



# IS THERE A RAND FLORA PATTERN - AND IS HYPERICUM PART OF IT?

INFERRING THE EVOLUTIONARY HISTORY OF AFRO-MEDITERRANEAN SECTIONS OF *HYPERICUM* (HYPERICACEAE)

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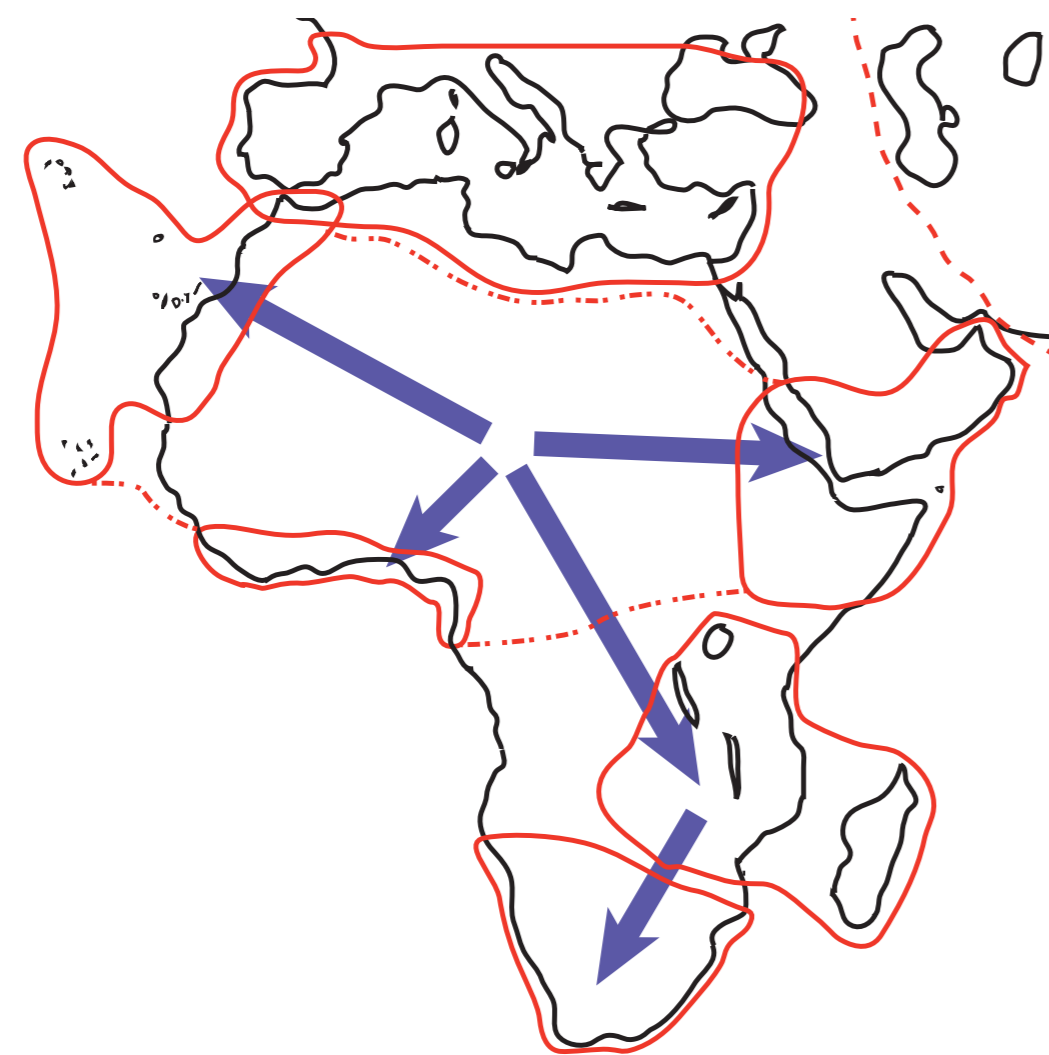
## THE "RAND FLORA"

The "Rand Flora" is a pattern of disjunct distributions across many plant groups, between northwest Africa-Macaronesia, Horn of Africa-southern Arabia, and east-south Africa. One of the most-cited examples of this enigmatic floristic pattern is the Canary Islands "dragon tree" (genus *Dracaena*), which has its closest relatives in Egypt and the Socotra Islands off the coast of Somalia.

### 2 MAIN HYPOTHESES ABOUT THE ORIGIN:

#### "VICARIANCE"

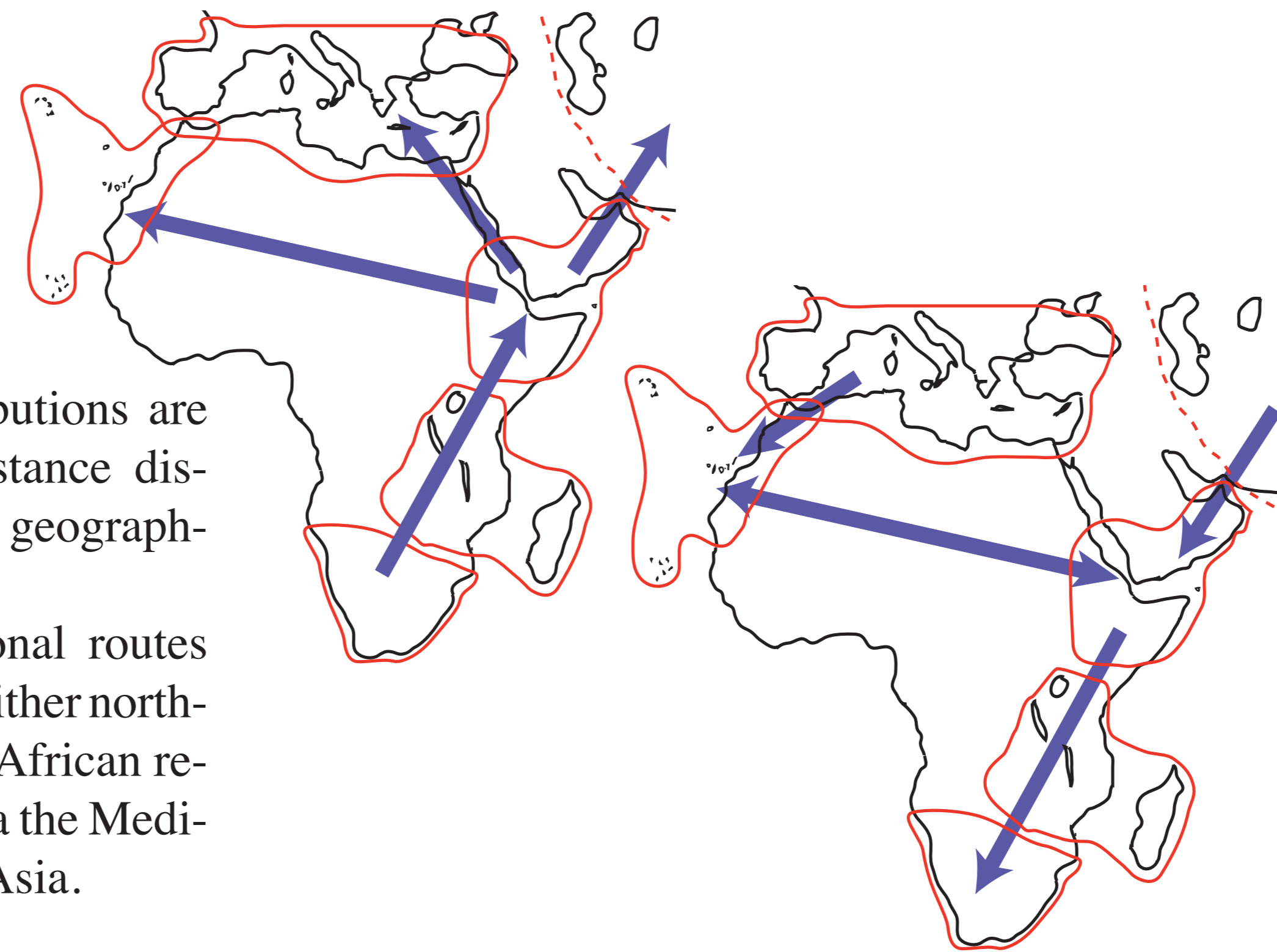
The extant species are relicts of a formerly larger distribution, a macrocontinental Tertiary flora that went partly extinct following the aridification that took place from the Miocene onwards.



#### "DISPERSAL"

The present distributions are the result of long-distance dispersal events between geographically isolated areas.

Two main directional routes have been proposed: either northwards from the south African region or southwards via the Mediterranean or western Asia.



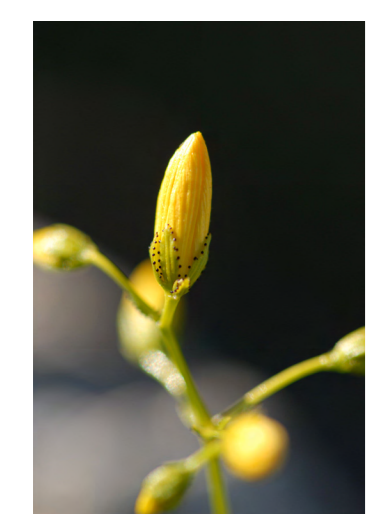
### RECONSTRUCTING THE EVOLUTIONARY ORIGINS OF THE RAND FLORA - WHY NOW?

- NEW MOLECULAR PHYLOGENIES of plant groups with this distribution have been published in the last decade.

- NEW DATING methods, that give more realistic results, have been developed.

- NEW GEOLOGICAL DATA from paleontology (Anderson et al., 2009), sedimentology and radiometrical analyses, have provided more detailed accounts of paleoclimate, paleogeography and vegetational changes in Africa and Macaronesia.

- NEW BIOGEOGRAPHICAL methods that can include temporal information from geological data or molecular dating have been developed in the last few years.



## HYPERICUM - A CASE STUDY

### HYPERICUM

The genus *Hypericum* L. contains more than 450 species, and has been treated either as a genus within Hypericaceae, or the subfamily Hypericoideae in an extended Clusiaceae. The family belongs to the order Malpighiales.

### DISTRIBUTION

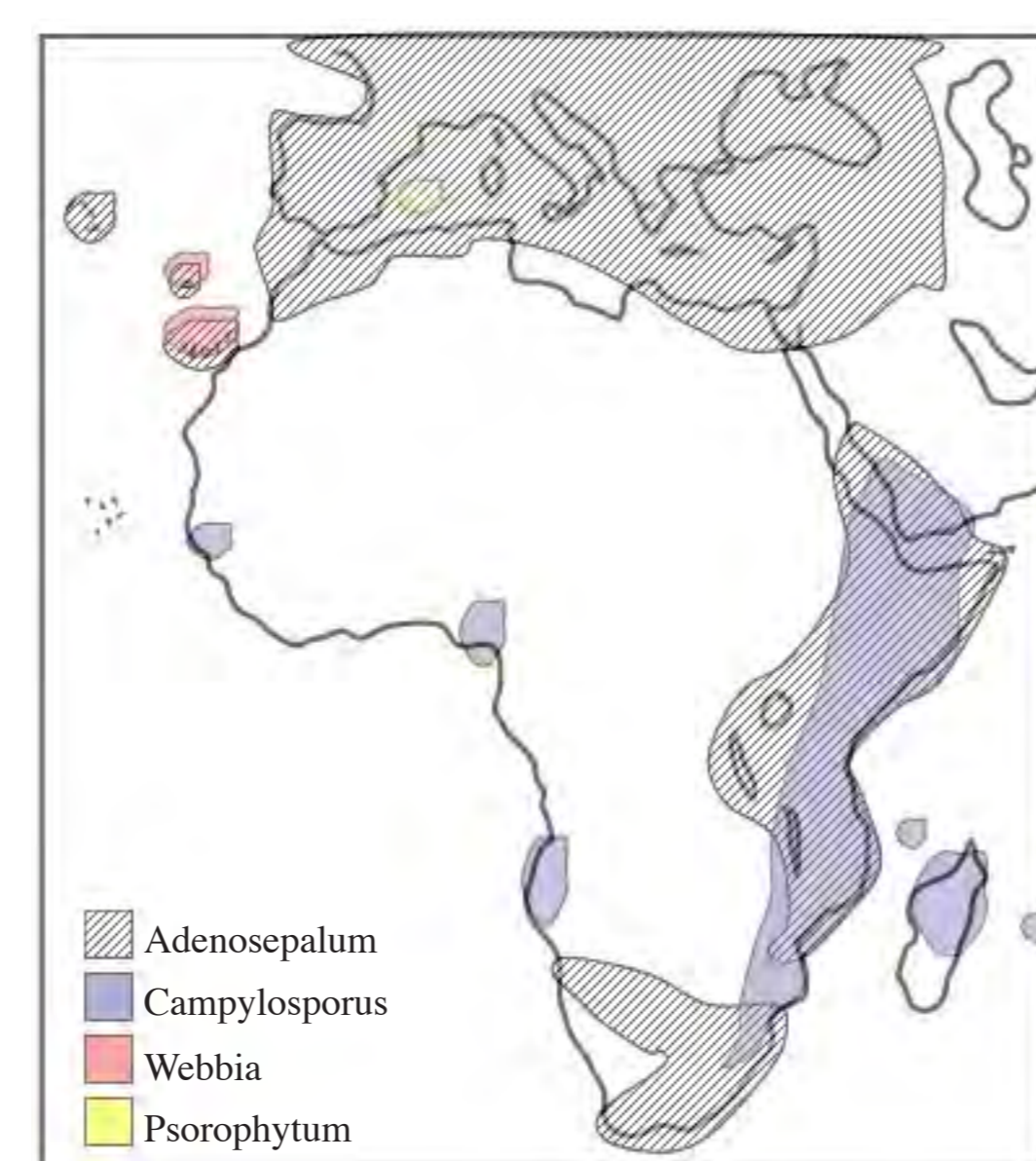
*Hypericum* has a worldwide distribution, with the largest diversity in the Holarctic and high-altitude tropical areas.

In the Afro-Mediterranean region *Hypericum* is present in most habitats except for deserts and tropical lowlands.

### PHYLOGENY

Robson (1977) made an infrageneric classification of *Hypericum*, and recognised 30 sections. Four of these sections (Adenosepalum, Campylosporus, Psorophytum and Webbia) have been proposed to show the Rand Flora pattern (see below).

However, only one phylogeny of *Hypericum* is published (Park & Kim, 2004), focusing on three Asian sections. Therefore we first need to reconstruct the phylogenetic "backbone" of the genus, and thereafter detailed phylogenies of the potentially interesting sections for the "Rand Flora Project".

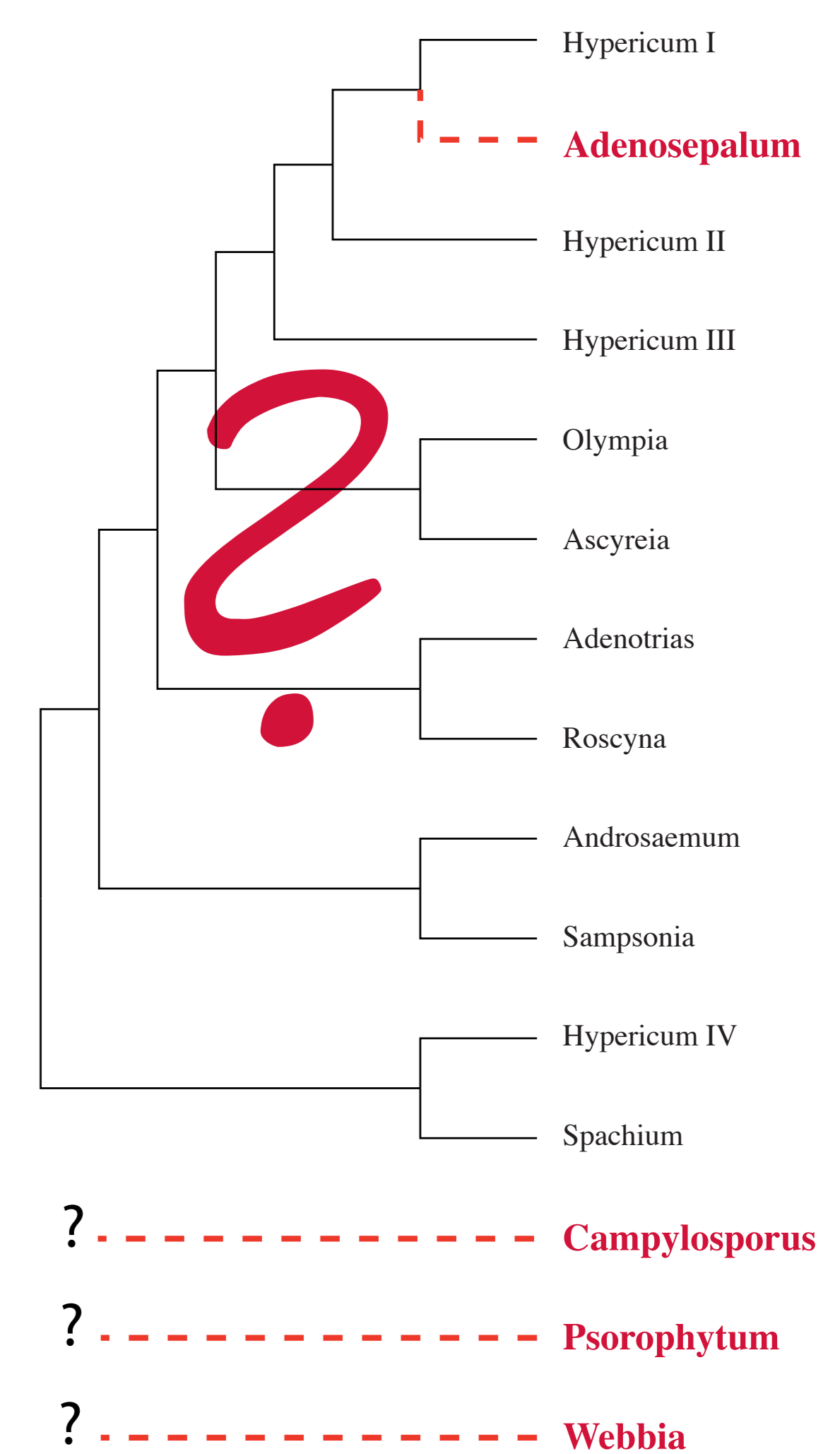


### FOSSIL RECORD AND AGE

Clusiaceae have a long fossil record, beginning with *Paleoclusia* from the Turonian, about 90 mya.

Molecular datings (e.g. Davis et al., 2005) have suggested Clusiaceae-Hypericaceae to be part of an "explosive" radiation of the Malpighiales in the mid-Cretaceous.

Fossil pollen of *Hypericum* from the lower Oligocene, about 30 mya, have been found in e.g. Spain. The genus and its presence in the Mediterranean is therefore regarded as older than the age of the hypothesized Oligocene-Miocene Rand Flora.



## How?

### HYPERICUM: WORKPLAN

- Sampling of all *Hypericum* sections, with special focus on Adenosepalum, Campylosporus, Psorophytum and Webbia
- Sequencing of mitochondrial and chloroplast genes
- Phylogenetic inference
- Molecular dating and biogeographical analyses
- Inclusion in the larger "Rand Flora Project"

### MOLECULAR DATING IN THE CONTEXT OF DISENTANGLING THE RAND FLORA PATTERN

Two plant groups can be of different ages, and therefore unlikely to have been affected by the same biogeographic events - but still show similar distributional patterns.

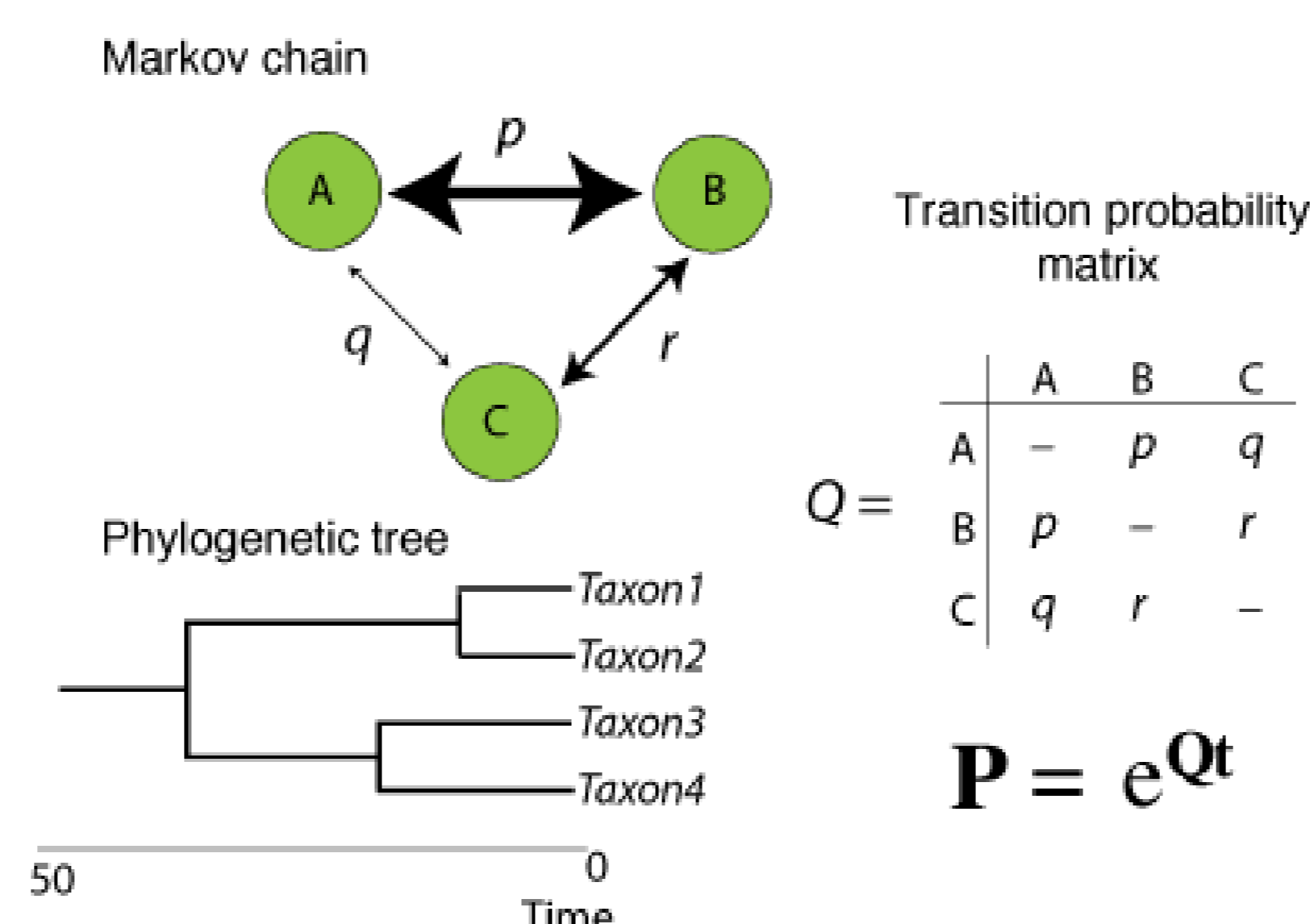
Different diversification periods has probably occurred in Africa, due to rapid changes in climate that started during the Oligocene-Miocene.

To disentangle the Rand Flora pattern we therefore need to distinguish between potentially pseudo-congruent patterns and "real" patterns; to do this molecular dating is necessary.

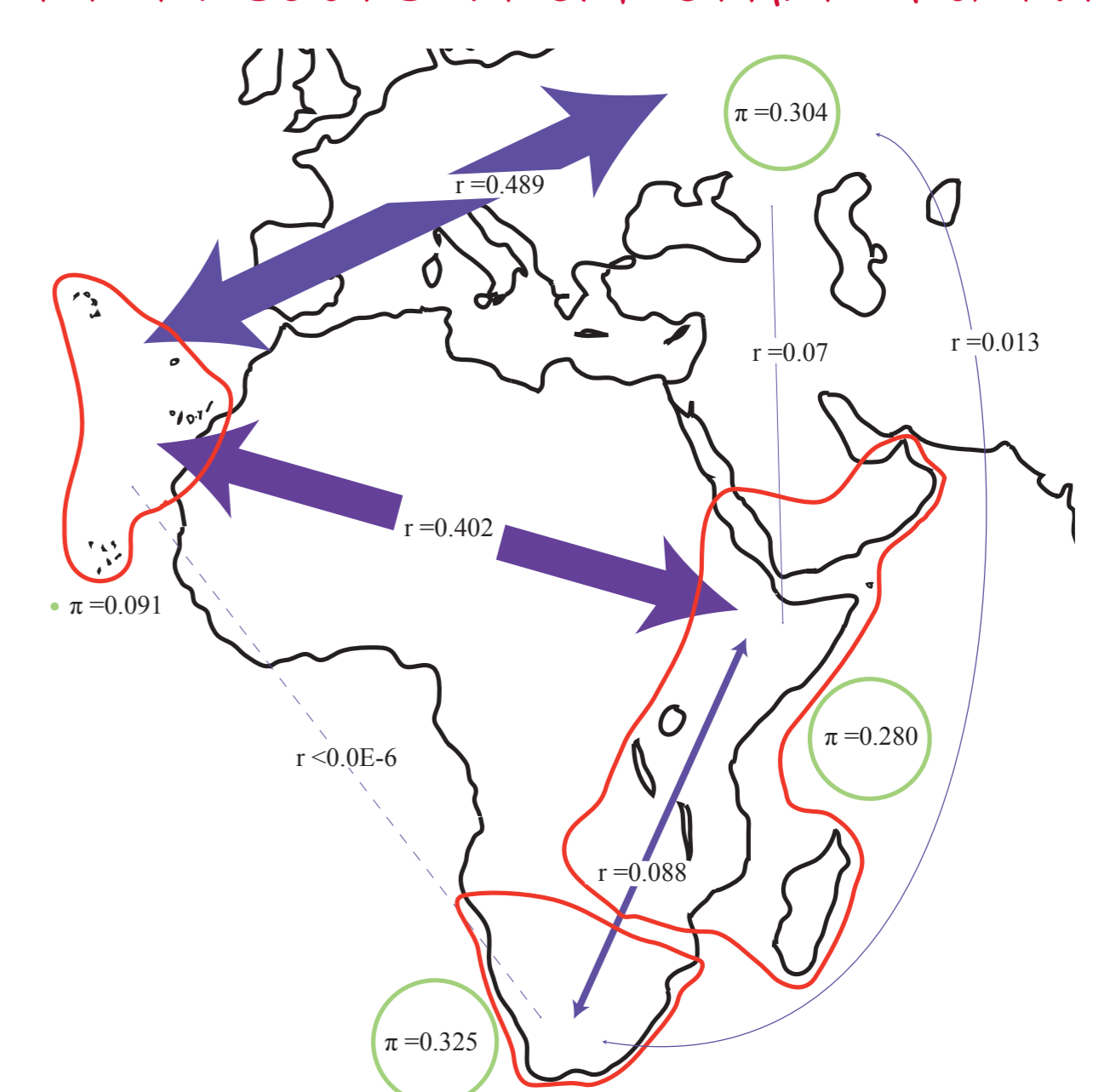
### MODEL-BASED BIOGEOGRAPHY METHODS

We are currently working on implementing the Bayesian island biogeography model (Sanmartín et al., 2008) in a continental setting. It is used to estimate rates of dispersal between geographic areas and area carrying capacities, from phylogenetic and distributional data, using an approach that integrates over phylogenetic and biogeographic uncertainty, and can be used across multiple lineages.

Range evolution is modelled as a stochastic process ("Markov chain") with discrete states (geographic ranges "A", "B", "C") that evolves along the branches of a phylogenetic tree according to a "matrix of transition probabilities, Q", e.g., "p" = dispersal rate from "A" to "B" (Sanmartín, 2009).



### PRELIMINARY RESULTS FROM OTHER PLANT GROUPS



- NORTHERN AFRICA shows the smallest carrying capacity but highest dispersal rate to other regions, suggesting that its flora was built up by immigration of lineages.

- SOUTH AFRICA shows the highest carrying capacity and lowest dispersal rate, suggesting a flora formed by in-situ diversification.

- There has been LITTLE EXCHANGE, or alternatively this exchange has been old, between south Africa and northern Africa, probably via the eastern African region.