and body size

Non-coastal lineages did not disperse at all and large
chameleons had a higher dispersal probability than lineages
110 with small body sizes in the past. The trait-dependent models
were selected as best models by the AICc-based model
comparison for coastal distribution and body size (Table 1;
Supporting information), split between just trait-dependent
115 (coastal distribution: 63%, body size: 74%) and distance-and-
trait-dependent models (coastal distribution: 37%, body size:
26%; Supporting information). The multiplier of the non-
dispersal-prone forms (m_2) was 0 for both traits. Phylogenetic
uncertainty had little effect on dispersal multiplier estimates
120 in the coastal distribution and body size analyses (Fig. 4).

0 Table 1. Best models per trait as selected by model comparison with AICc. Only models with an AICc weight greater than 1% are included. m2: dispersal multiplier of species in the non-dispersal-prone form: non-coastal distribution, small bodied, intermediate life history (m2 > 1 indicates that species with non-dispersal-prone traits were more successful dispersers than species in trait state 1, and m2 < 1 indicates the inverse); x: dispersal multiplier of geographic distance.

Trait set	Best models	LnL	AICc weight (%)	m2	x
Coastal distribution	DECm2	-272	63	0	0
	DECm2x	-271	37	0	-0.11
Body size	DECm2	-253	74	0.0028	0
	DECm2x	-253	26	0.0028	-10 ⁻⁶
Extreme life history	DECm2	-248	74	0.15	0
	DECm2x	-248	26	0.15	-10 ⁻⁶
Dispersal syndrome	DECm2	-234	74	0.02	0
	DECm2x	-234	26	0.02	-10 ⁻⁶

10 Using different distances to the sea (2, 15, 25 km) to classify species as coastal did not change interpretation of our results (Supporting information). Neither did moving the cutoff during binarization of body size 10% in either direction, i.e. considering the first 40% and 60% of species as large, respectively (Supporting information).

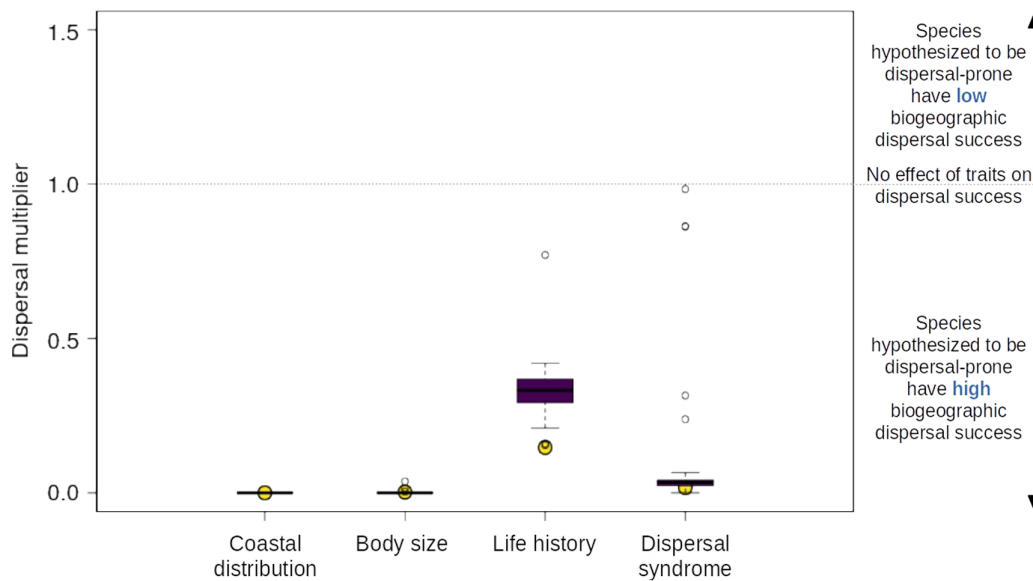
15 **Life history strategy**

Initial results suggested that fast lineages had generally higher dispersal probabilities than slow lineages: m2 of the median-split classification of life history strategies was 0.84, trait-dependent models accruing an AICc weight of 27% (Supporting information), and m2 was 0.22 when comparing the fastest 25% of all species against the rest, trait-dependent

61 models accruing an AICc weight of 93% (Supporting information). However, when comparing the fastest 75% against the rest, m2 of the best model was 2.19 (AICc weight of trait-dependent models = 68%; Supporting information), indicating that the slowest 25% of all species had a higher dispersal probability than the fastest 75%, contrary to the initial results. We therefore developed an ad hoc hypothesis and tested whether the extremes of the life history spectrum may be advantageous to dispersal. When comparing the fastest 25% and slowest 25% of species jointly against the rest, m2 was 0.15 and trait-dependent models accrued an AICc weight of 100% (Table 1; Supporting information), indicating that species with an extreme life history strategy had an 85% higher dispersal probability than species with an intermediate one. Phylogenetic uncertainty influenced the extreme life history result more than coastal distribution and body size, with the median m2 being at 0.33 ± 0.07. Moving the cutoff during binarization 10% in either direction, i.e. hypothesizing the extreme 40% and 60% of species to be dispersal-prone, respectively, did not change our results (Supporting information).

20 **Dispersal syndrome**

According to the life history results, our prediction for the dispersal syndrome changed to expecting that chameleons dispersed more when they were at the same time coastal, large-bodied and with extreme life history strategy (instead of only a fast one). We identified 34 species (ca 19%) as having such a dispersal syndrome, significantly more than could have been expected by chance (Supporting information). Species that did not hold this combination of traits had a 98% lower probability of dispersal (m1 was fixed to 1, m2 estimated



25 Figure 4. Values of the dispersal multiplier parameters as estimated by trait-dependent DEC models (DEC+m2). m1 (multiplier of the dispersal-prone forms) was fixed to 1. All multipliers presented here are estimations of m2, the multiplier for the non-dispersal-prone forms. The yellow points indicate the m2 parameter estimation from the consensus tree; the boxplots reflect the uncertainty in m2 parameter estimates due to phylogenetic uncertainty: the models were run on a set of 100 trees from the posterior.

0 as 0.02; Fig. 4), and trait-dependent models accrued an
AICc weight of 100% (Table 1; Supporting information).
When running the trait-dependent model on a set of trees,
5 m2 values varied around 0.03 ± 0.14 but a small number
of trees (3%) generated low log-likelihood models with m2
parameters close to 1 (Supporting information).

Biogeographic history of chameleons and trait evolution

10 Trait-dependent models were consistently better supported
by AICc comparison than trait-independent models.
Notably, two nodes were estimated identically in all trait-
dependent models but differently in the trait-independent
15 model (Supporting information). All trait-dependent models
agreed on the most recent common ancestor (MRCA)
of *Bradypodion pumilum* and *B. damaranum* occupying
southeast and southwest Africa (Supporting information).
20 The trait-independent model, however, inferred this node to
be restricted to southeast Africa which then led to the inference
of two independent range expansions by *B. pumilum* and
B. damaranum to southwest Africa (Supporting information).
Similarly, the trait-dependent models estimated a more
25 widespread ancestor for part of *Trioceros* than the trait-
independent model (Supporting information).

Despite all trait-dependent models being better supported
than trait-independent models, there were also differences in
estimations of ancestral ranges within trait-dependent models.
30 Shortly after the split of Brookesiinae and Chamaeleoninae,
the ancestor of the Chamaeleoninae developed a dispersal-
prone form and expanded its range to the Seychelles and
Madagascar, but the order of events is unclear (coastal
distribution and life history models inferred that Madagascar
35 was colonized first; body size and dispersal syndrome models
inferred that the Seychelles were colonized first; Supporting
information).

The biogeographic history of the genus *Chamaeleo* was
40 well supported by all models, except for the timing of the
colonization of Socotra and North Africa and Arabia. The
coastal distribution and dispersal syndrome models agreed on
an ancestor occupying central Africa, north Africa and Arabia,
and Socotra ca 20 mya. In other models this same ancestor
Q12 was restricted to central Africa and colonized Socotra about
18 mya (Supporting information).

Several range expansions and retractions took place in
Bradypodion but the order and timing of events is uncertain
50 (Supporting information). The MRCA of *Bradypodion* either
occupied central Africa and southeast Africa (body size, life
history and trait-independent models) or central Africa,
southeast and southwest Africa (coastal distribution and
dispersal syndrome models). All trait-dependent models then
55 agreed on the MRCA of *B. pumilum* and *B. damaranum*
occupying southeast and southwest Africa. The MRCA
of *Bradypodion* excluding *B. pumilum* and *B. damaranum*
(Supporting information) was estimated to have occupied
the same model-specific range as the MRCA of the whole
60 genus; only the coastal distribution model inferred a range

61 retraction. Furthermore, in the body size and life history
models the ancestor of *B. thamnobates* occupied southeast
Africa and dispersal into central Africa only took place with
B. thamnobates, which occurs today on the edge of both
65 regions. In the other models, the ancestor of *B. thamnobates*
was already present in both regions. Similarly, it is unclear
whether *B. gutturale* expanded its range from southeast to
southwest Africa or if the expansion happened before.

In *Trioceros*, range expansions to north Africa took place
70 repeatedly, but the number of range expansion events differed
between trait-dependent models (coastal distribution,
body size: 6; life history: 4; dispersal syndrome: 5; Fig. 5;
Supporting information).

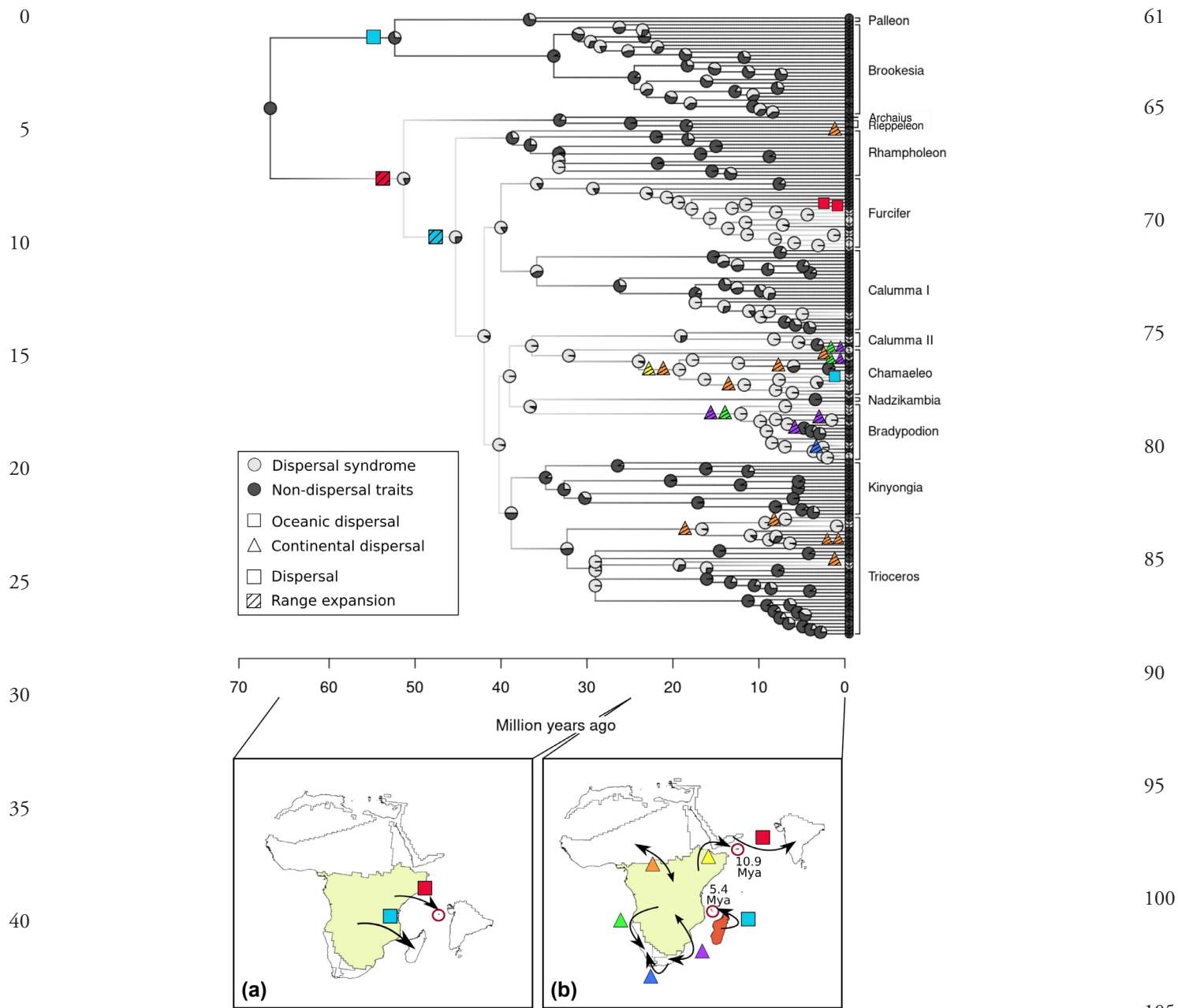
Discussion

75 We tested on an evolutionary timescale whether three traits
(coastal distribution, body size and life history) and their
combination in chameleons were related to biogeographic
dispersal success. Lineages of coastal chameleons and large
chameleons were more likely to disperse than non-coastal and
80 small lineages in the past. Instead of a fast life history strategy,
an extreme life history strategy, i.e. either particularly early
sexual maturity and short gestation time (fast) or late maturity
and a long gestation time (slow) relative to body size, was
linked to dispersal success. Our analyses revealed uncertainties
90 in ancestral range estimations: there were differences in
timing of dispersal events between trait-independent and
trait-dependent models, as well as within trait-dependent
models depending on which trait was included. However,
95 trait-dependent models were better supported by AICc
comparison than trait-independent models in all cases,
demonstrating that including traits in analyses of historical
biogeography is essential for more accurate estimations of
species' pasts.

Trait-dependent biogeographic models

Coastal distribution and body size

100 Coastal distributions are positively related to biogeographic
movement in chameleons, as has been shown for
105 *Cryptoblepharus* lizards and crocodiles (Blom et al. 2019,
Nicolai and Matzke 2019). While it seems logical that
coastal distributions should promote trans-oceanic dispersal,
most dispersal events that we identified were continental.
110 Possibly chameleons dispersed along the coast, either by their
own movement on land, or on vegetation adrift on the sea.
Alternatively, coastal lineages may have dispersed through
the interior of the continent. Coastal lineages tend to have
115 larger ranges and there may be other factors that facilitate
their overland and overwater dispersal, e.g. an underlying
trait correlated with coastal distribution, possibly related to
micro-habitat (e.g. arboreal species having a higher chance
of being transported on vegetation compared to terrestrial
120 species) or other morphological traits (da Silva and Tolley
2013, 2017).



45 Figure 5. Biogeographical movements and evolution of the dispersal syndrome of chameleons mapped onto their phylogeny (using trait-
 50 dependent biogeographical model). The pie charts represent the probabilities of nodes being in a certain trait state: white indicates species
 55 holding all three hypothesized biogeographic dispersal traits (coastal distribution, large body and extreme life history strategy), and black
 60 indicates a form with two, one or no dispersal traits. Estimated dispersal (i.e. lineage completely left the previously occupied region; plain
 65 symbols) and range expansion events (i.e. the new regions were added to the lineage's range; striped symbols) are indicated on the tree by
 70 different symbols next to the pie charts. Different symbols correspond to oceanic (square) and continental (triangle) dispersal events and
 75 the colours indicate the direction of the dispersal events. The maps below the tree show where these dispersal and range expansion events
 80 took place, and where chameleons presumably occurred at the beginning of the period (coloured regions). Note: although we included five
 85 time slices in our analysis, only two maps are presented here for simplification. The time of emergence of the Comoros Islands and Socotra's
 90 split-off from Africa are indicated in map (b).

Q13

60 Furthermore, body size (and associated life history trait covariation) also strongly influenced natural biogeographic dispersal processes, as in crocodylians (Nicolai and Matzke 2019). Large size possibly favours dispersal success because the lower metabolic rate relative to body size of large species

is related to lower relative energy requirements (Andrews and Pough 1985) which may improve resistance to stress, such as long periods of food and water shortage, and increase survival probability during the dispersal process. Moreover, body size in reptiles is highly correlated to clutch size (Meiri et al. 2020)

0 and species with big clutches may have an advantage at the
establishment stage. To distinguish between the correlated
effects of body size and clutch size, further research should
explore the role of body size in biogeographic dispersal
5 in taxonomic groups where body size does not correlate
positively with clutch size (e.g. reptile clades with relatively
invariant clutch sizes, such as geckos, or in mammals).

Life history strategy

10 Model selection did not confirm that chameleons with a fast
life history were better dispersers than slow chameleons in the
past. Instead, lineages with an extreme life history strategy
had a higher dispersal probability than lineages with an
intermediate life history strategy.

15 Our results for historical dispersal may indeed reconcile
two seemingly conflicting theories on how life history strategy
influences range expansion and dispersal. On one hand, species
with a fast life history strategy may be successful establishers
because they have the capacity for fast population growth
20 and can quickly overcome the period in which stochastic
extinction is particularly probable (Caswell et al. 2003,
Reynolds 2003, Blackburn et al. 2015). Also, fast population
growth facilitates local adaptation in niche requirements if
newly colonized areas are ecologically different from areas of
25 origin (Lavergne et al. 2010). In present-day invasions, for
instance, a fast life history strategy was found to be more
successful than a slow one in non-avian reptiles (Fujisaki et al.
2010, van Wilgen and Richardson 2012, Allen et al. 2017).
30 On the other hand, species with a slow life history strategy can
wait for favourable conditions to reproduce (Cáceres 1997)
and they are less vulnerable to environmental stochasticity
since they exhibit less demographic variability (Sæther and
Bakke 2000, Jeppsson and Forslund 2012). This is apparent
35 in bird invasions today where characteristics of a slow life
history strategy, such as long lifespan and big brain size, are
linked to success (Sol et al. 2012). Our results confirm that
one strategy is not necessarily better than the other and that
40 there might be more than one road to dispersal success.

Another reason for an extreme life history strategy being
related to dispersal success in our study, rather than a fast one,
may be that we did not exclusively study oceanic dispersal.
Sol et al. (2012) proposed that a founder population needs
45 to be very small for a strategy of fast population growth to
be advantageous for colonization success. A small founder
population is most likely the origin of island populations,
but it may not always be the case for continental dispersal
(e.g. climatic barriers can be temporarily alleviated over
50 evolutionary time scales). Indeed, all recent purely oceanic
dispersals in chameleons (*Furcifer polleni* and *F. cephalolepis*
to the Comoros Islands and *Chamaeleo zeylanicus* to India)
were associated with an extremely fast life history strategy
55 (Fig. 3b). However, since there were few clear oceanic dispersal
events in the history of chameleons, it is impossible to draw
strong conclusions from this fact. More research is necessary
to distinguish between the effect of life history strategy in
continental versus oceanic dispersal; maybe a different
60 strategy is advantageous for different modes of dispersal.

Dispersal syndrome

61 While we suggest the three traits tested are linked to specific
stages of the dispersal process, it is possible that they are also
linked to other stages of the dispersal process, either directly or
65 indirectly through correlations with other traits (Uyeda et al.
2018). In addition, traits may have multiplicative effects
on dispersal probability. This underlines the importance of
also testing dispersal syndromes in relation to biogeographic
dispersal success (Van Bocxlaer et al. 2010, Nicolai and Matzke
70 2019). We found the combination of coastal distribution,
large body size and an extreme history strategy had ca 98%
higher dispersal rate than lineages with a non-dispersal
syndrome. Moreover, more than one-third of all identified
dispersal and range expansion events took place in the genus
75 *Chamaeleo*, a relatively small genus (14/181 species) in which
most extant species and their ancestors were identified to
hold or to have held all three hypothesized dispersal traits.
Since coastal distributions were strongly related to dispersal
success (the dispersal multiplier for non-coastal species was 0
80 which is the maximum detectable effect), we were not able
to formally detect an additive or multiplicative effect of all
hypothesized dispersal traits.

The number of species that held the dispersal syndrome
85 was significantly higher than expected by chance, which may
indicate that lineages with a dispersal syndrome have higher
speciation rates. In other clades (birds: *Zosterops*, Moyle et al.
2009; amphibians: Bufonidae, Van Bocxlaer et al. 2010),
patterns of high dispersal ability combined with high
90 speciation rates were found as well. Rare dispersal to distant
locations may open opportunities for divergence by creating
isolated populations (Gillespie et al. 2012). However, the
fact that more species than expected held the dispersal
syndrome may be a result of coevolving traits that produce
95 convergent trait syndromes. Several traits can, for example,
be jointly selected for by a given environment (Ronce and
Clobert 2012, Stevens et al. 2014). More detailed studies
are necessary to elucidate the link between dispersal and
100 speciation in chameleons, and to determine whether the
dispersal syndrome may be a product of coevolution.

New insights into the biogeographic history of chameleons

105 Trait-dependent models accrued 100% of the AICc weight for
all four traits that we tested. This underlines the importance
of including species' ecology in models of historical
biogeography and emphasizes that different biogeographic
110 processes may be relevant to different lineages, which means
that they should not be treated interchangeably (Sukumaran
and Knowles 2018).

The inclusion of traits allows us to pinpoint which parts
115 of a clade's biogeographic history are subject to uncertainty.
While in some nodes there were uncertainties throughout
all models, two nodes were estimated identically in all trait-
dependent models but differently in the trait-independent
model (MRCA of *Bradypodion pumilum* and *B. damaranum*,
120 and the ancestor of part of *Trioceros*; Supporting information).

0 In both cases, the trait-independent model inferred a more restricted ancestral range, which led to more estimated range expansion events later on. In *Bradypodion*, there is an indication that the MRCA of *B. pumilum* and *B. damaranum* may have occupied a more widespread range including southwest and eastern cape floristic regions (Tolley et al. 2006), supporting results from trait-dependent models in our study. Q14
Q15
In *Trioceros*, all trait-dependent models inferred an ancestor occupying parts of central Africa and the region north Africa and Arabia already ca 15 mya, whereas the trait-independent model inferred two separate dispersal events later on. For clades with an uncertain biogeographic history, an analysis at a smaller spatial scale is preferable to allow a tailored definition of biogeographic regions and more detailed estimations (see Tolley et al. 2006 for *Bradypodion* and Ceccarelli et al. 2014 for *Trioceros*).

20 Conclusions

Our study emphasizes the importance of including species' ecological and biological characteristics in historical biogeography. Coastal distribution, body size and life history strategy are likely to have indeed played a decisive role in shaping the biogeographic history of chameleons. We found evidence that lineages with extreme life histories were more successful dispersers than lineages with an intermediate life history. Our results complement findings from invasion ecology but indicate that dispersal on an evolutionary timescale and in the Anthropocene may not be directly comparable. We show how life history strategy has influenced the biogeographic history of chameleons, which invites new key questions: Which effect has life history strategy had in the biogeographic history of other clades? How has it influenced and will it influence range shifts, invasions and global biodiversity patterns?

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55 Author contributions

Sarah-Sophie Weil: Conceptualization (supporting); Data curation (equal); Formal analysis (lead); Writing – original draft (lead); Writing – review and editing (equal). **Laure Gallien:** Conceptualization (equal); Funding acquisition (equal); Supervision (equal); Writing – review and editing

(equal). **Sébastien Lavergne:** Supervision (equal); Writing – review and editing (equal). **Luca Börger:** Supervision (equal); Writing – review and editing (equal). **Gabriel Hassler:** Formal analysis (supporting); Methodology (equal); Writing – original draft (supporting); Writing – review and editing (equal). **Michaël P. J. Nicolai:** Data curation (equal); Writing – review and editing (equal). **William L. Allen:** Conceptualization (equal); Data curation (equal); Funding acquisition (equal); Supervision (equal); Writing – review and editing (equal).

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Data availability statement

Data are available from the Dryad Digital Repository: <<https://doi.org/10.5061/dryad.XXXX>> (Weil et al. 2022). 80
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Supporting information

The Supporting information associated with this article is available with the online version. 85

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40		100
45		105
50		110
55		115
60		121

Author Queries

JOB NUMBER: 06323

JOURNAL: OIK_ECOG

- Q1 Please check that all author names are correctly spelled and confirm that all author affiliations are correctly listed. Note that affiliations should reflect those at the time during which the work was undertaken. Please check that the ORCID addresses are accurate and listed for all authors who wish to add it.
- Q2 Confirm that the email address for the corresponding author is accurate.
- Q3 AQ: The text that follows is within inverted commas. Does this indicate it is a quotation? Please note it is not usual to include quoted material in an abstract (and quotations must always be accompanied by a citation/reference). Can you rephrase in your own words?
- Q4 Ensure that all the figures, tables and captions are correct, and all figures are of the highest quality/resolution. Please note that figure quality in the online proofing tool appears low. The PDF proofs should be used as a reference of how the figures/images will look like when published. Note that figures and tables must be cited sequentially.
- Q5 AQ: Please adjust figures to avoid combinations of red/orange and green in the same figure. These can be difficult for visually impaired readers to distinguish. Note: This comment applies throughout the paper.
- Q6 AQ: 'north Africa' (and other regional descriptors). Many such terms generally take upper-case (e.g. 'North Africa'). Please check all such descriptors carefully and ensure they are used consistently throughout the text.
- Q7 AQ: Please spell out UPGMA. Is this your own map? If it comes from another publication/source, please provide citation/reference and any acknowledgement that is requested.
- Q8 AQ: please check this addition is correct.
- Q9 AQ: by 'snout-vent-length', are you describing the length between the snout and the vent? If so, could the term be expressed as 'snout-vent length' (i.e. using an en rule rather than a hyphen)? Note the query applies throughout the text.
- Q10 AQ: Should 'panel 2a' read 'panel 3a'?
- Q11 AQ: should 'panel 2b' read 'panel 3b'?
- Q12 AQ: You refer to both 'north Africa' and 'North Africa'. If there a deliberate distinction between the terms, please add a note to explain this.
- Q13 AQ: for consistency, please also refer explicitly to map (a) in your caption.
- Q14 AQ: should 'southwest and eastern cape' be replaced with 'Southwest and Eastern Cape'? Please check expression of all regional descriptors carefully.
- Q15 AQ: Could 'inferred an ancestor occupying parts of central Africa and the region north Africa and Arabia already ca 15 mya' be replaced with 'inferred an ancestor already occupying parts of Central Africa and the region comprising North Africa and Arabia ca 15 mya'? Please check carefully (especially the expression of regional descriptors).
- Q16 Please confirm that the CRediT taxonomy of contributor roles (author contributions) is correct and that all author names are spelled correctly.
- Q17, Q23 Please confirm that the Data availability statement is accurate and, if necessary, update the link to the data repository. Note that the data supporting your paper must be publicly accessible. If your data was private during the peer review process, please ensure that they are now publicly available and that you provide a permanent link to the dataset (not the temporary link available during the peer review process).
- Q18 Please update the reference 'GEBSCO Compilation Group 2021'.
- Q19 AQ: Graham and Fine 2008 provided in the list, but not cited in the text.
- Q20 Please update the reference 'Hassler et al. 2021'.
- Q21 AQ: IUCN 2019. Should '2019-2' read '2019-20'?
- Q22 Please provide the page range for the reference 'Ronce and Clobert 2012'.