Global patterns and a latitudinal gradient of flower disparity: perspectives from the angiosperm order Ericales.

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SUPPLEMENTARY INFORMATION

1. Methods S1	2
1.1. Taxon sampling and scoring of the morphological dataset	2
1.2. Growth form, habitat, climate, and geographic region	2
1.3. Creation of the association network.	3
1.4. Latitudinal distribution of species richness and disparity	4
1.5. Potential methodological shortcomings	4
2. Note S1 - Supplemental results	6
2.1. Morphological description and comparison of factor categories	6
Character states coding:	7
Factor growth form	9
Factor habitat	15
Factor climate	19
Factor region	25
2.2. Visualisation of factor categories in the morphospace	32
2.3. Variation of disparity when isolating factor categories	34
Growth form	35
Habitat	36
Climate	37
Region	38
2.4. Permutation test (latitudinal disparity gradients of disparity vs. species richness)	39
2.5. Latitudinal distribution of all Ericales from GBIF.	40
3. Note S2 - Distribution maps of the study species	41
4. References	99

1. Methods S1

All analyses were performed using the software R v.3.5.1 (R Core Team, 2018). Functions are referred to in the following format: *function name*{*package name*}.

1.1. Taxon sampling and scoring of the morphological dataset

To analyse morphological diversity (disparity), we used the morphological dataset and taxon sampling from Chartier *et al.* (2017). This dataset describes 380 species belonging to 274 genera (79.5 % of all Ericales genera) covering all major clades of the order identified in taxonomic/phylogenetic studies (Rose *et al.*, 2018; Schönenberger *et al.*, 2005). It is composed of 36 morphological characters, describing the perianth (12 characters), the androecium (13 characters), the gynoecium (six characters), and general features (e.g. flower sex and size, five characters) of the anthetic flower. We recorded the dataset in the database PROTEUS (Sauquet, 2019). It contains a total of 12,512 data entries, with 13.4 % missing data. We took a strict exemplar approach for scoring traits, which means that we only scored a trait state for a given species if we could confirm that it was observed in this species (that is, we did not use any general family descriptions or make any assumptions that all species of a genus share the same character states). In addition, each data record is directly linked with the reference from which we have retrieved the information. The total morphological data set, including references and a detailed description of all characters and character states, is available in the online supplemental information of Chartier *et al.* (2017).

1.2. Growth form, habitat, climate, and geographic region

All species from the morphological dataset were coded also for the four following factors using the exact same scoring approach as outlined above: *growth form, habitat, climate type*, and *region*. In this manuscript, we use abridged expression such as « floral disparity of trees », or « disparity in cold areas ». Each of these expressions should be understood as for instance « floral disparity in species displaying an arborescent growth form », or « floral disparity in species distributed in cold areas ».

For each factor, the assignment of each species to one or more categories was made retrieving information from the literature cited in Chartier *et al.* (2017) for each species, and by crossing this information with the maps and descriptions from (Cox, 2001; Peel *et al.*, 2007; Loarie *et al.*, 2009). This new dataset is available as Supplementary Information and stored in the online database Proteus (Sauquet, 2019), with at least one bibliographic reference linked to each entry. It contains 1,800 new data entries (3.6 % missing data).

We divided *growth forms* into the five categories occurring in Ericales Kubitzki (2004): (1) *trees*, (2) *shrubs*, (3) *lianas and climbers*, (4) *herbs* (*including aquatic herbs*), and (5) *root parasites*.

We defined *habitat* categories by taking the biome descriptions from Loarie *et al.* (2009), and simplifying them into the three habitat states: (1) *forests*, (2) *open habitats*, and (3) *wet habitats* (the latter including mangroves and flooded grassland/savannas).

For *climate type* (Fig. 4 a), we used the Köppen-Geiger climate classification based on temperature and precipitation applying the five main categories described in Peel *et al.* (2007): (1) *tropical* (temperature of the coldest month \geq 18 °C, either rainforest, monsoon, or savannah), (2) *arid* (desert and hot or cold steppes), (3) *temperate* (temperature of the hottest month > 10 °C, temperature of the coldest month between 0 °C and 18 °C, either dry summer, dry winter, or without dry season), (4) *cold* (temperature of the hottest month > 10 °C, with dry summer or dry winter), and (5) *polar* (temperature of the hottest month < 10 °C, either tundra or frost).

Finally, we divided *regions* into (1) *North America*, (2) *Eurasia*, (3) *South America*, (4) *Africa*, (5) *Indo-Pacific*, and (6) *Australia* (Fig. 4 b). We followed the revised biogeographical delimitations of Floral Kingdoms as suggested by Cox (2001), dividing the Holarctic Kingdom into North America and Eurasia to account for continent delimitations. Each species was assigned to its native region only.

As pointed out above, our taxon sampling aimed to cover all major ericalean clades and most genera with the goal to optimize the estimation of disparity for the order as a whole (Chartier *et al.*, 2017). For this study, we thus assume that the distribution of the sampled species for each factor category is also representative for the order.

1.3. Creation of the association network.

Multiple correlations/associations are usually visualized on a correlation table (Fig. S1a). Instead, we propose to use an ordination, on which associated categories are grouped together, and significantly associated categories are linked by lines whose colour represent the strength of the association (here red for a positive association, blue for a negative association, Fig. S1b). This type of representation allows visualizing multiple associations very easily.

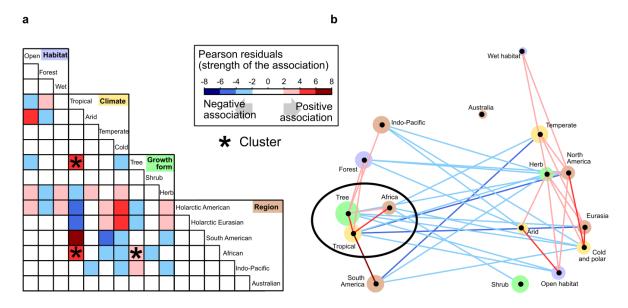


Figure S1. a correlation table displaying positive (in red) and negative (in blue) significant associations among categories, obtained after a series of chi-square tests and based on the value of Pearson residuals. As an example, a group of three categories that are significantly positively associated is highlighted by black stars. **b** association network representing the same associations from the same dataset. Significantly associated categories are linked by a line, whose colour indicates the strength of the association. The cluster highlighted in **a** by stars is shown in **b** with a black circle.

For significant chi-squared tests, the strength of the association can be estimated from the Pearson residuals (PR). PR > 2 indicates more observations than expected and PR < -2 indicates fewer observations than expected (Hawkins, 2014). To easily visualize clusters of associated factor categories, we transformed the PR into a distance index, d_{PR} , varying between 0 and 1, so that, for a pair of factors:

$$d_{PR} = (PR + m)/2m$$

with m the maximum absolute Pearson residual value from the analyses (in our case, PR ranged from -5.98 to 7.28 so m was set to 8). This way, d_{PR} is minimum when two categories are associated more often than expected (i.e. when their PR is maximum), d is maximum when two categories are associated less often than expected (i.e. when their PR is minimum), and close to 0.5 when two categories are not associated. We created a distance matrix containing d_{PR} for all pairs of categories, with a value of d_{PR} set to 0.5 for pairs of categories belonging to the same factor. This matrix was then visualized with a non-metric multidimensional scaling (nMDS) using the function $metaMDS\{vegan\}$ (Oksanen et al., 2017). The nMDS is a method consisting in representing at best distances from a distance matrix in a number of dimensions specified by the user. The way we calculated d and using this method leads associated categories to fall close together in the representation, allowing an easy graphical identification of clusters of associated factor categories. The

strength of the association (*PR* values) is depicted by the colour of lines linking the categories that are significantly associated (interpretations of this type of graph should be made based on those lines rather than on the distances between dots on the graph).

1.4. Latitudinal distribution of species richness and disparity

We estimated the latitudinal distribution of the species from the dataset by extracting data from the Global Biodiversity Information Facility online database (GBIF, https://www.gbif.org/). For each species, location records (latitude and longitude) were extracted and filtered using the function $occ_search\{rgbif\}$ (Chamberlain, 2017). Records where retained if they had "no geospatial issue", and if they belonged to the categories "HUMAN_OBSERVATION", "LITERATURE", "PRESERVED_SPECIMEN", or "OBSERVATION". Distribution maps (Supplementary Information) were then plotted using the package maptools (Bivand & Lewin-Koh, 2017) and all of these maps were manually checked for atypical and non-native records by using data from the literature and online trustworthy websites (such as the IUCN website, http://www.iucnredlist.org). This allowed us to estimate the presence/absence of 347 (91 %) of the study species in each ten-degree latitude interval across the globe.

Disparity (\overline{D}) was then calculated for the species occurring in each given latitude interval. Finally, we tested for the correlations between latitude and species richness, latitude and disparity, and species richness and disparity (for each latitudinal interval) with Pearson correlation tests using the functions $cor.test\{stats\}$ and $lm\{stats\}$.

1.5. Potential methodological shortcomings

- [1] GBIF data only provide an underestimation of species richness. We corrected each distribution by hand and deleted the observations that were outside the natural distribution range of the study species. The distribution of some species might be underestimated, as we did not add records that were not in GBIF.
- [2] To verify if the GBIF sample of Ericales we worked with is representative of the whole order, we extracted the latitudinal distribution of all Ericales (7,152 species) from GBIF and compared it to the distribution of species from our dataset (350 species). The two distributions were very similar, with a discrepancy in the northern hemisphere, where our sample contained proportionally more species than there were in the total distribution. This is could be due to the fact that our sample contains numerous cultivated species that, in the non-corrected dataset, are recorded in Europe and North America (e.g. *Actinidia* or *Camelia*). Correlation between these two distributions (number of species per latitudinal interval): r²=0.91, p<10⁻⁶; linear regression: slope=0.77 (probably because of the bias in the northern hemisphere), intercept=1.27.
- [3] The gradient of disparity could be due to the increase in sample size near the tropical latitudes (although disparity is an index that is quite robust to sample size differences). The rarefaction analysis below shows that our result holds even when correcting for sample size:

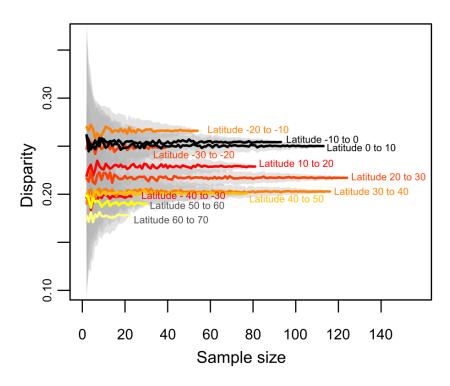


Figure S2. Disparity, averaged for each latitudinal slice over 200 random samples of the dataset. Sample sizes (x axis) range from 2 species to the maximum number of species possibly sampled for each latitudinal slice. In grey: standard deviation.

2. Note S1 - Supplemental results

2.1. Morphological description and comparison of factor categories

We used non parametric multivariate analyses of variance (npMANOVAS) to compare the morphological traits of each factor category, with the function *adonis*{*vegan*} in R and the same test used as posthoc, with a Bonferroni correction. Each factor category was then described using barplots as follow: *green* barplots give the distribution (frequency) of all morphological character states for a given factor category. *Gray* barplots give the frequencies of the same morphological states for the *rest* of the dataset. In case of polymorphism, species are included in each category they belong to (here in the green and in the gray barplots).

Such a representation allows visualising what makes a factor category different from the other categories (e.g. what differentiates *trees* from the other *growth forms*).

The number of species sampled per factor category is given in the first cell of each plate.

Legend for the following figures: barplots displaying the frequency of each character state for each factor state. In green: number of species of a given category (for example "trees") displaying a given character state (for example "bisexual flowers only"). In gray: number of species of all the other categories from the same factor (for example "shrubs" and "lianas" and "herbs") displaying the same character state.

Character states coding:

Functional sex:

a = bisexual flowers onlyb = unisexual flowers only

c = both

Structural sex:

a = bisexual flowers onlyb = unisexual flowers only

c = both

Nectaries and oil:

a = absenceb = presence

Flower length:

a = small (< 1cm)

b = medium (1 to 3 cm)

c = large (>3cm)

Flower diameter:

a = small (< 1cm)

b = medium (1 to 3 cm)

c = large (>3cm)

Perianth differentiation:

a = no/weak differentiation

b = continuous differentiation

c = marked differentiation

Sepal phyllotaxis:

a = whorled

b = spiral

Petal phyllotaxis:

 $\boldsymbol{a} = \boldsymbol{whorled}$

b = spiral

Sepal aestivation:

a = apert

b = imbricate

c = valvate

Petal aestivation:

a = apert

b = imbricate

c = valvate

Perianth symmetry:

a = polysymmetric

b = monosymmetric

c = disymmetric

d = asymmetric

Sepal union:

a = free/basally united

b = more than 10% union

Petal union:

a = free/basally united

b = more than 10% union

Distal filament union:

a = absent

b = present

Androecium phyllotaxis:

a = whorled

b = stamens in pairs (whorled)

c = ring primordium

d = fascicles

Number of androecium whorls:

a = one

b = two

c = more than two

Androecium symmetry:

a = polysymmetric

b = monosymmetric

Filament union:

a = free/basally united

b = more than 10% united

Anther union:

a = not united

b = united

Anther orientation:

a = introrse

b = latrorse

c = extrorse

d = apical

Anther attachment:

a = basifixed

b = dorsifixed

c = ventrifixed

Anther dehiscence:

a = longitudinal slit

b = apically poricidal

c = basally poricidal

d = common stomium of confluent

thecae

e = transverse (horizontal) slit

Filament insertion to corolla:

a = no fusion or basally fused

b = lower half inserted

c = upper half inserted

Filament fusion to corolla:

a = no fusion or basally attached

b = more than 10% fusion

Staminodes:

a = fused to form a corolla-like

structure

b = stamen-like

c = hood-like structure

d = scale-like

e = petaloid

f = triangular, wooly or hairy, applied

to the style at anthesis

g = no staminodes

h = petal-like

Ovary position:

a = inferior

b = superior

Gynoecium symmetry:

a = polysymmetric

b = monosymmetric

c = disymmetric

Style union:

a = free or basally united

b = more than 10% union

Placentation:

a = axile

b = free-central

c = parietal

Number of ovules per carpel:

a = one

b = two

c =three to ten

d = more than ten

Ovule integuments:

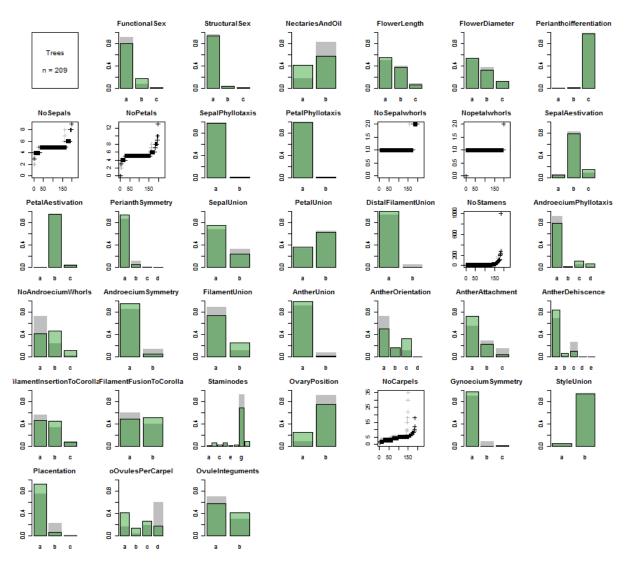
a = one (unitegmic)

b = two (bitegmic)

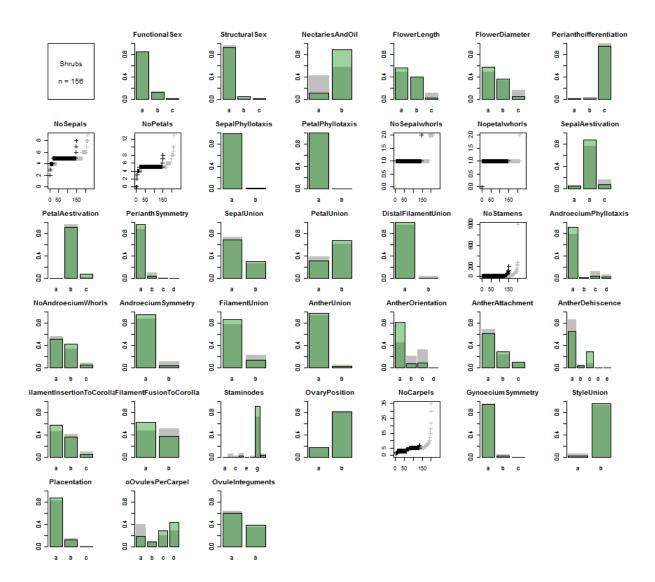
Factor growth form

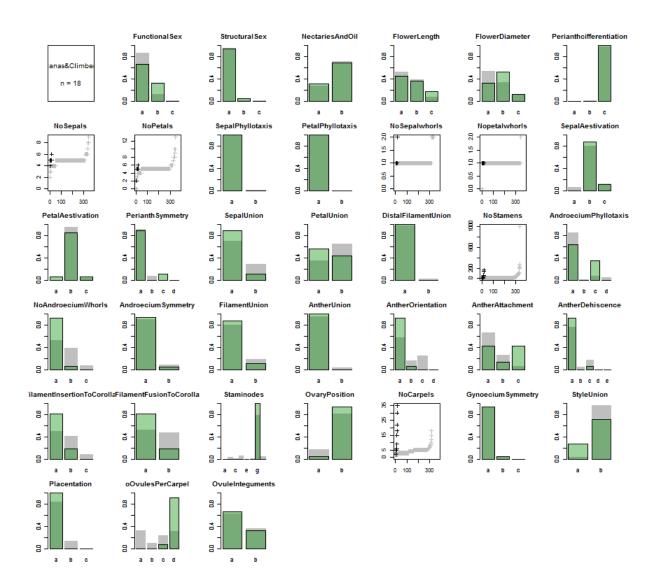
There were significant floral morphological differences among growth forms (npMANOVA: F = 7.60, $r^2 = 0.05$, $p < 10^{-03}$). According to posthoc tests, only *lianas and climbers* did not significantly differ from the other growth forms.

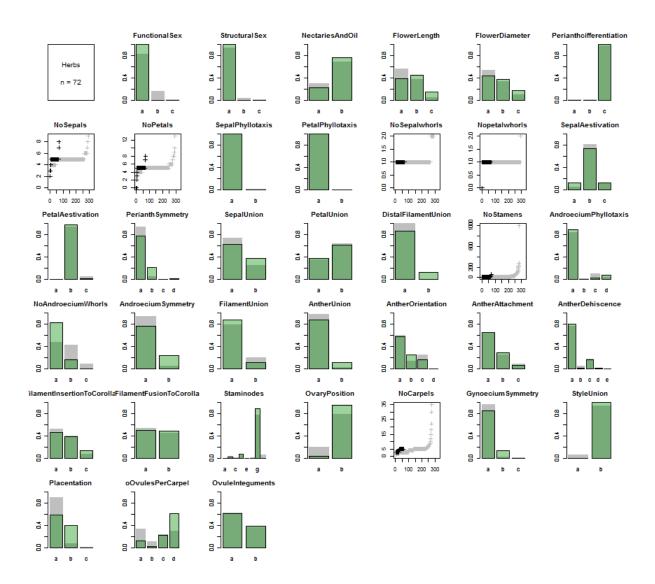
```
##
                     Df SumsOfSqs MeanSqs F.Model R2 Pr(>F)
##
                           0.5994 0.199815 7.6001 0.04812 1e-04 ***
## Residuals
                    451
                          11.8573 0.026291
                                                  0.95188
## Total
                    454
                          12.4568
                                                  1.00000
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "POSTHOC Corrected alpha: 0.008333"
upper diagonal: r2
lower diagonal: p
        Herb Lian
##
                     Shr
                           Tre
## Herb
          NA 0.031 0.023 0.018
## Lian 0.037
                NA 0.008 0.016
## Shr 0.002 0.233
                      NA 0.036
## Tre 0.002 0.009 0.001
upper diagonal: F
lower diagonal: significance level (* = significant p-value, ns = non significant
p-value).
##
       Herb Lian
                    Shr
                           Tre
## Herb <NA> 2.793 5.33 5.161
## Lian ns <NA> 1.324 3.742
## Shr
         *
                  <NA> 13.720
               ns
## Tre
               ns
                   *
```

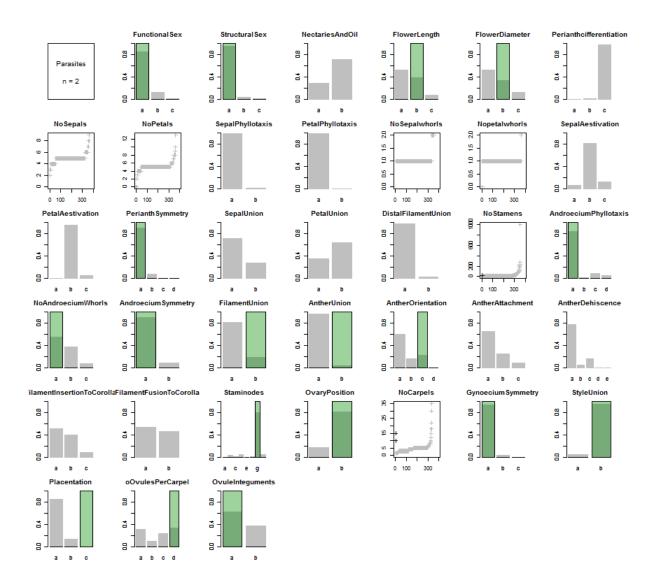


E.g.: in green: distribution of the morphological character states for trees; in gray: for the other growth forms present in the dataset.







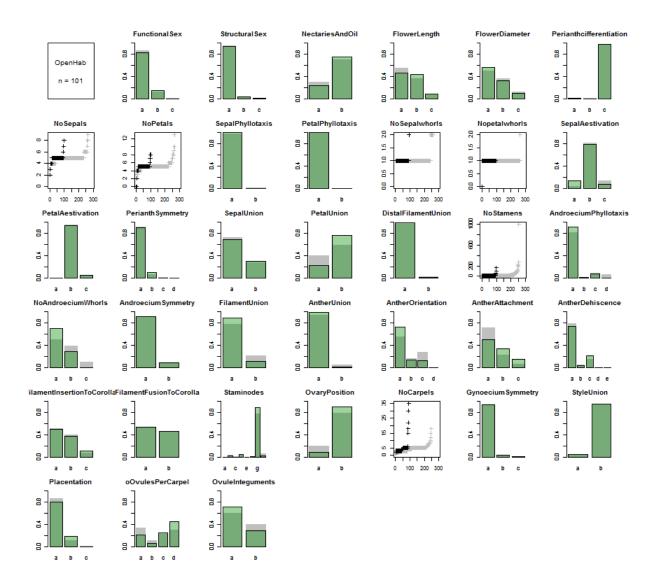


There were significant floral morphological differences among types of habitat (npMANOVA: F = 2.36, $r^2 = 0.01$, p = 0.0182). According to posthoc tests, only *forests* and *open habitats* significantly differed.

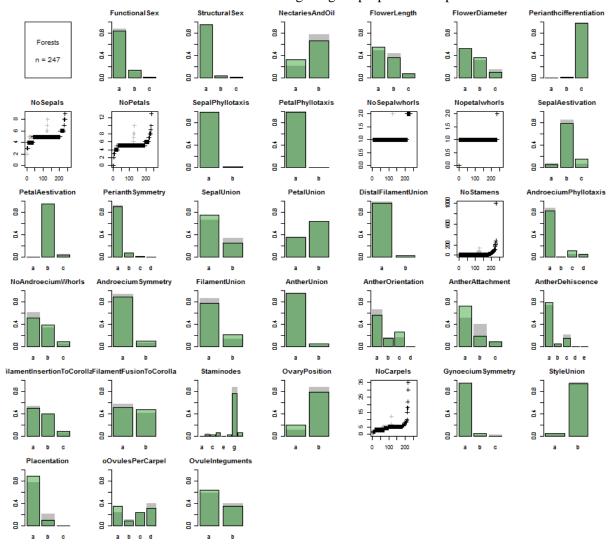
```
##
                      Df SumsOfSqs MeanSqs F.Model
                                                           R2 Pr(>F)
##
                             0.1272 0.063599 2.3568 0.01258 0.0182 *
                        2
## Residuals
                      370
                             9.9847 0.026986
                                                      0.98742
## Total
                      372
                            10.1119
                                                      1.00000
## ---
                   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Signif. codes:
## [1] "POSTHOC Corrected alpha: 0.016667"
upper diagonal: r<sup>2</sup>
lower diagonal: p
##
         For
               0pe
                     Wet
## For
          NA 0.016 0.005
## Ope 0.001
                NA 0.014
## Wet 0.225 0.123
upper diagonal: F
lower diagonal: significance level (* = significant p-value, ns = non signi
ficant p-value).
##
        For
              0pe
                    Wet
## For <NA> 5.707 1.381
## Ope
          *
             <NA> 1.825
## Wet
       ns
               ns
                     NA
```

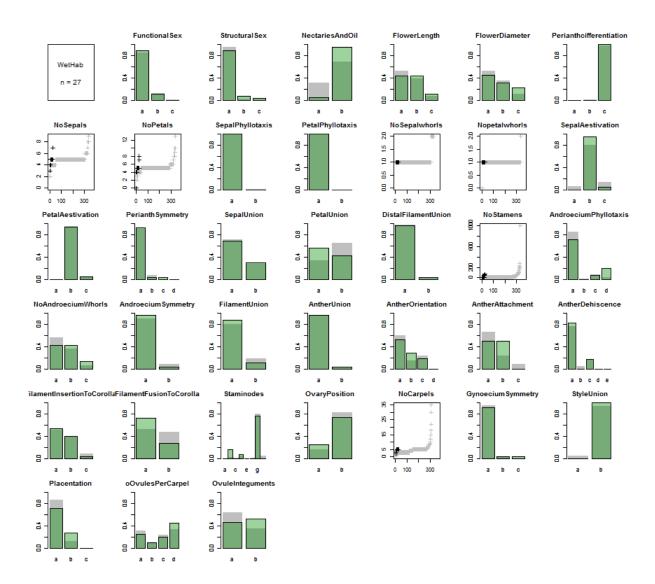
The morphological characteristics of each habitat category can be read on the graphs below.

Open habitats differ from the rest of the dataset in having a higher proportion of flowers with apert petals, of flowers with united petals, of stamens inserted in one whorl, of free filaments, of introrse anthers, of dorsifixed and ventrifixed (instead of basifixed) anthers, of superior ovaries, of numerous carpels, of more than 10 ovules per carpel and of unitegmic ovules.



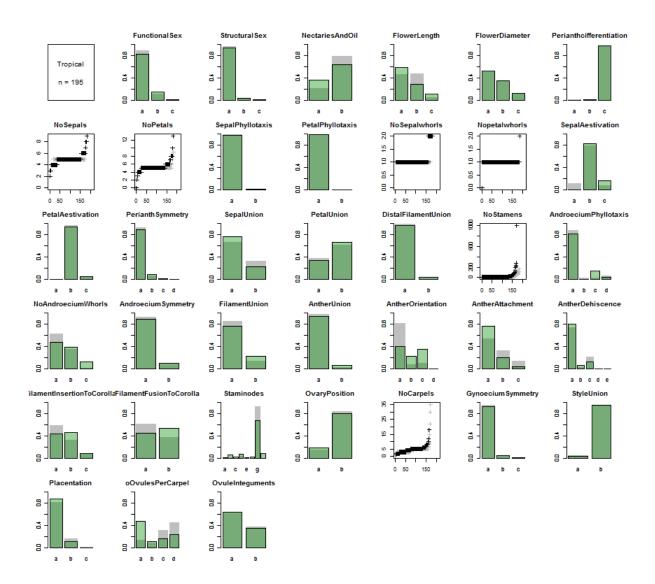
Forests differ from the rest of the dataset in having a higher proportion of species whose flowers

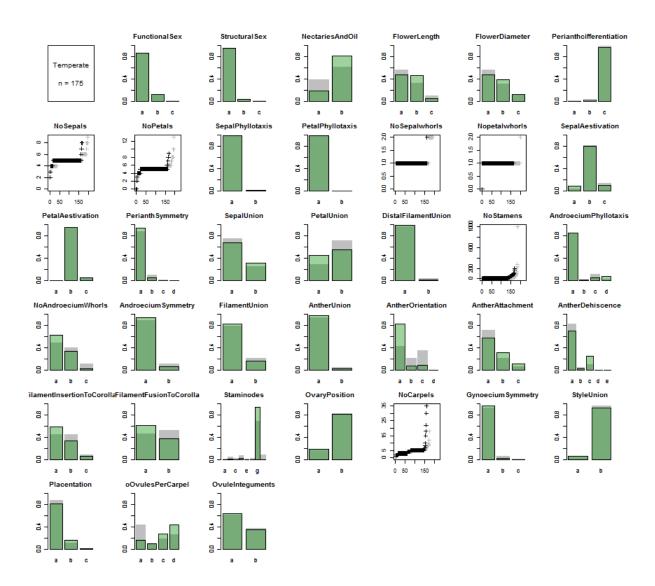


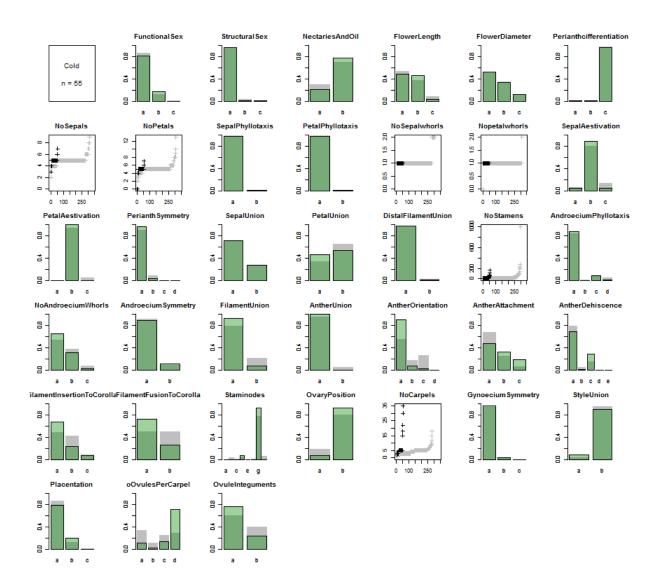


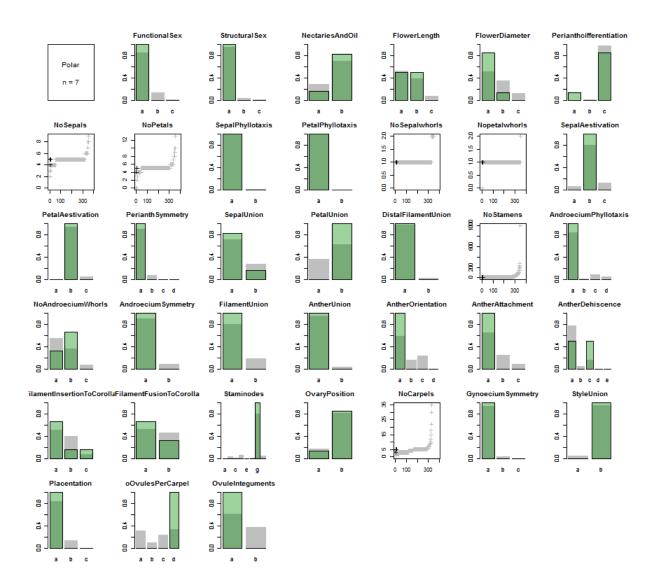
There were significant floral morphological differences among climate categories (npMANOVA: F = 3.75, $r^2 = 0.03$, $p < 10^{-03}$). According to posthoc tests, only species growing under *tropical* climate significantly differed from the other categories (all but *arid*). The morphological characteristics of each *climate* category can be read on the graphs below.

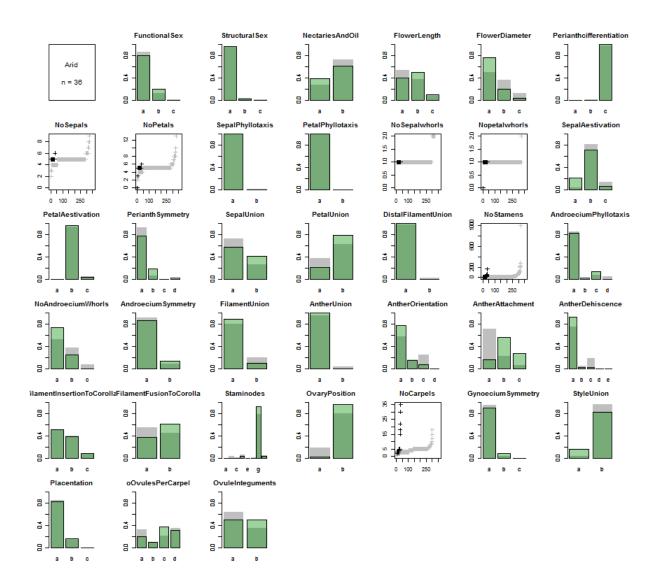
```
##
                      Df SumsOfSqs MeanSqs F.Model
                                                         R2 Pr(>F)
##
                            0.3862 0.096548 3.7527 0.03153 1e-04 ***
                       4
## Residuals
                           11.8605 0.025728
                                                    0.96847
                     461
## Total
                     465
                           12.2467
                                                    1.00000
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "POSTHOC Corrected p-value: Corrected p-value: 0.005"
upper diagonal: r2
lower diagonal: p
##
          Ari Cold
                            Pol Trop
                      Tem
## Ari
           NA 0.029 0.011 0.093 0.015
## Cold 0.041
                 NA 0.003 0.054 0.034
## Tem 0.059 0.660
                       NA 0.021 0.039
## Pol 0.007 0.015 0.012
                             NA 0.037
## Trop 0.011 0.001 0.001 0.001 NA
upper diagonal: F
lower diagonal: significance level (* = significant p-value, ns = non
significant p-value).
##
         Ari Cold
                     Tem
                           Pol
                                 Trop
## Ari
        <NA> 2.699 2.315 4.216
                                3.600
## Cold
              <NA> 0.617 3.444
                                8.861
          ns
## Tem
          ns
                    <NA> 3.743 14.697
                ns
## Pol
          ns
                ns
                      ns
                          <NA>
                                7.778
## Trop
                                   NA
          ns
```





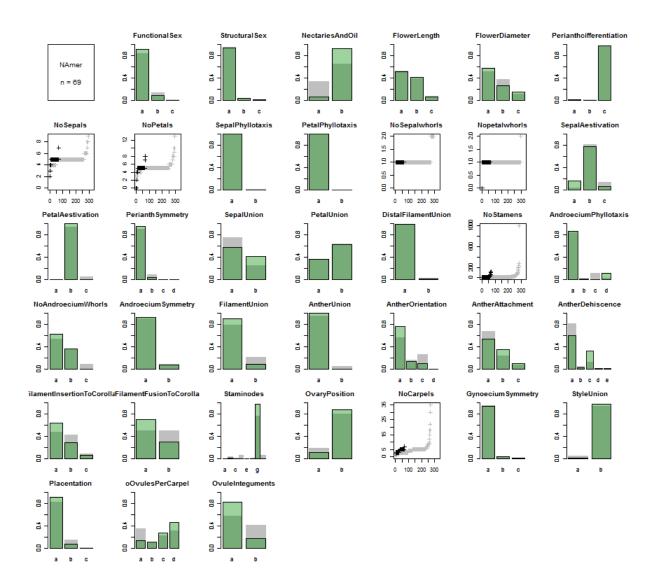


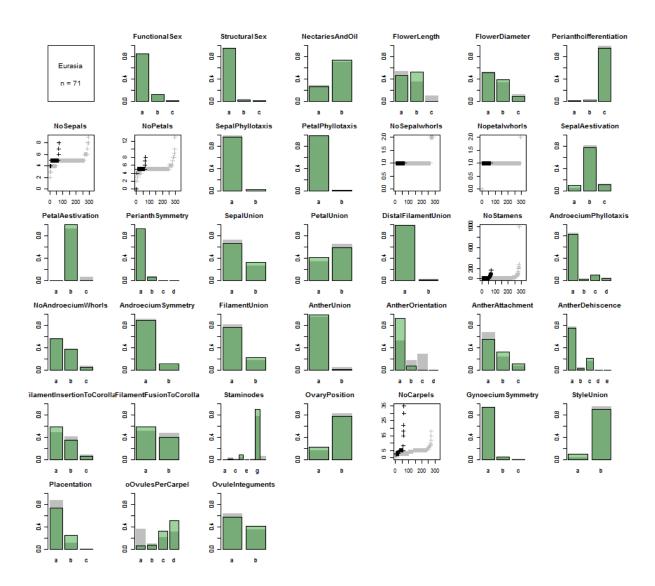


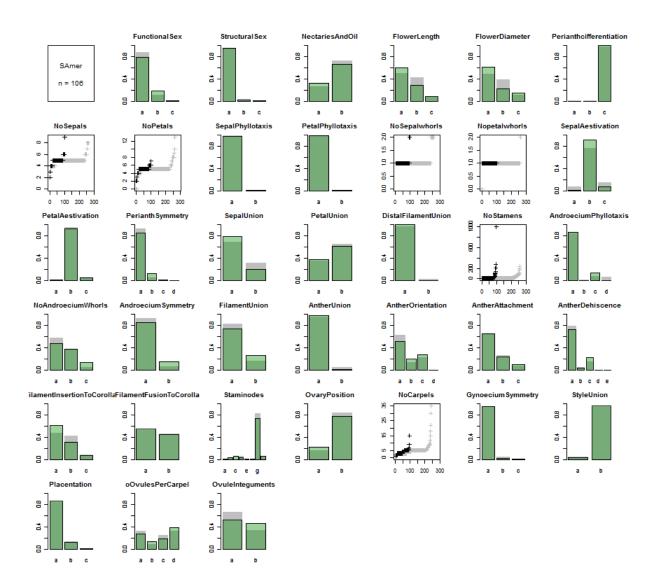


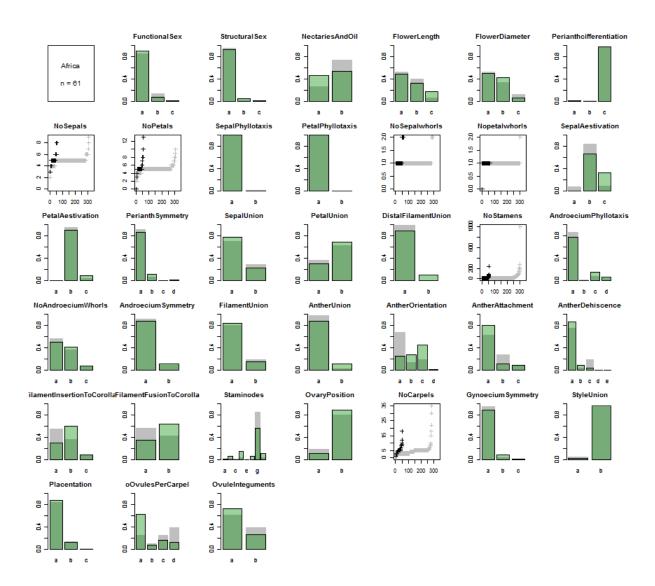
There were significant floral morphological differences among regions (npMANOVA: F = 3.3, $r^2 = 0.04$, $p < 10^{-03}$). According to posthoc tests, species from *Africa* where the ones that differed from the most other regions. *North America* and *Australia* differed from Indo-Pacific. The morphological characteristics of each *region* category can be read on the graphs below.

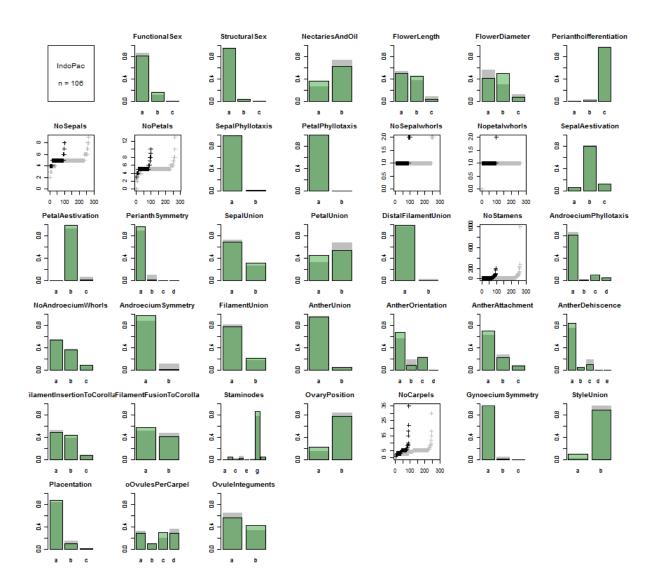
```
##
                      Df SumsOfSqs MeanSqs F.Model
                                                          R2 Pr(>F)
##
                             0.4311 0.086222
                                                 3.3 0.03806 1e-04 ***
                       5
## Residuals
                     417
                           10.8952 0.026127
                                                     0.96194
## Total
                     422
                           11.3263
                                                     1.00000
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
## [1] "POSTHOC Corrected alpha: 0.003333"
upper diagonal: r<sup>2</sup>
lower diagonal: p
##
         Afr
                           NAm
                                  SAm
               Eur
                     Ind
                                        Aus
## Afr
          NA 0.057 0.037 0.108 0.034 0.087
## Eur 0.001
                NA 0.007 0.026 0.007 0.055
## Ind 0.001 0.290
                      NA 0.033 0.006 0.038
## NAm 0.001 0.007 0.001
                            NA 0.020 0.030
## SAm 0.001 0.241 0.297 0.014
                                   NA 0.024
## Aus 0.001 0.004 0.003 0.047 0.042
upper diagonal: F
lower diagonal: significance level (* = significant p-value, ns = non
significant p-value).
        Afr
              Eur
                    Ind
                           NAm
                                  \mathsf{SAm}
                                        Aus
## Afr <NA> 7.902 6.285 15.575 5.795 6.805
## Eur
             <NA> 1.179
                         3.639
                                  1.3 4.711
## Ind
               ns
                   <NA>
                         5.852 1.15 4.561
## NAm
               ns
                          <NA> 3.514 2.469
## SAm
               ns
                     ns
                            ns
                               <NA> 2.784
## Aus
                            ns ns NA
               ns
```

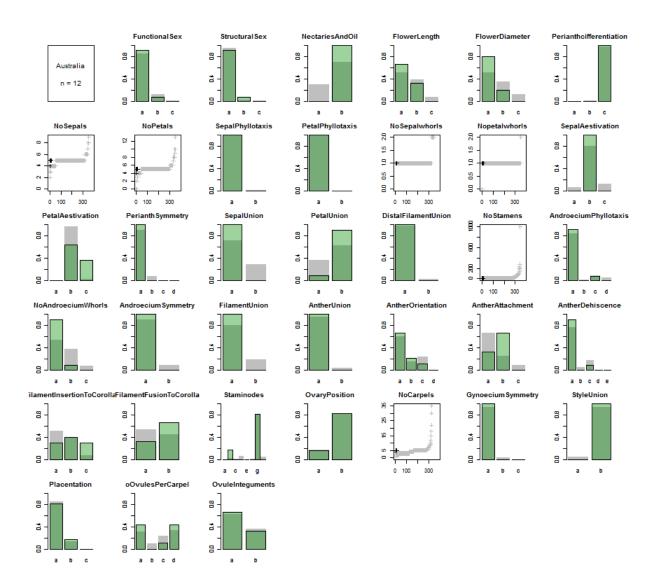






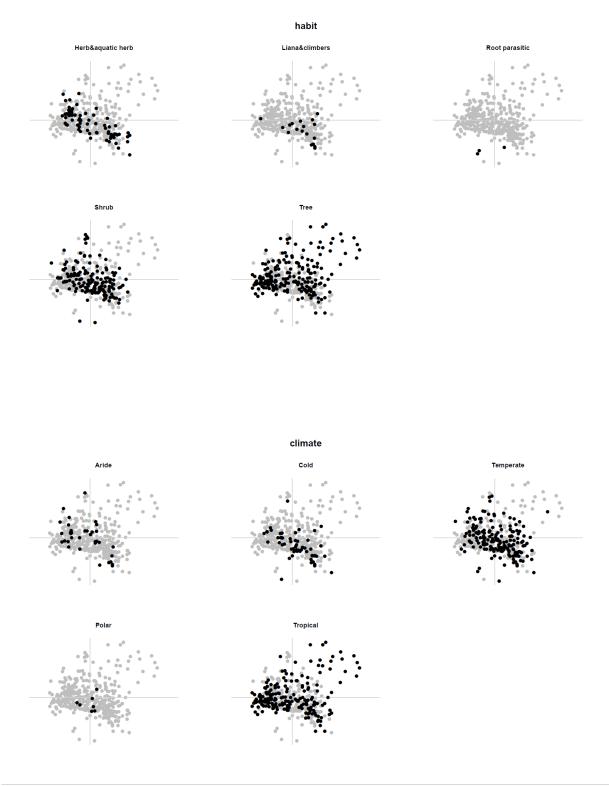


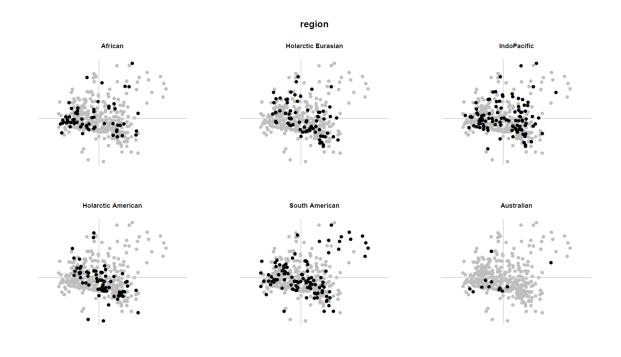


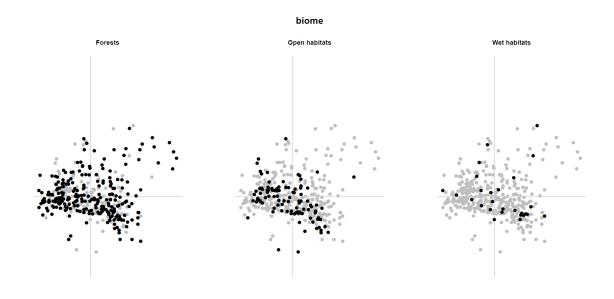


2.2. Visualisation of factor categories in the morphospace

In the following figures, the position in the floral morphospace of each factor category is highlighted by black dots. Gray dots represent the rest of the dataset. The following representation of the morphospace was obtained with a principal coordinate analysis, taking as input the original morphological dissimilarity matrix. The significance of the correlation between distances in the distance matrix and distances in the morphospace ordination presents the following statistics: Pearson's r = 0.71, p < 0.001. All details about the creation of the representation of this morphospace can be found in Chartier et al. (2017).







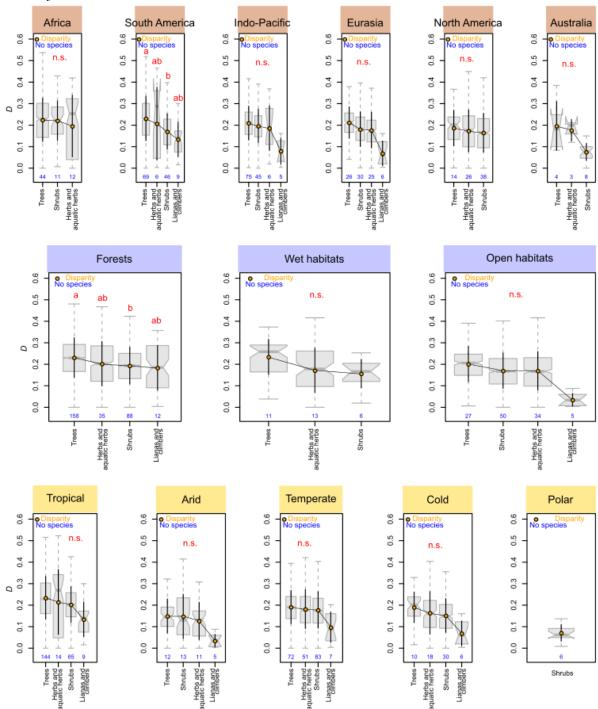
2.3. Variation of disparity when isolating factor categories.

Investigation of disparity variation among the different categories (e.g. *tree*, *shrub*, *herbs*) of one factor (e.g. *growth form*) for each category of the other factors.

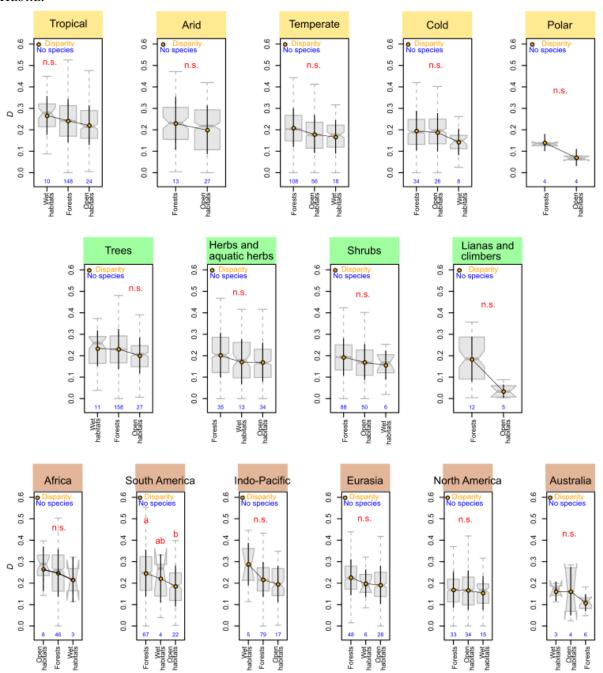
In the following graphs: D= mean character difference between two taxa, $\overline{D}=$ mean pairwise differences for a group of taxa. For each boxplot, sample size is given below each box and disparity (the average $\overline{D}\pm SD$) is represented by orange circles and orange error bars. Post hoc test results are summarized in red. When the overall Kruskal-Wallis test was significant (p \leq 0.5), letters indicate groups that are not significantly different according to posthoc tests. NS means that the overall test was not significant (p > 0.05) and therefore no posthoc test was made.

Note that sample size is given as number of species, but that disparity (\overline{D}) is calculated for pairs of species. This means that, for n species, disparity is calculated by averaging $(n^2 - n) \div 2$ values.

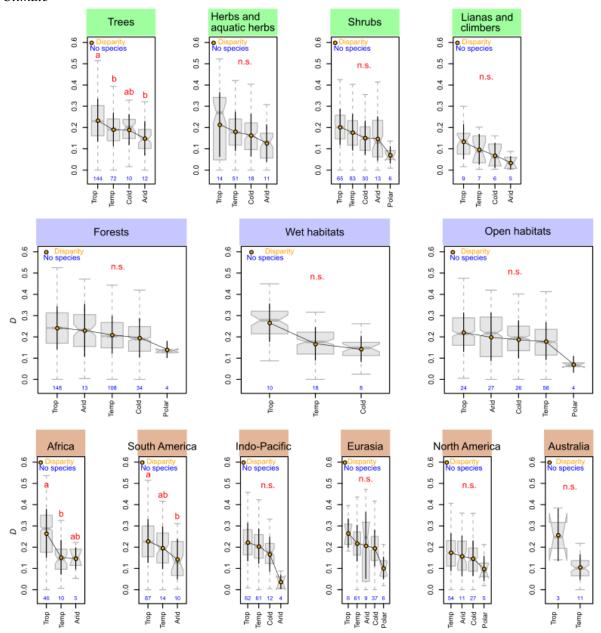
Growth form



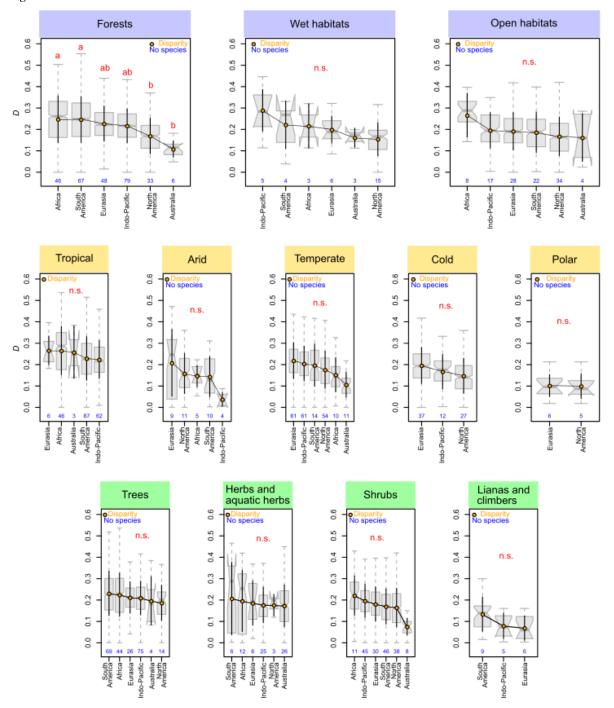
Habitat



Climate



Region



2.4. Permutation test (latitudinal disparity gradients of disparity vs. species richness)

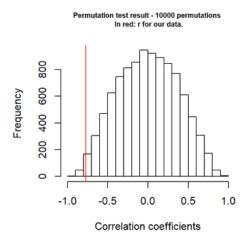
In this analysis, we show that the higher disparity found at low latitudes is not due to the fact that there are more species in the tropics, but that it is rather due to the fact that these tropical species are morphologically more diverse.

To test this, we randomized floral morphologies among species 10,000 times, and recalculated disparity for each latitudinal interval in each case (each 10° latitudinal interval containing the real number of species, but the morphologies of these species being randomly mixed without replacement).

If the higher disparity at low latitudes is not due to the higher number of species in these areas, we expect that once the morphologies are randomized, disparity gets homogenized across all latitudes and there is no more disparity gradient even if a species number gradient is still present. In this case, the distribution of r (the coefficients of correlation of a Pearson correlation test between latitude and disparity), should follow a normal distribution centered to zero (0 is the value of r in the case of no correlation).

If, on the contrary, if the higher disparity at low latitudes is due to the fact that there are more species at low latitudes, we expect a negative correlation between latitude and disparity in all cases, and the distribution of r should be asymmetrical towards -1 (-1 is the value of r in the case of a perfect negative correlation).

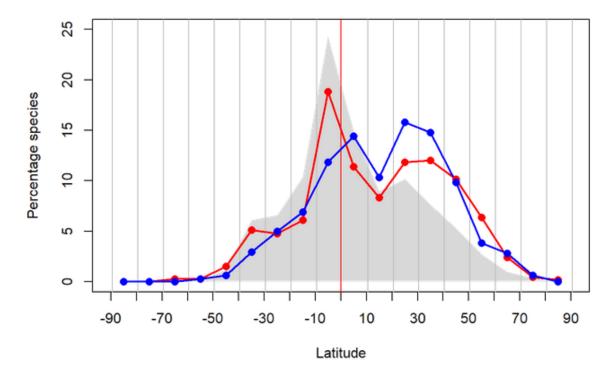
The distribution of r once the data are randomized is shown below. It is centered to 0, and in 99% cases, r is higher than the value or r (-0.77) in the unaltered dataset. This shows that, in our sampling, the higher disparity at lower altitudes is not an effect of higher species numbers in these areas.



[1] "Proportion of cases where r is inferior or equal to r in our data (p-value of this permutation test): 0.008"

2.5. Latitudinal distribution of all Ericales from GBIF.

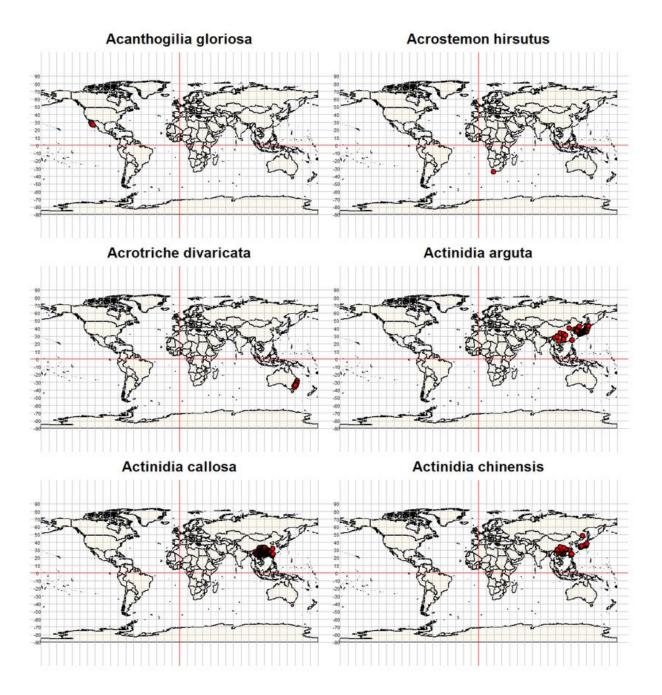
The graph below shows the latitudinal distribution of Ericales species when taking into account all species available in GBIF (n=7152, gray area). The red line shows the distribution of the uncorrected GBIF data for the species sampled in this study (n=347). The blue line shows the distribution for the species sampled for this study after manually correcting the raw GBIF distribution data to only keep native distribution areas.



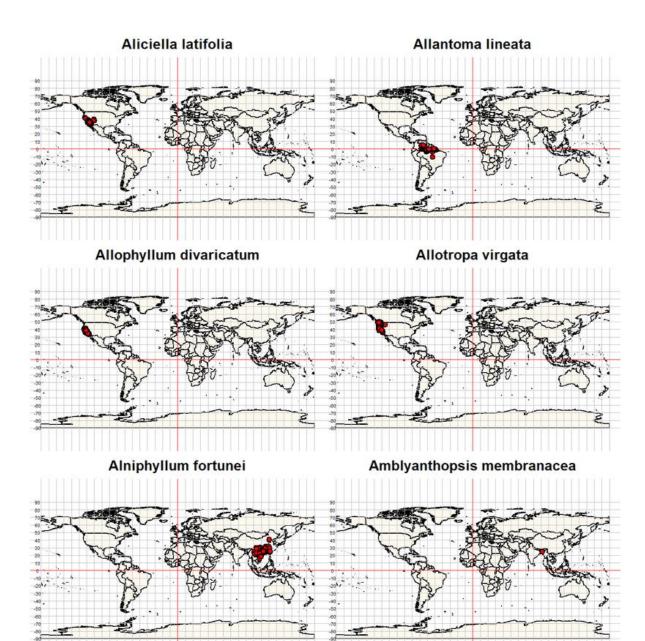
There are data for 7,152 ericalean species in GBIF, c.a. 65% of the order. A discrepancy between the distribution of the full Ericales dataset extracted from GBIF (gray area on the graph above) and our data without correction (in red, 347 species) is mainly present in the Northern hemisphere with more species in our sample compared to the total Ericales recorded in GBIF between latitudes 20 and 60. Apart from that difference, the shapes of the two curves are similar, and both show a latitudinal gradient. The shape of the curve changes significantly once the data is manually corrected (blue curve).

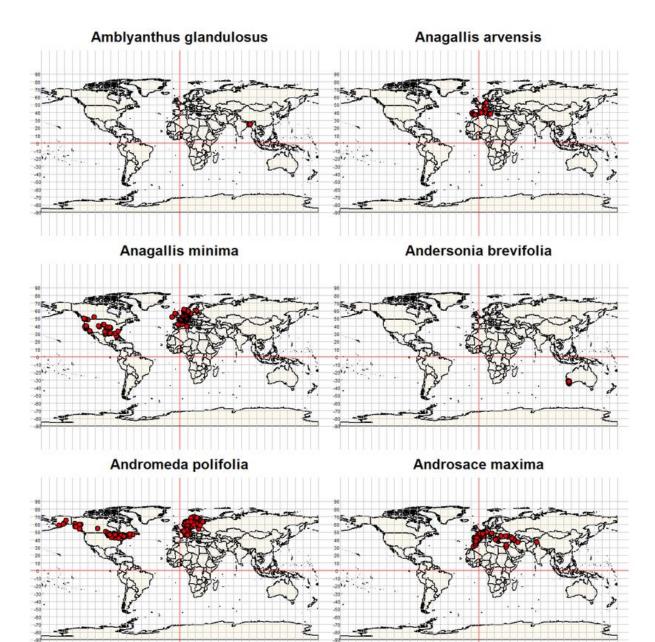
3. Note S2 - Distribution maps of the study species

Manually corrected distribution of the study species. Original occurence data were extracted from the database GBIF, and distributions manually corrected using floras and other scientific litterature (references are stored in the database Proteus (http://eflower.myspecies.info/)).



Actinidia kolomikta Actinidia melanandra Adinandra formosana Agapetes serpens Agarista albiflora Agarista sleumeri



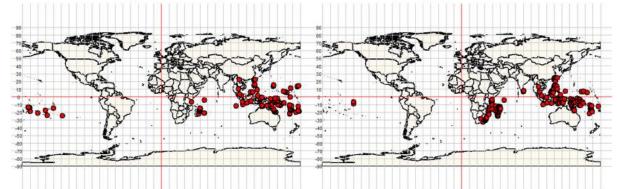


Anneslea fragrans Anomalanthus marlothii Apterosperma oblata Arbutus menziesii Archboldiodendron calosericeum Ardisia calycosa

Ardisiandra primuloides Argania spinosa Asteranthos brasiliensis Aubregrinia taiensis Autranella congolensis Baillonella toxisperma

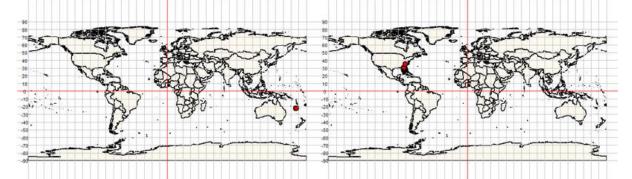
Barringtonia asiatica

Barringtonia racemosa



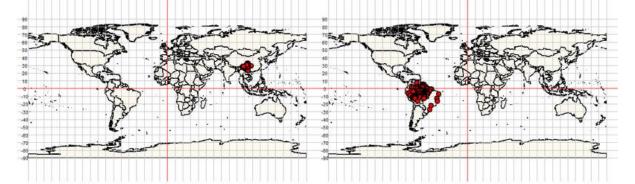
Beccariella sebertii

Bejaria racemosa

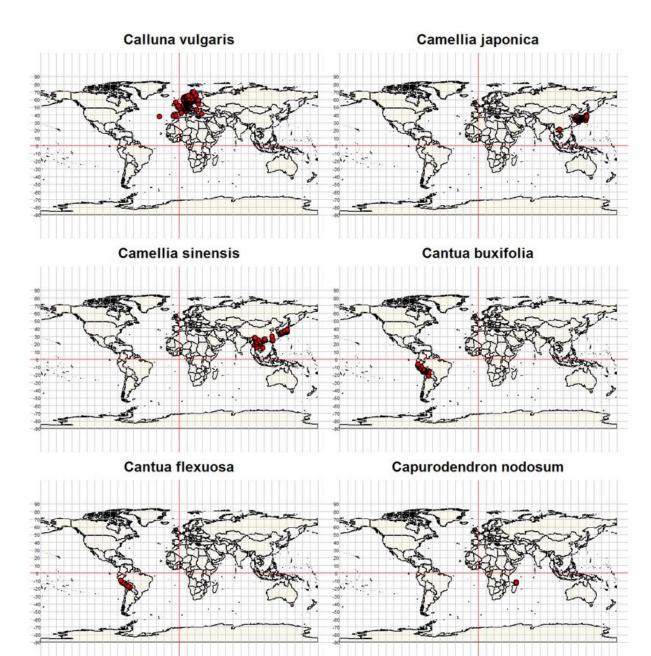


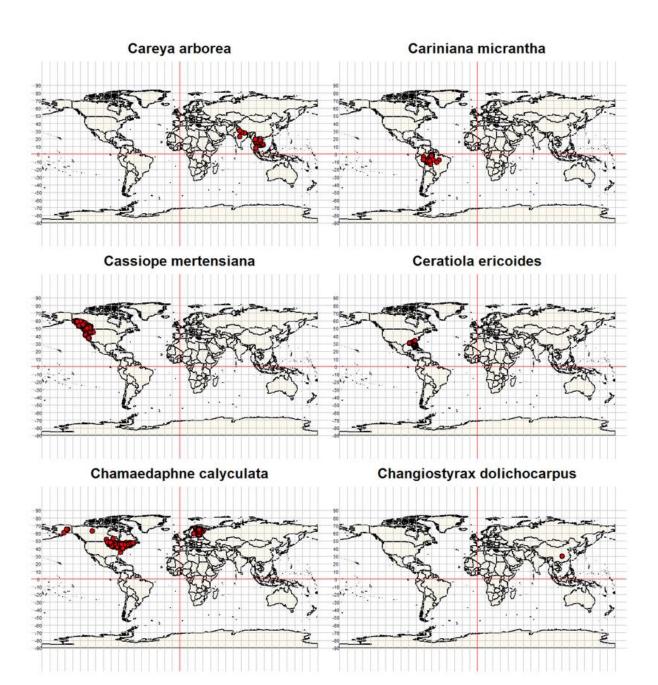
Berneuxia thibetica

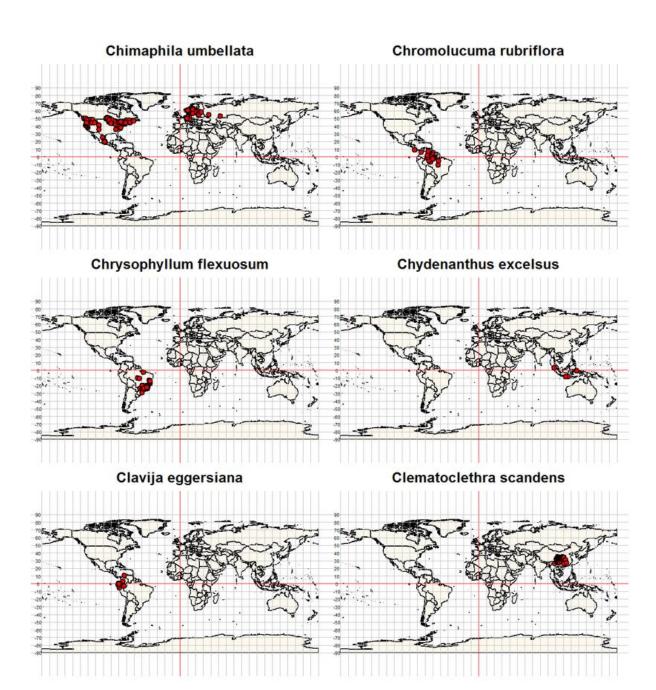
Bertholletia excelsa

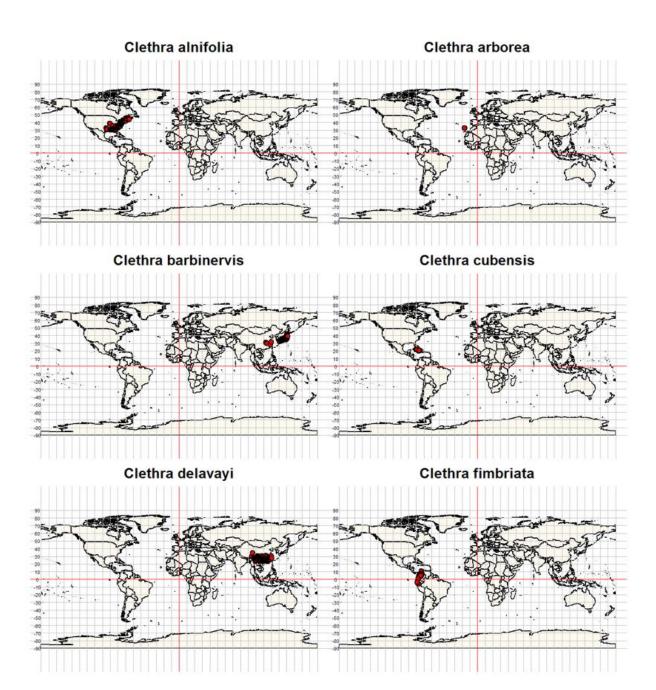


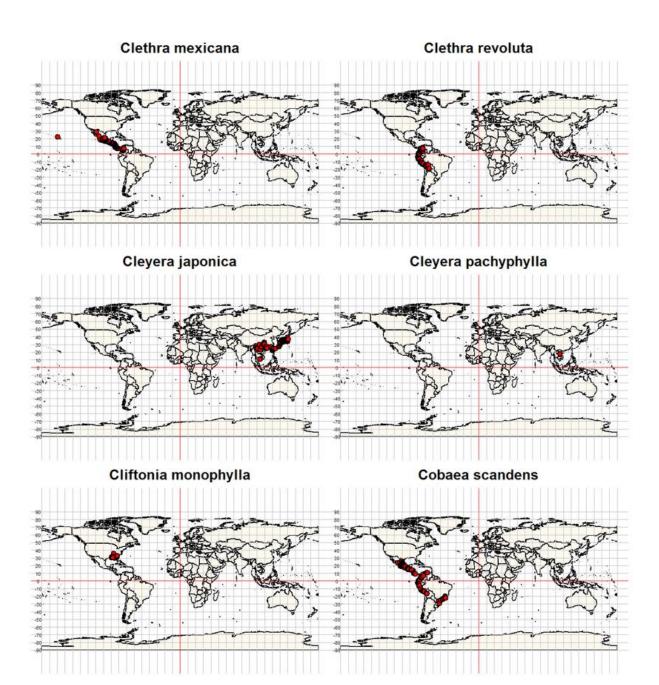
Bonellia albiflora Bonplandia geminiflora Breviea sericea Bruinsmia styracoides Bryantiella palmeri Bryocarpum himalaicum

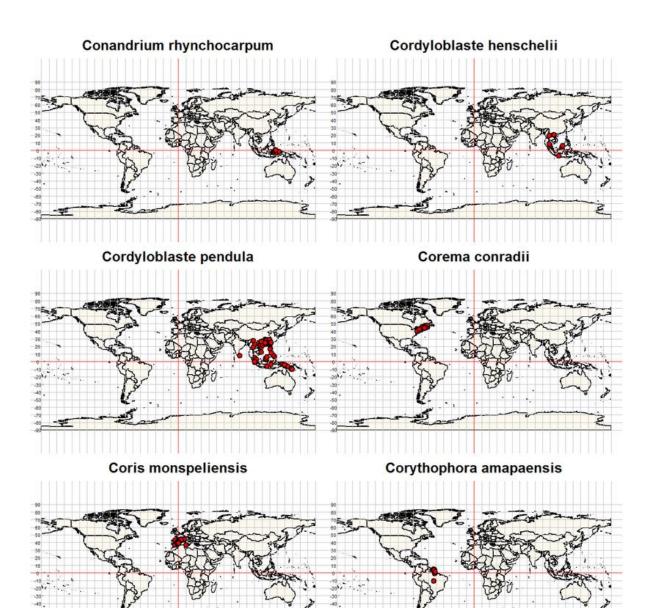


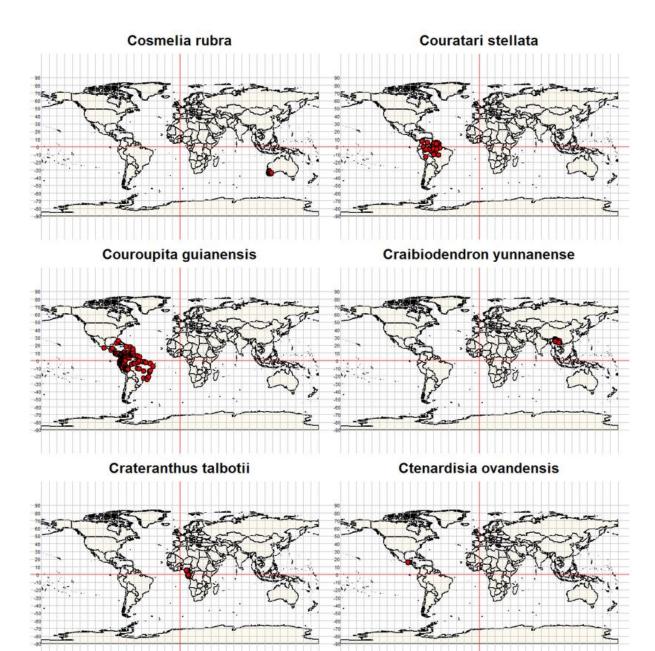


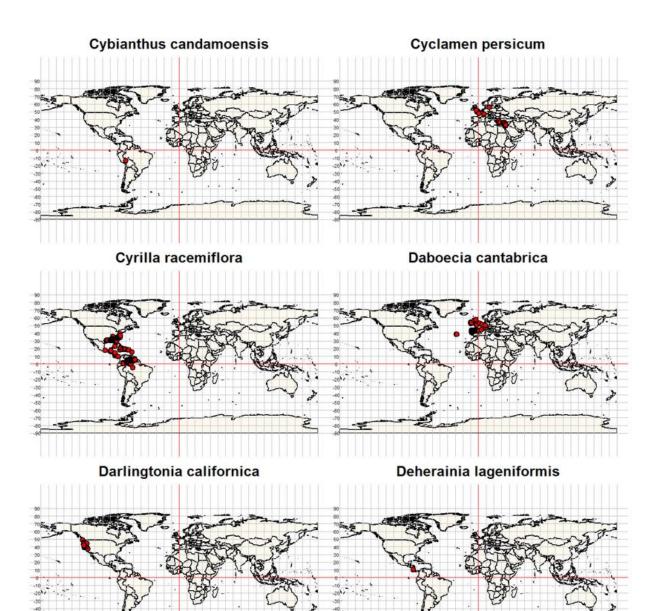


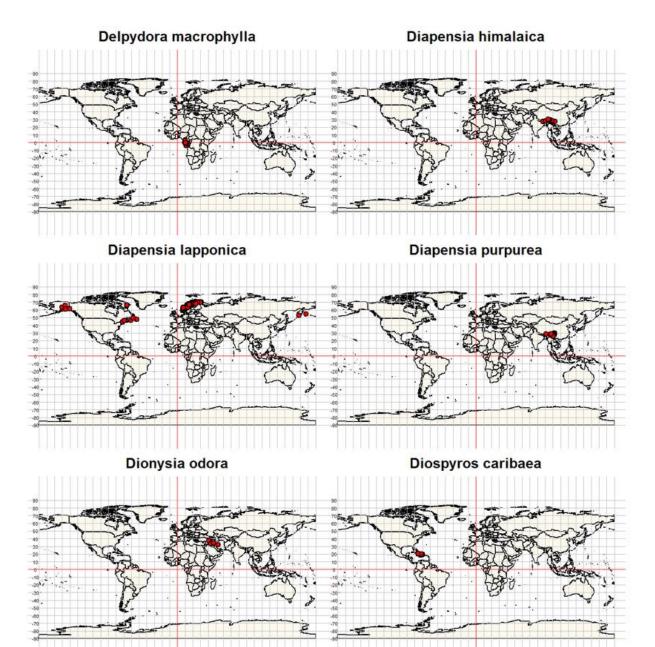


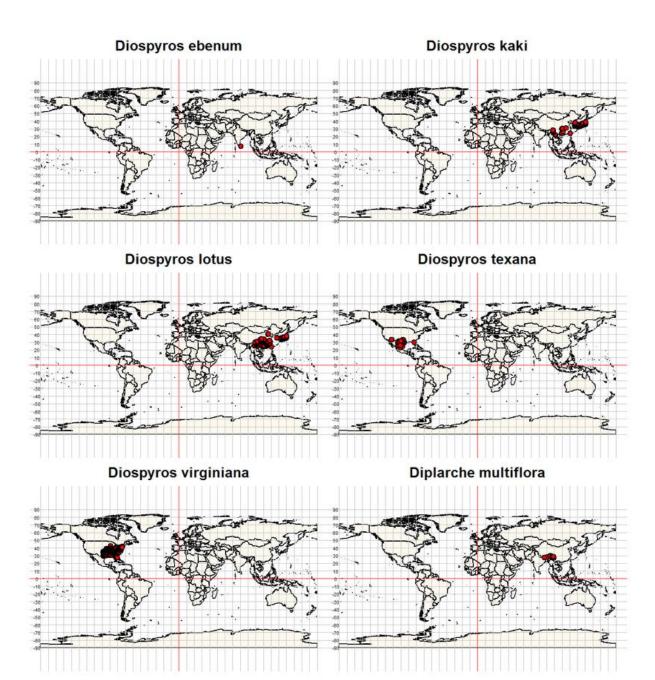


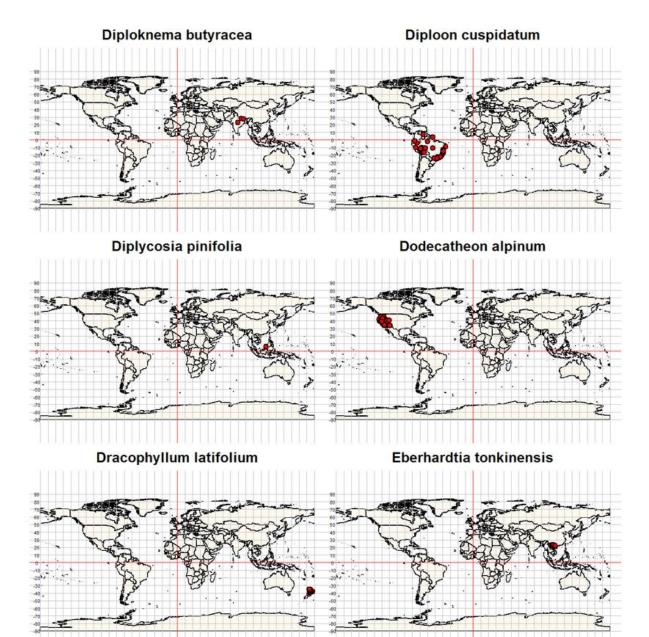




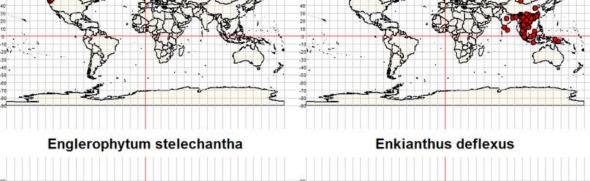


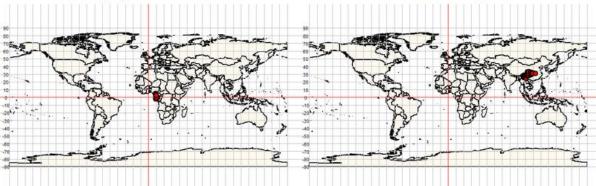


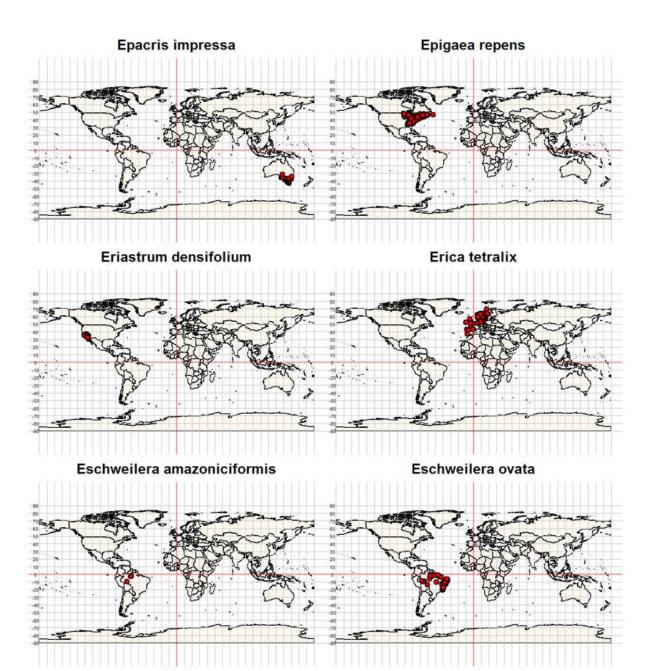


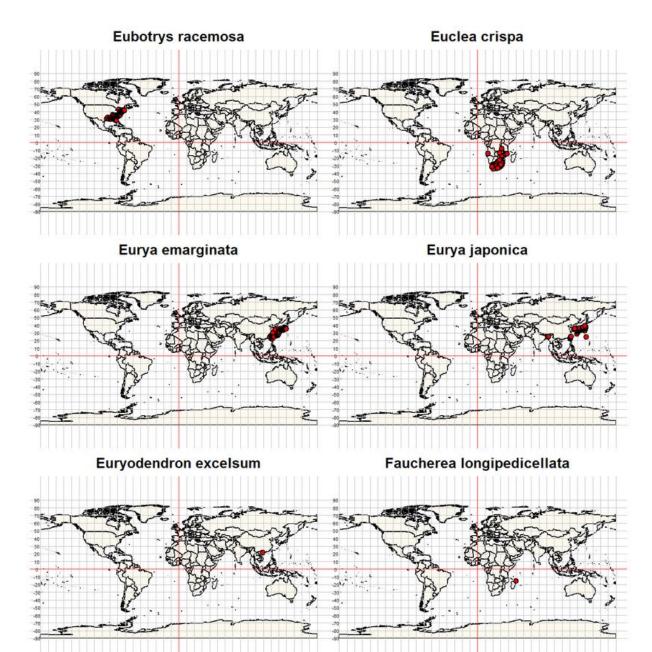


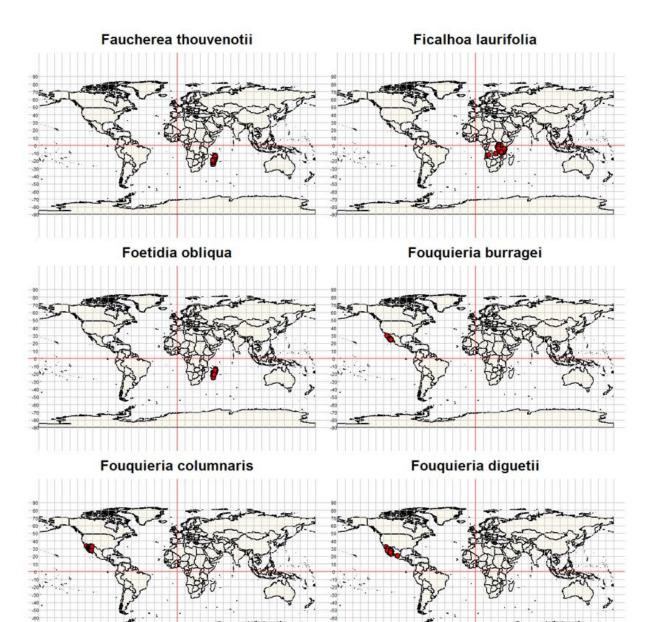
Ecclinusa ulei Elaeoluma glabrescens Elliottia pyroliflora Embelia ribes



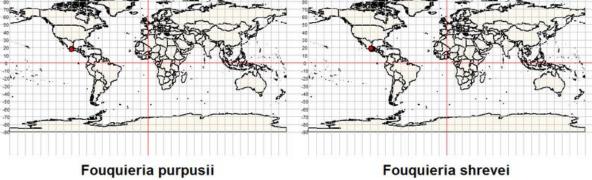


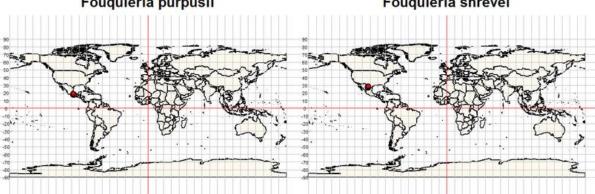






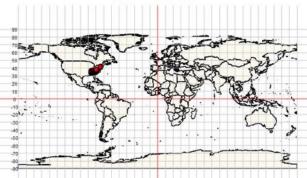
Fouquieria fasciculata Fouquieria formosa Fouquieria leonilae Fouquieria ochoterenae





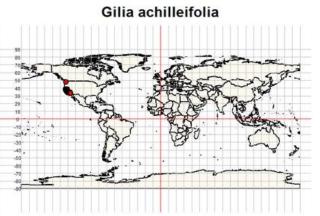
Freziera cuatrecasasii

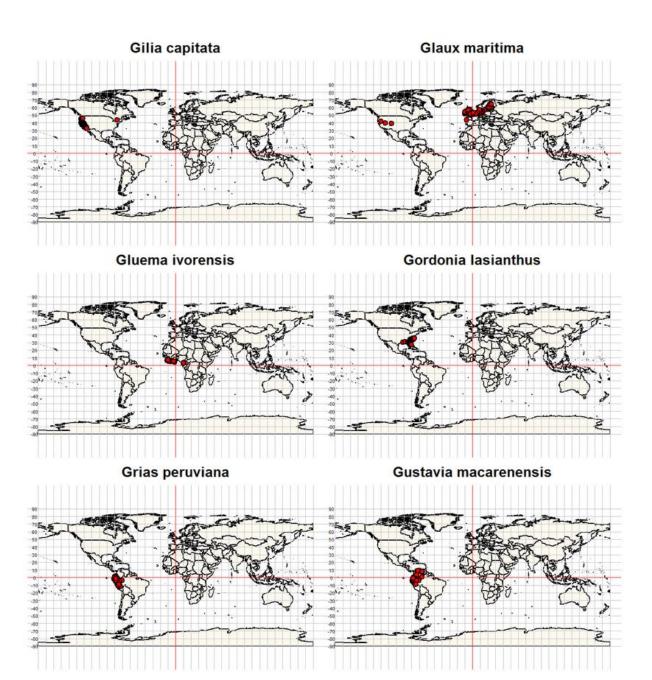


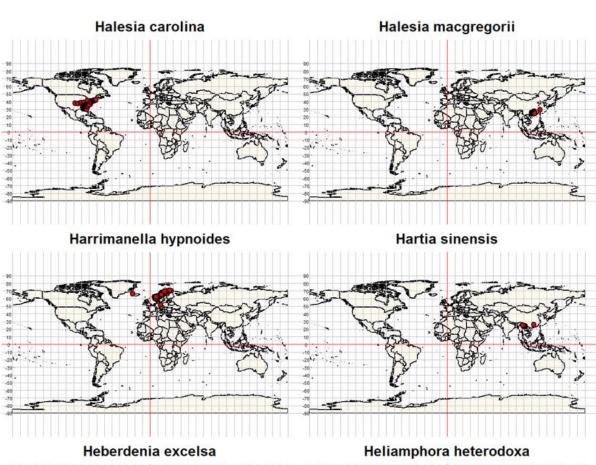


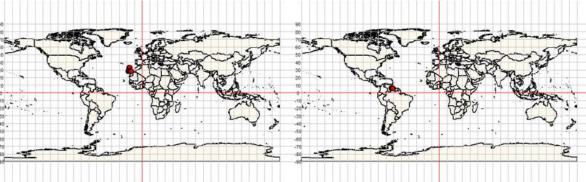
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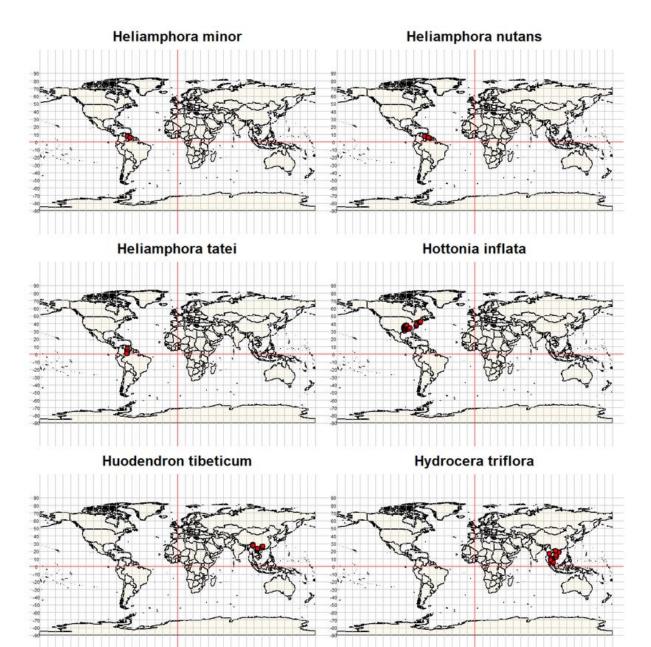
Geissanthus cogolloi

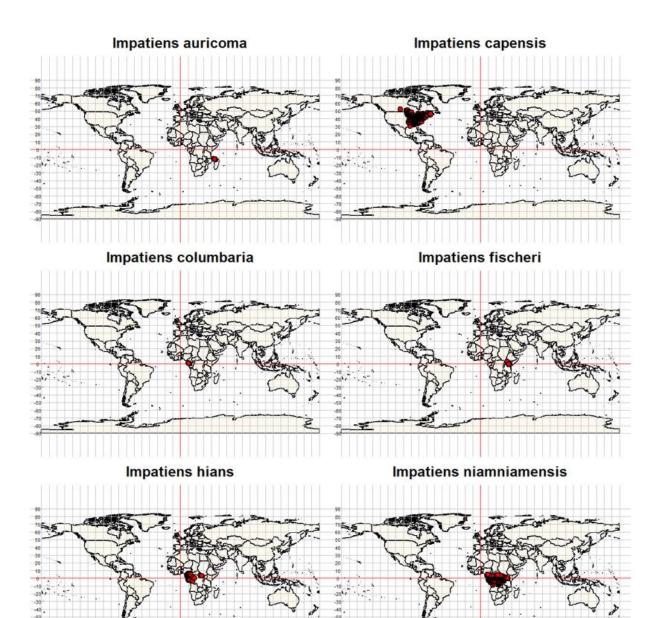






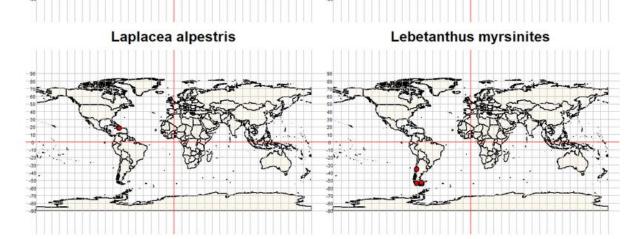


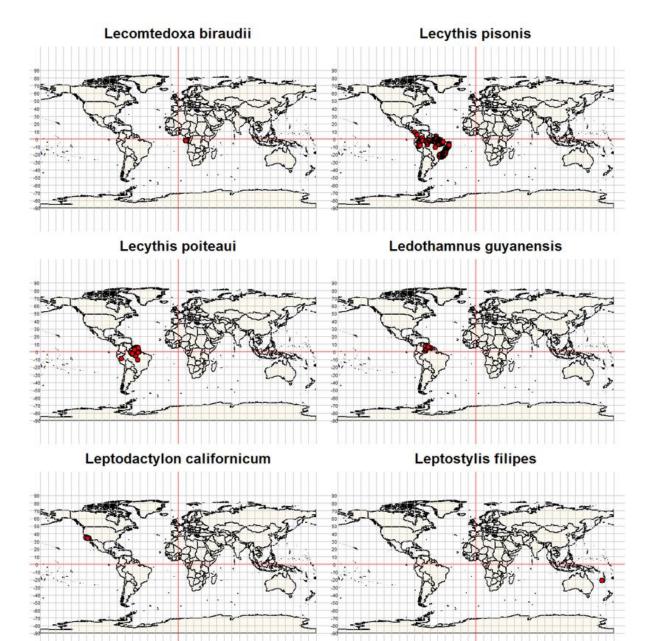


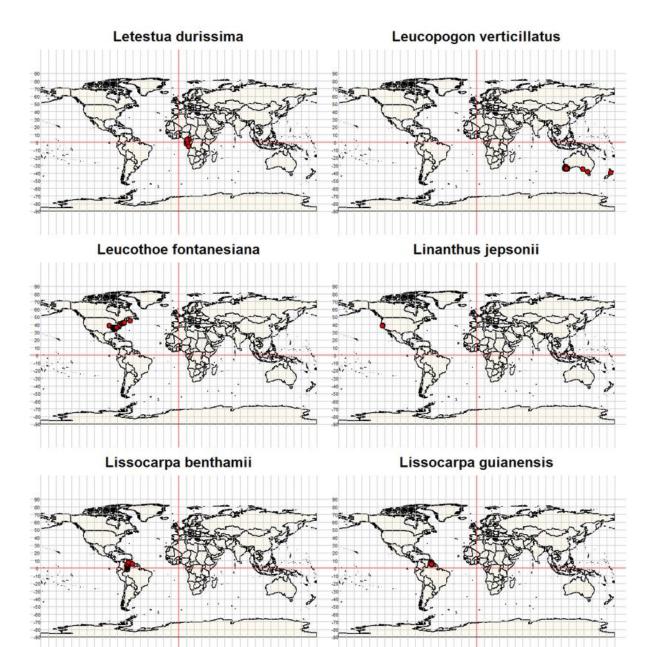


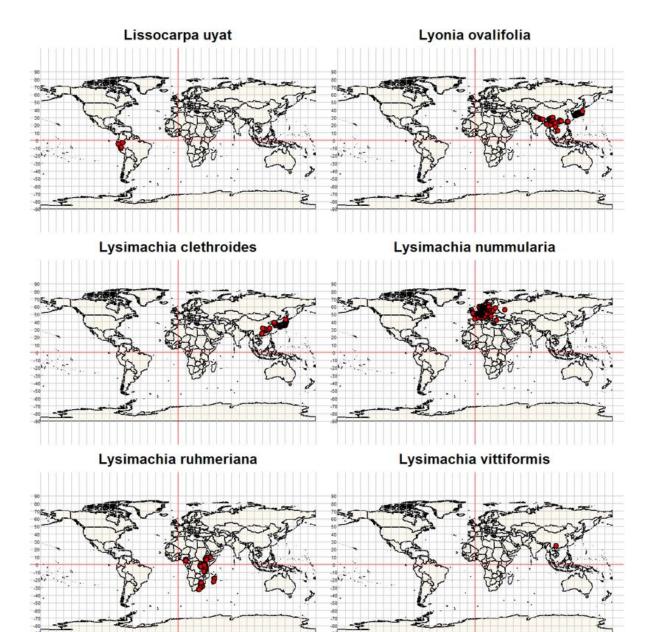
Impatiens parviflora Impatiens pseudoviola Ipomopsis tenuifolia Isonandra lanceolata Jacquinia armillaris Kalmia buxifolia

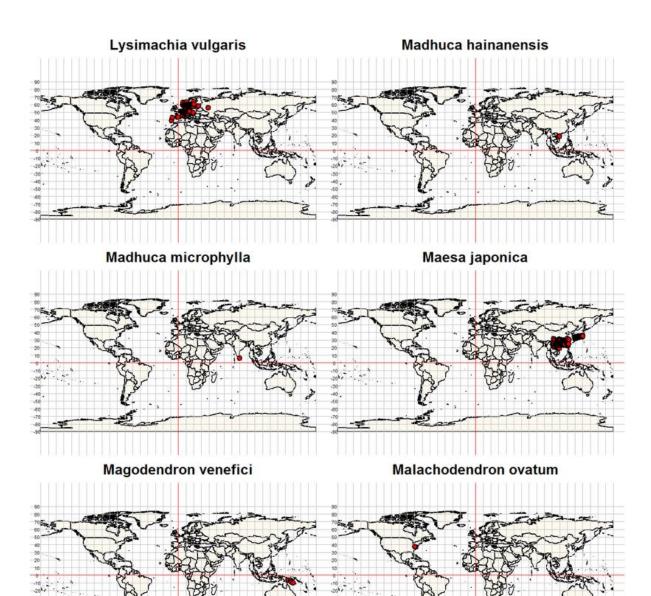
Kalmiopsis leachiana Labisia pumila Labourdonnaisia madagascariensis Labramia costata





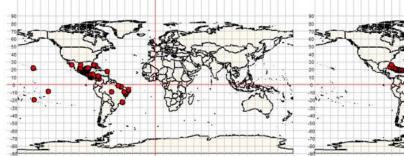


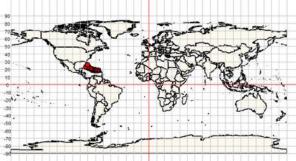




Manilkara zapota

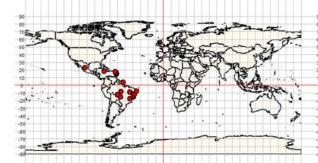
Marcgravia rectiflora

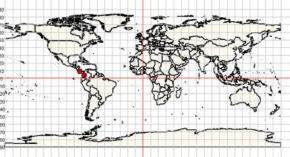




Marcgravia umbellata

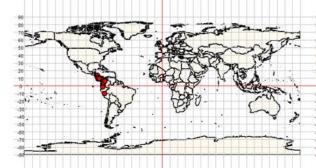
Marcgraviastrum pauciflorum

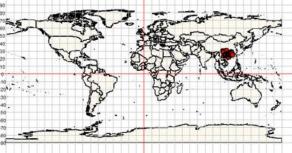


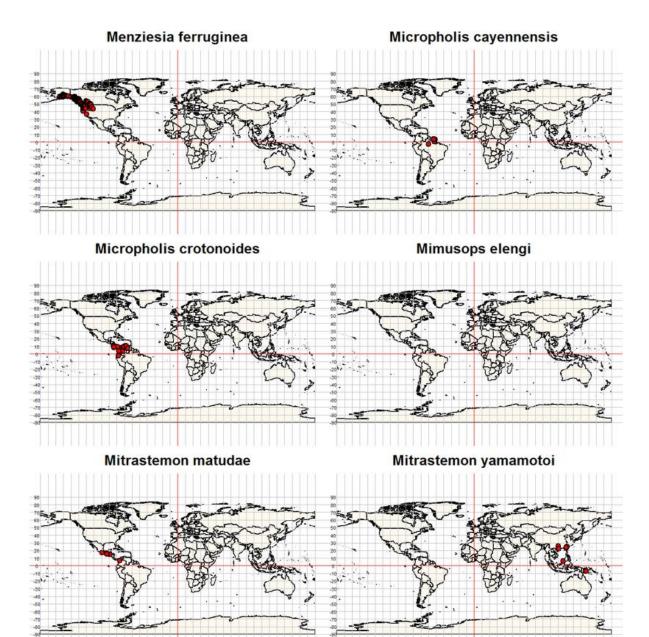


Marcgraviastrum subsessile

Melliodendron xylocarpum

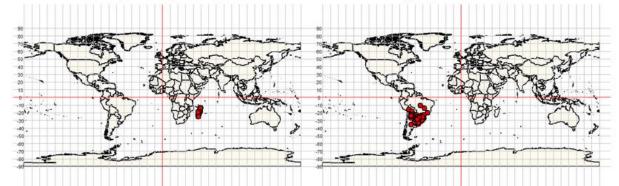






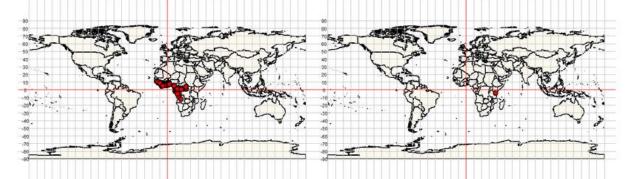
Monoporus spathulatus

Myrsine laetevirens



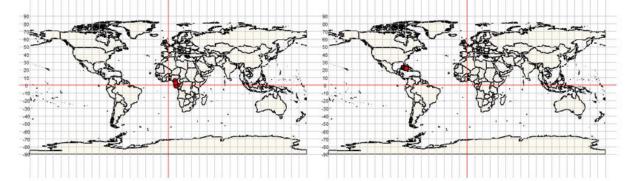
Napoleonaea vogelii

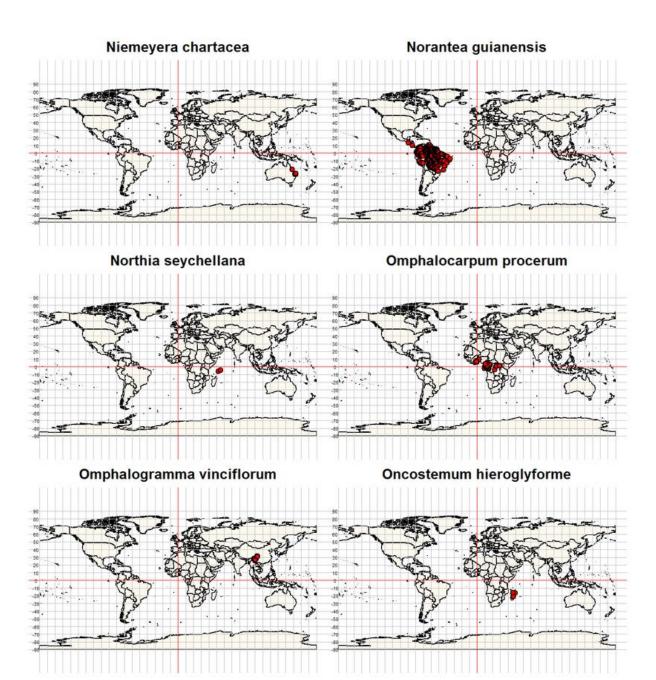
Neohemsleya usambarensis



Neolemonniera ogouensis

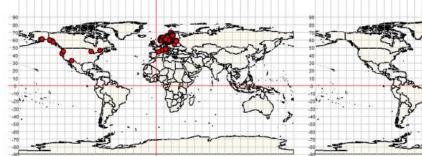
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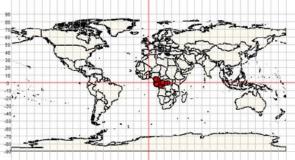




Orthilia secunda

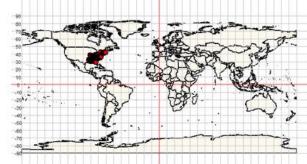
Oubanguia africana

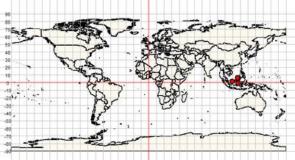




Oxydendrum arboreum

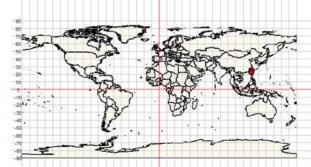
Palaquium beccarianum



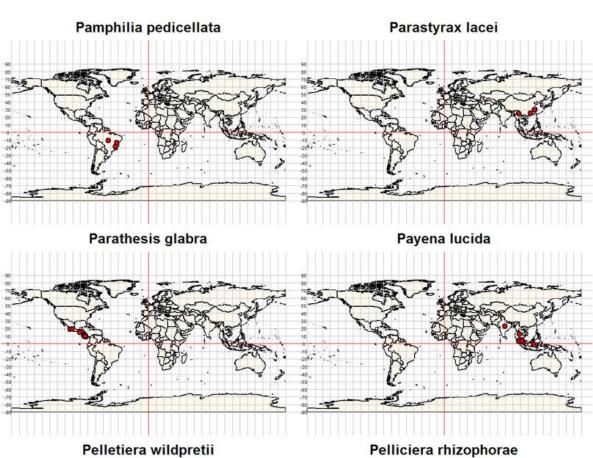


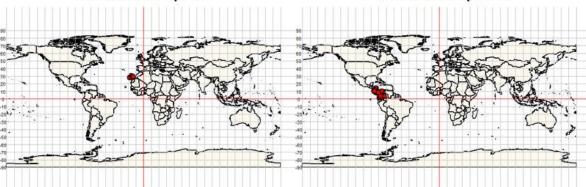
Palaquium formosanum

Palaquium obovatum



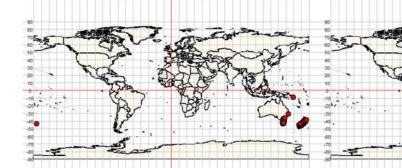






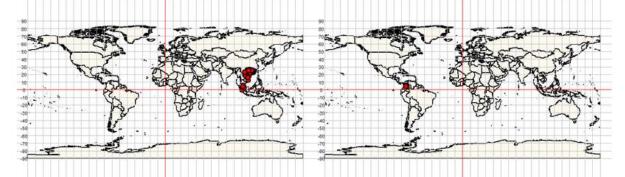
Pentachondra pumila

Pentamerista neotropica



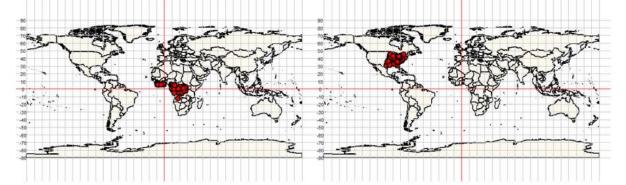
Pentaphylax euryoides

Pernettya hirta



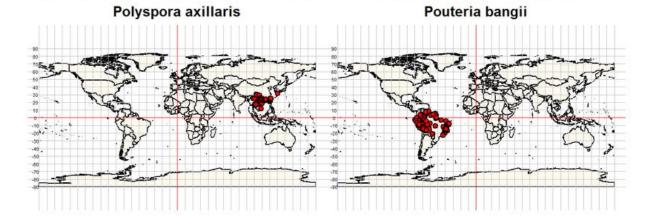
Petersianthus macrocarpus

Phlox divaricata



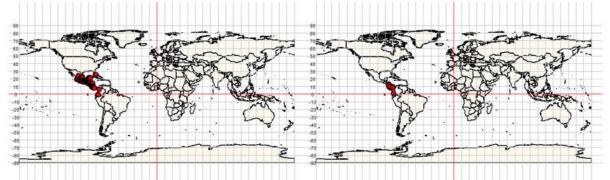
Pieris cubensis Pierrina zenkeri Planchonella kuebiniensis Planchonella obovata

Planchonia careya Pleiomeris canariensis Polemonium caeruleum Polemonium reptans



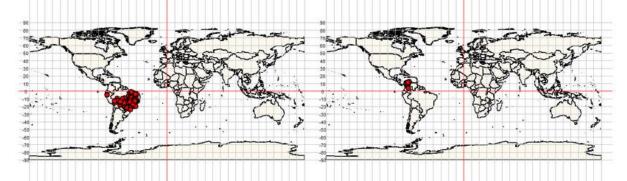
Pouteria campechiana

Pouteria foveolata



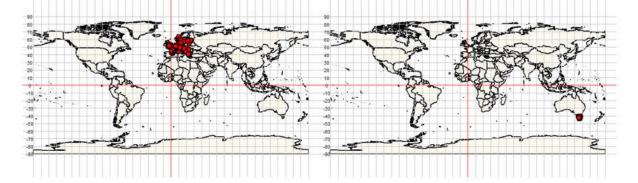
Pouteria ramiflora

Pradosia colombiana



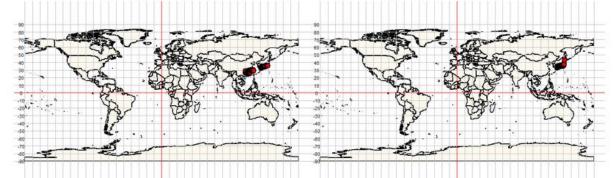
Primula veris

Prionotes cerinthoides



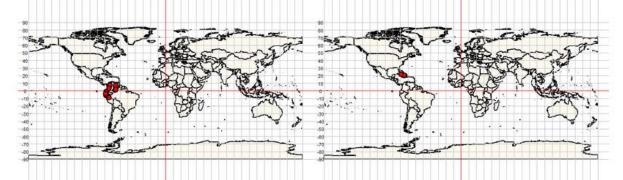
Pterostyrax corymbosus

Pterostyrax hispidus



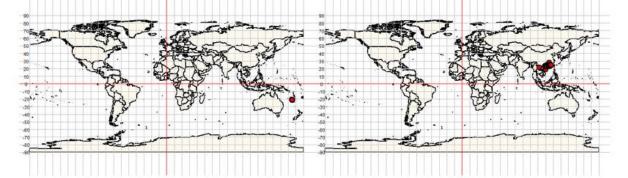
Purdiaea nutans

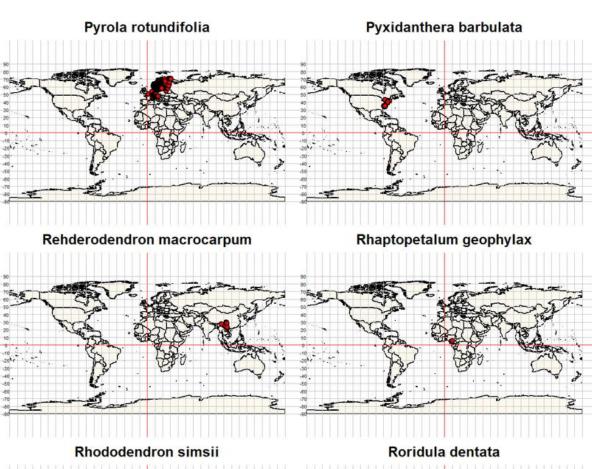
Purdiaea stenopetala

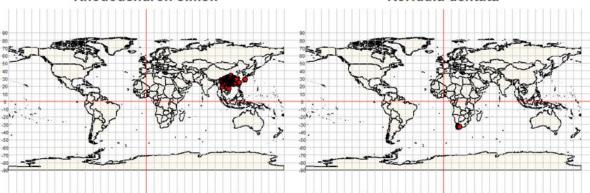


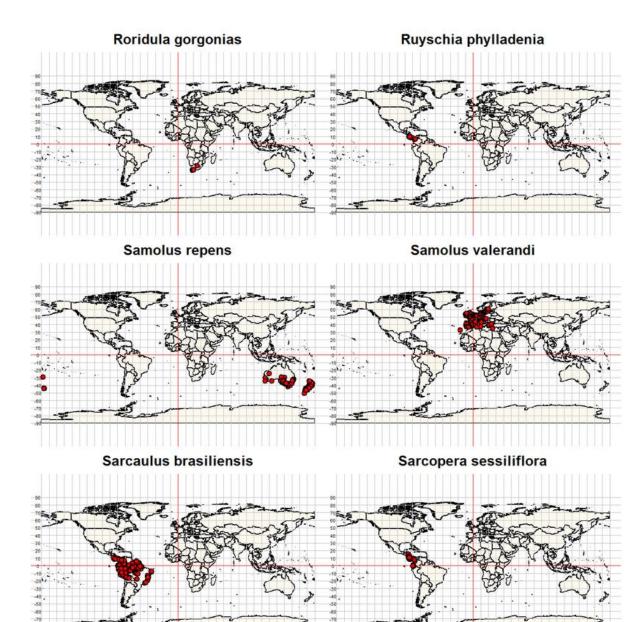
Pycnandra benthamii

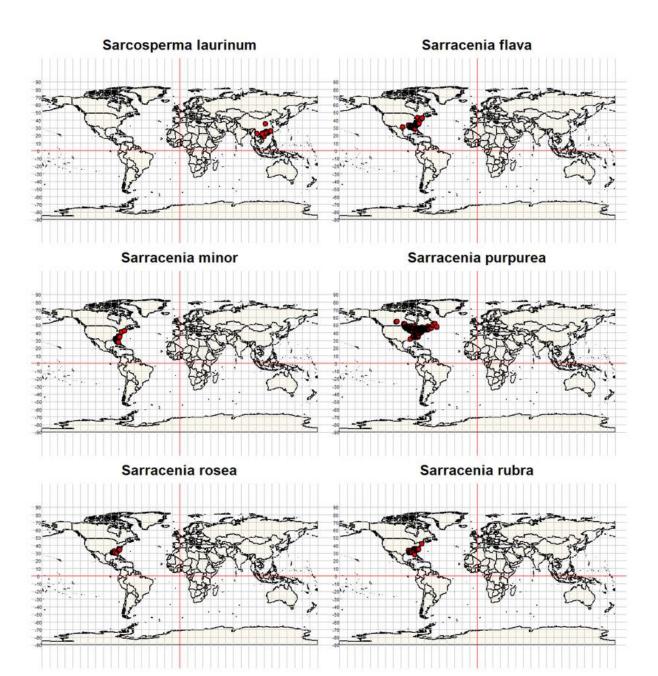
Pyrenaria spectabilis

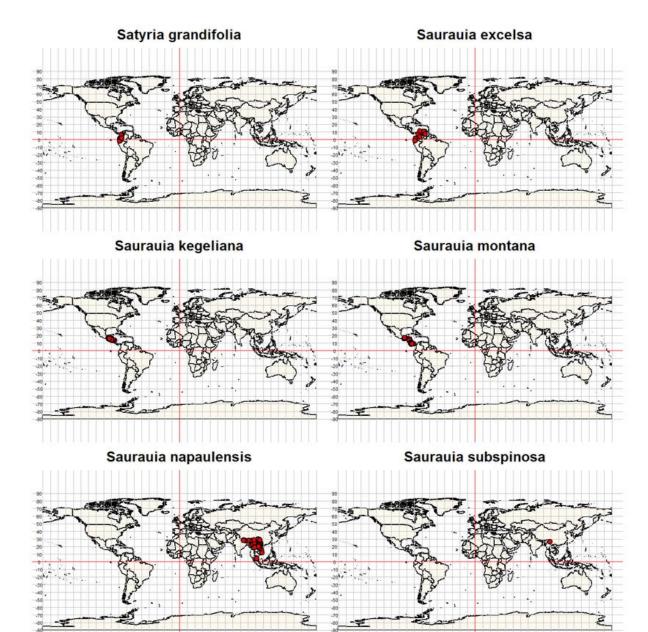


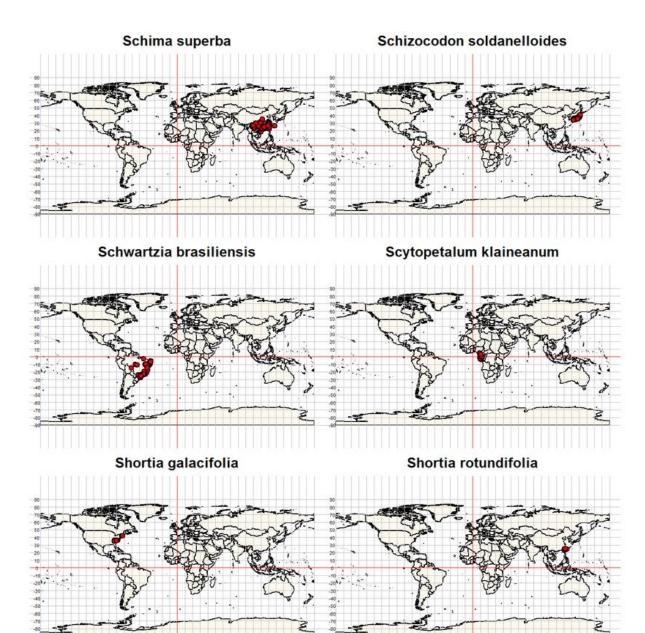


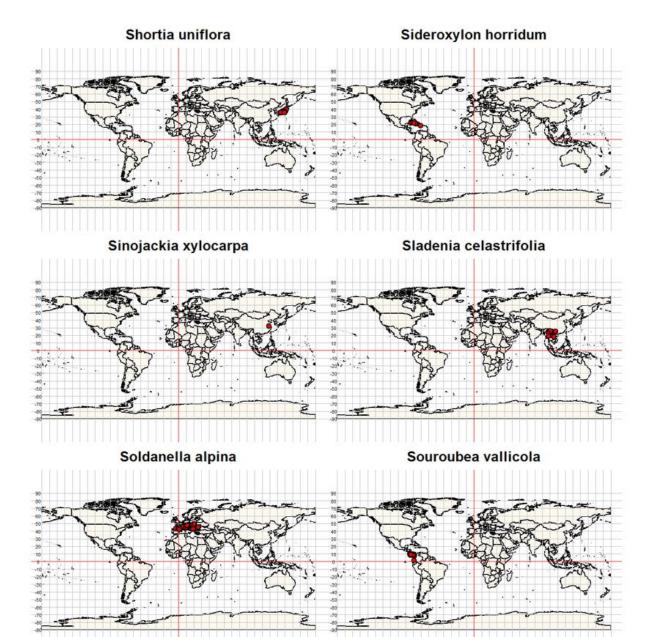




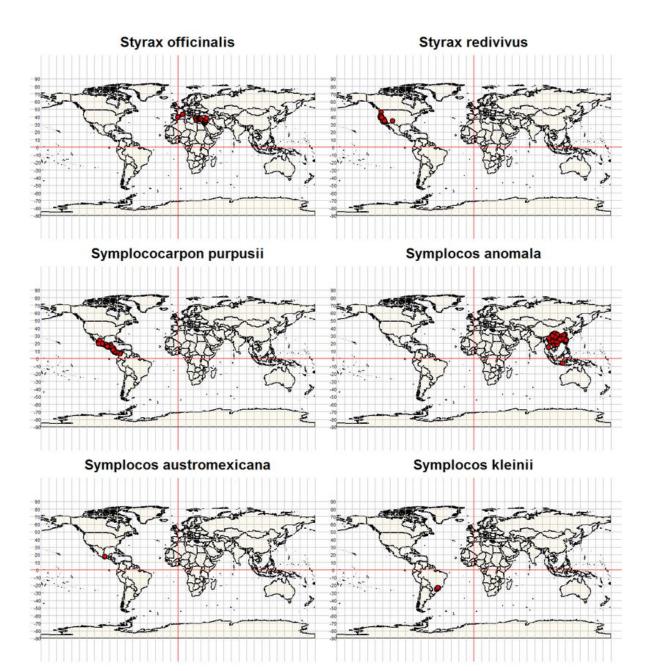


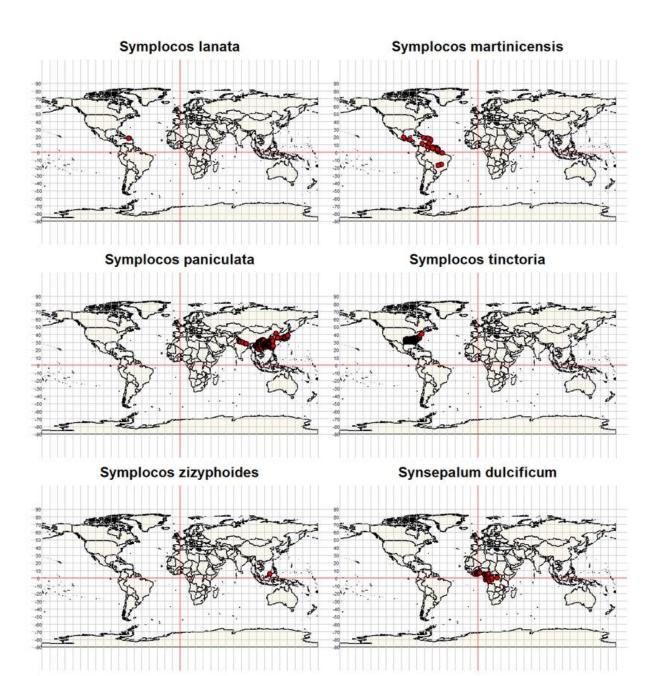




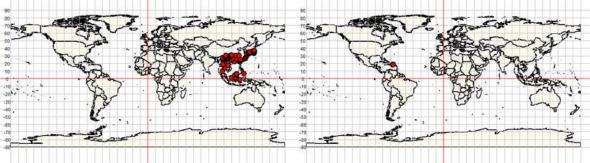


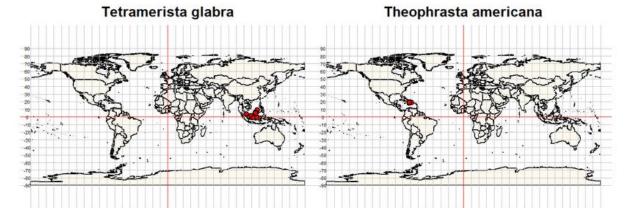
Stewartia pseudocamellia Stimpsonia chamaedryoides Styrax americanus Styrax chinensis Styrax japonicus Styrax obassia

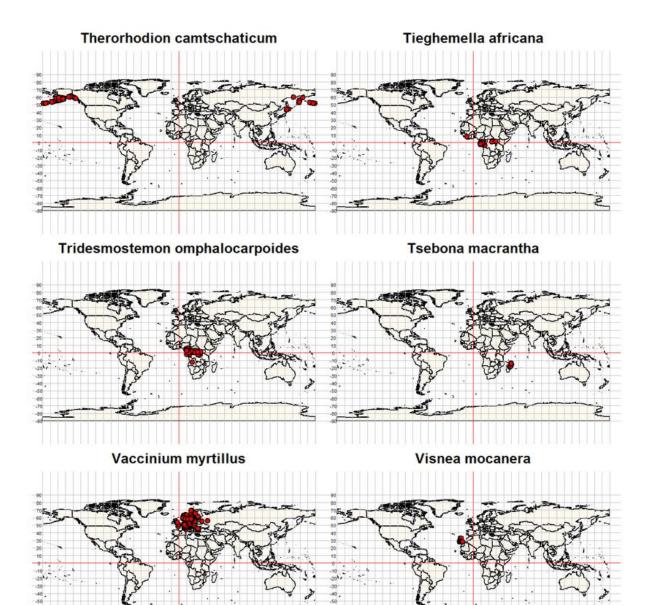


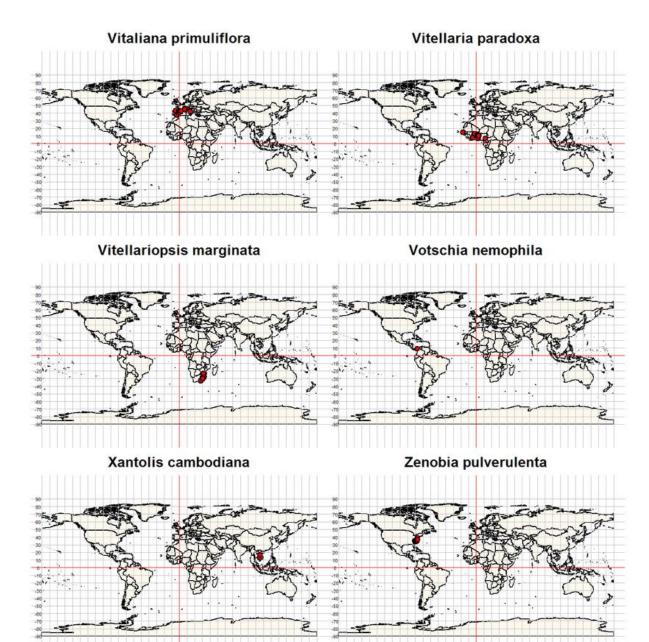


Taonabo stuebelii Tepuia venusta Ternstroemia gymnanthera Ternstroemia stahlii









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