Taxonomy and morpho-molecular investigations

Summary

I. Basic knowledge in a historical perspective

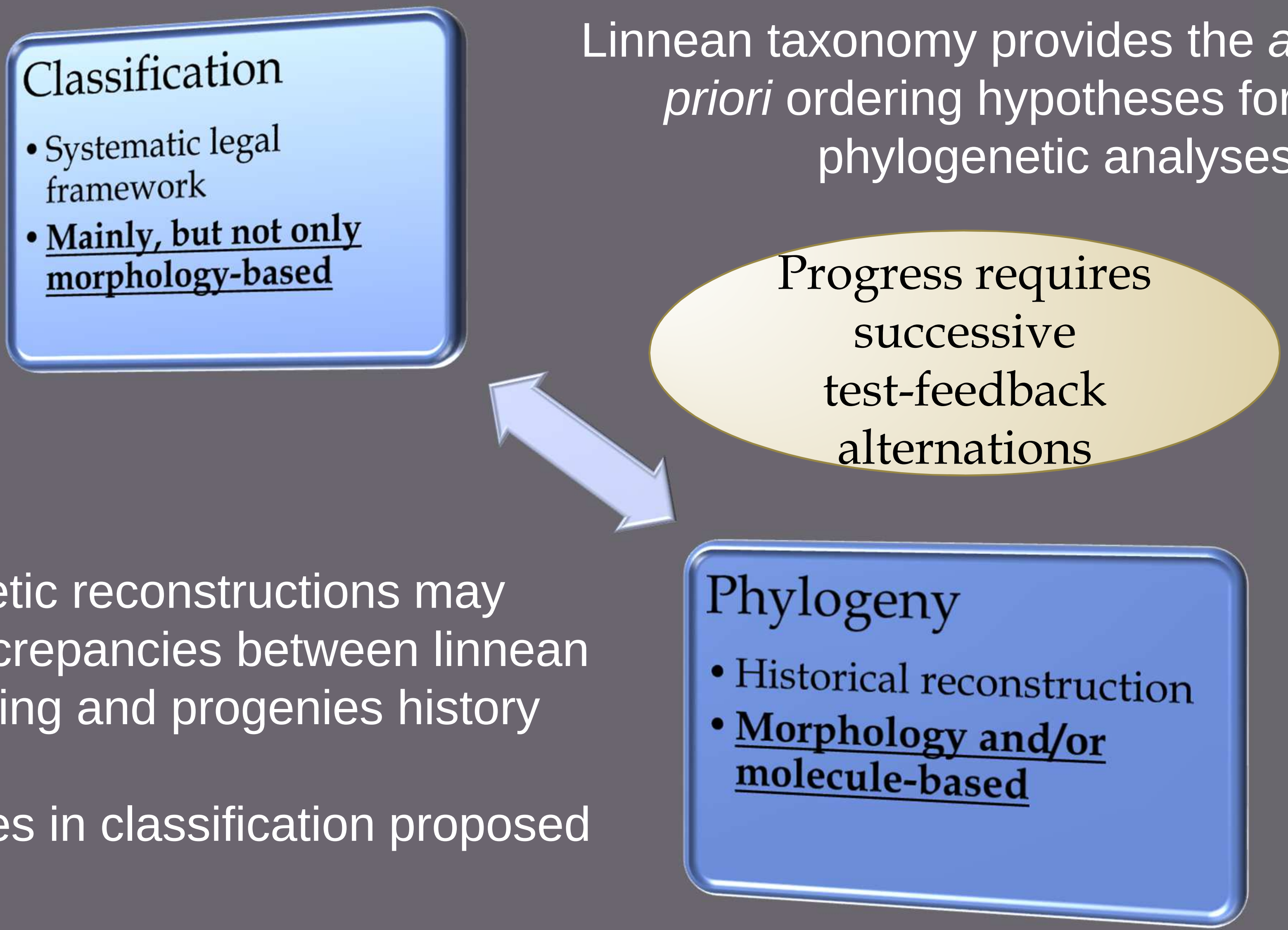
- a) Linnean systematics
- b) Problems with mite taxonomy
- c) The phylogenetic approach

II. How are phylogenetics and traditional taxonomy working together?

Objectives

- Clearing up the confusion between legislative part of taxonomy and natural groups / classification consistency
- Identifying the effective contributions of molecular biology
- Understanding how crucial the confrontation of different lines of evidence is (nothing all right, DNA brings complimentary information, never all information)

How do phylogenetic works interact with linnean systematics?



Classification

- Systematic legal framework
- **Mainly, but not only morphology-based**

Linnean taxonomy provides the *a priori* ordering hypotheses for phylogenetic analyses

Progress requires successive test-feedback alternations

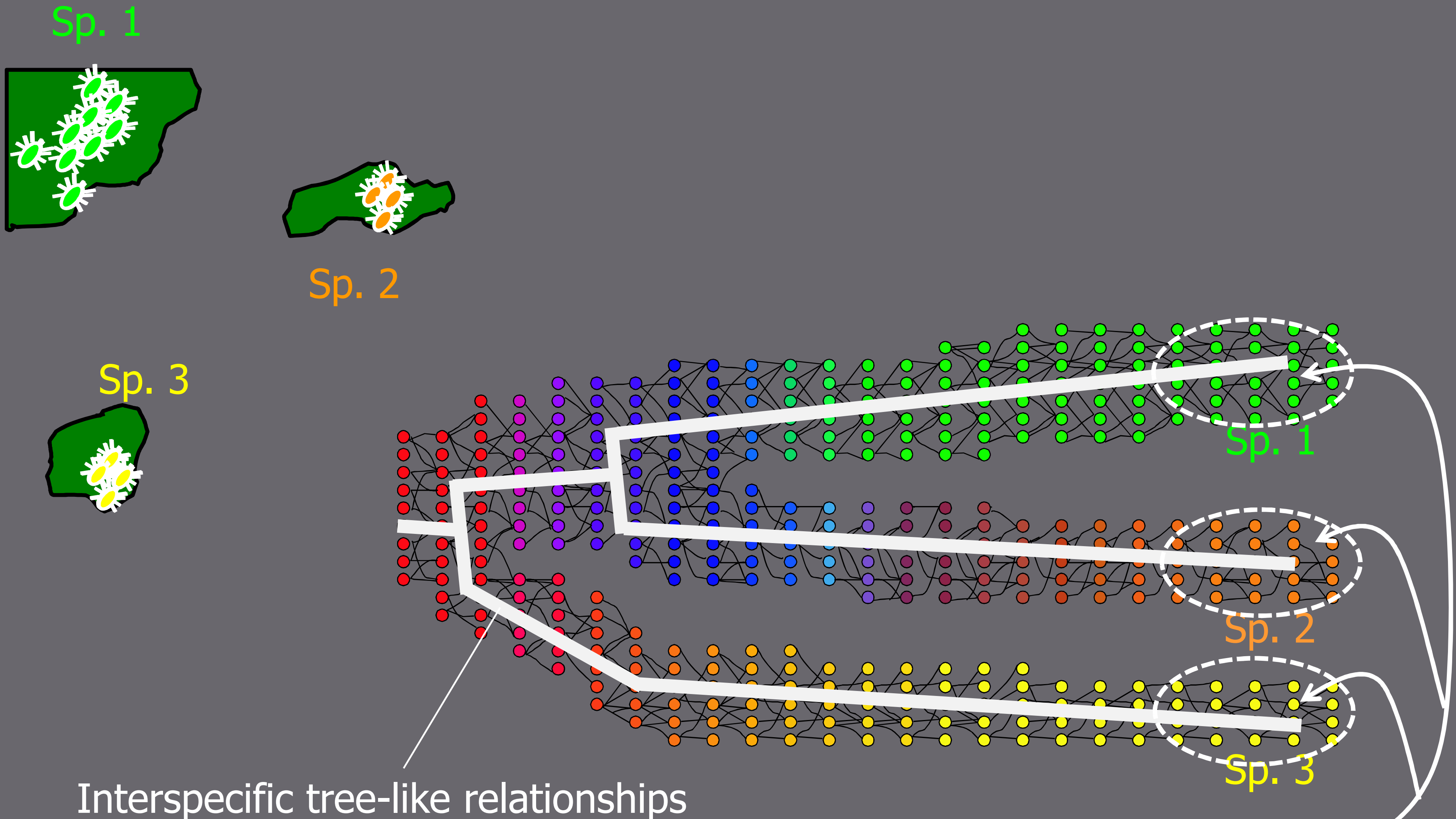
Phylogeny

- Historical reconstruction
- **Morphology and/or molecule-based**

Phylogenetic reconstructions may reveal discrepancies between linnean taxa ordering and progenies history

→ Changes in classification proposed

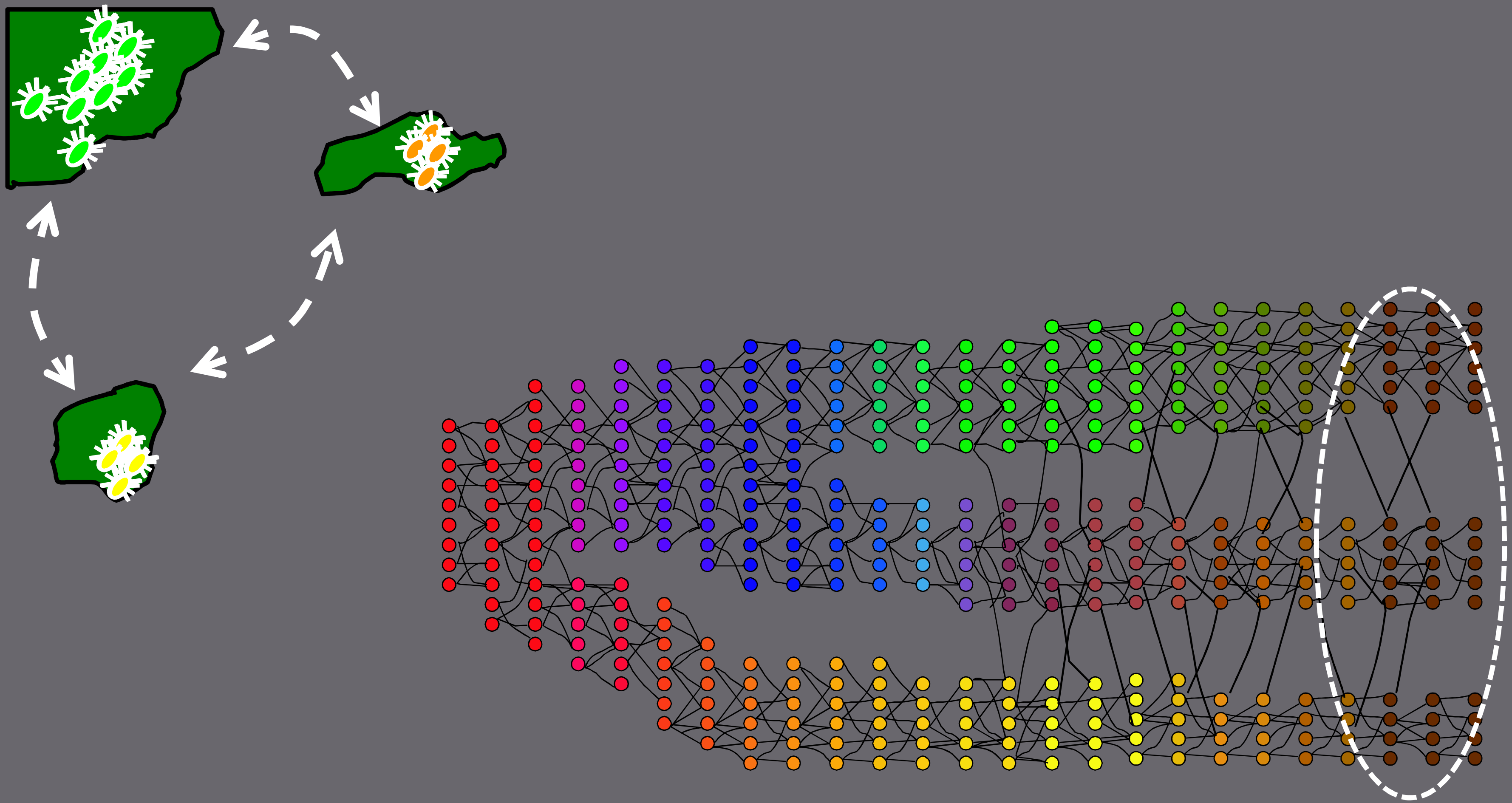
/!\ Differentiate between interspecific and intraspecific relationships



Interspecific tree-like relationships

Intraspecific network
(interconnected genealogy-like trees)

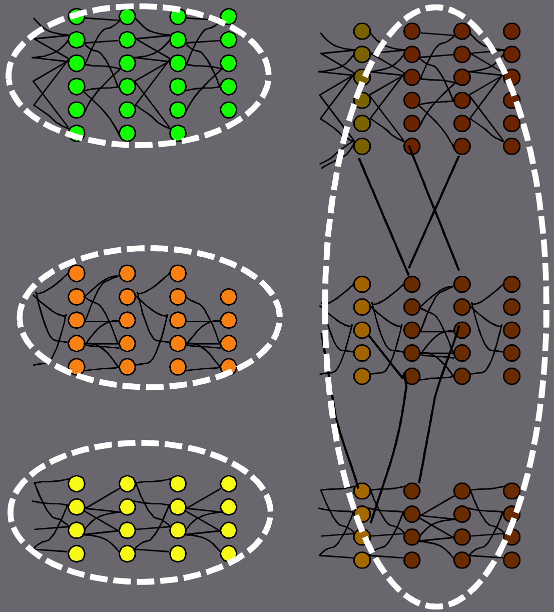
/!\ Differentiate between interspecific and intraspecific relationships



Intraspecific network
(interconnected genealogy-like trees)

Intraspecific structure

Within network studies require population genetics tools rather than phylogenetics *sensu stricto*



Various statistics tools that must be applied to rather large samples (>20 individuals per isolate)

→ based on allelic and/or genotypic frequencies, eventually alleles' relationships estimates via coalescent models…

Objectives: tracing spread routes, testing for bottleneck events and the effect of some given selective pressure …

⇨ out of scope in the present training school

What are we talking about when dealing with classification?

Interspecific relationships: tree-like organisation

/!\ REMINDER:
NOT TO BE CONFUSED TO EACH ANOTHER:

Today:

- **Concept**: evolutionist
- **Criteria:** diverse (increasing use of relatedness as estimated using phylogenetic tools, but simple comparaison still in use)
- **Nomenclature:** based on Linnaeus' system

What are we talking about when dealing with classification?

- *Just nominalism*

Essentialism

- *The diverse species are differing between each another in essence*
- *Concept = nature in made of distinct, discontinuous things*
- → ***fixist concept***

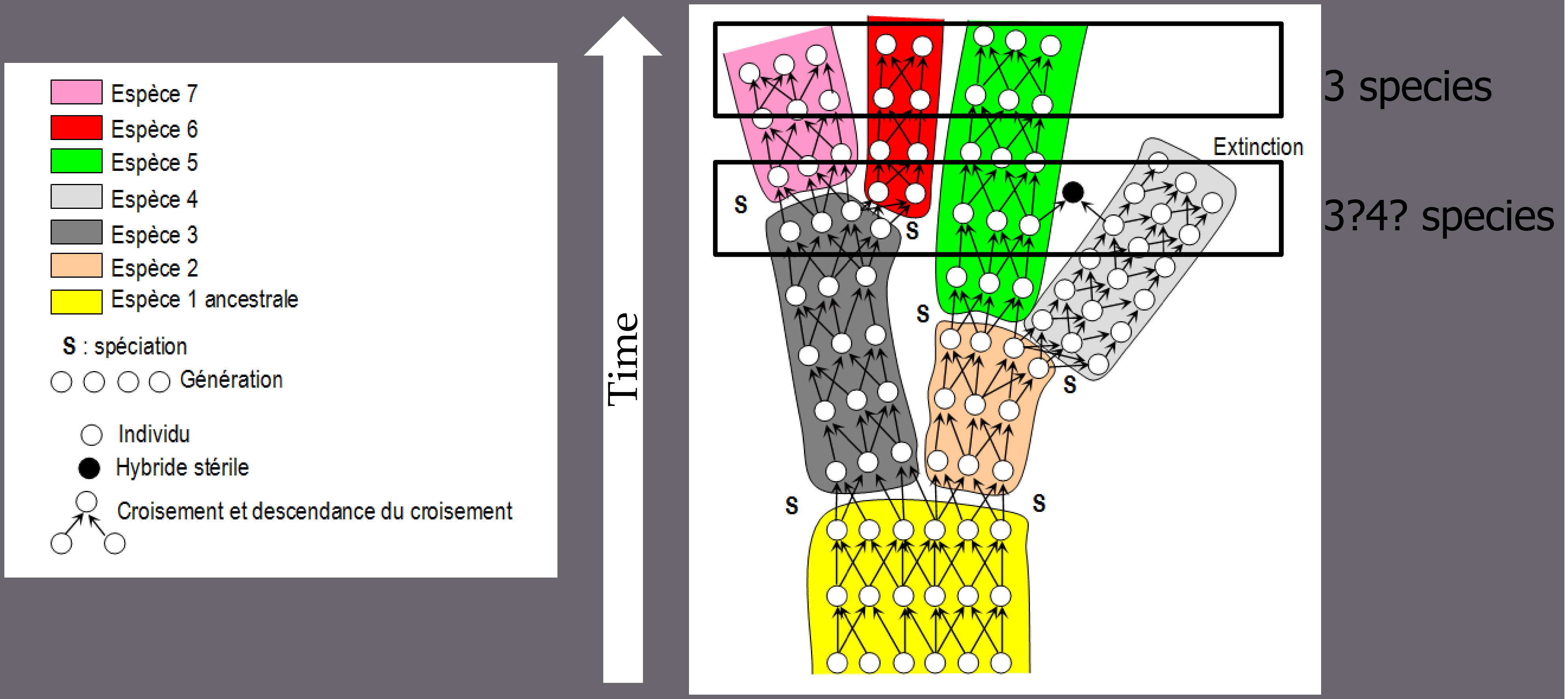
Nominalism

- Categories are nothing more than abstract constructs amongst the huge continuum of nature
- Concept: species = the product of a continuous evolution

⇨ no perfect classification
⇨ more of a trade-off

Putting populations into species boxes

- Species delineation is inherently dependent of time … yet we only access to current populations

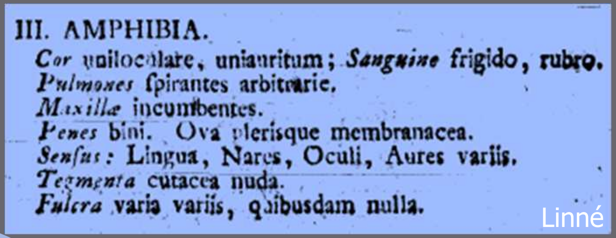


Don’t underestimate traditional taxonomic works!

- Classification based on strict comparisons often did generate good hypotheses:
  - Often (not always), the degree of relatedness is consistent with the category definition provided by traditional taxonomists
  - Many traditional taxonomists are very good observers and detect finest morphological common points
    - Huge, skill- and time-consuming work

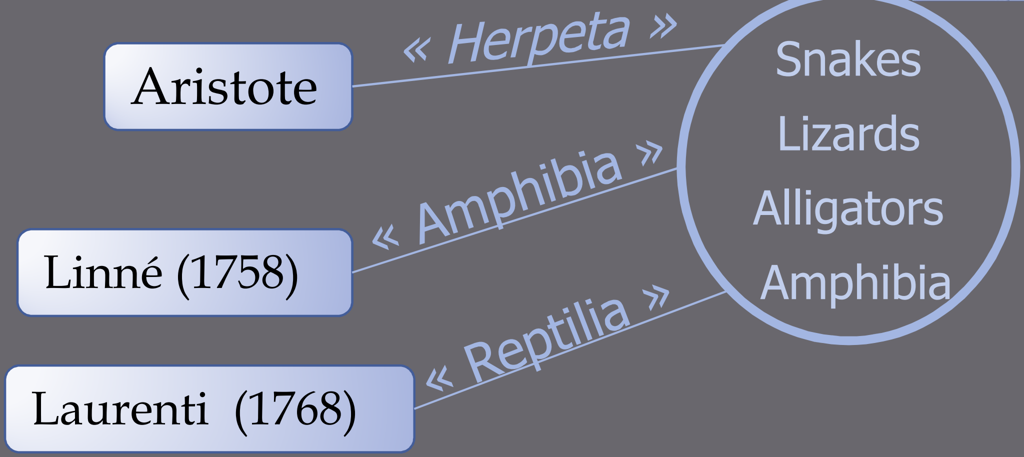
Don’t underestimate traditional taxonomic works!

- A example with ”reptiles”



III. AMPHIBIA.
Cor uniloculare, uniauritum; *Sanguine* frigido, rubro.
Pulmones ſpirantes arbitrarie.
Maxillæ incumbentes.
Penes bini. Ova plerisque membranacea.
Senſus: Lingua, Nares, Oculi, Aures variis.
Tegmenta coriacea nuda.
Fulcra varia variis, quibusdam nulla.

Linné



Aristote

« Herpeta »

Linné (1758)

« Amphibia »

Laurenti (1768)

« Reptilia »

Snakes
Lizards
Alligators
Amphibia

Don’t underestimate traditional taxonomic works!

- A example with ”reptiles”

Aristote

« Herpeta »

Linné (1758)

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Laurenti (1768)

« Reptilia »

Brongniart (1799)

« Reptilia »

Snakes

Lizards

Alligators

~~Amphibia~~

Turtles

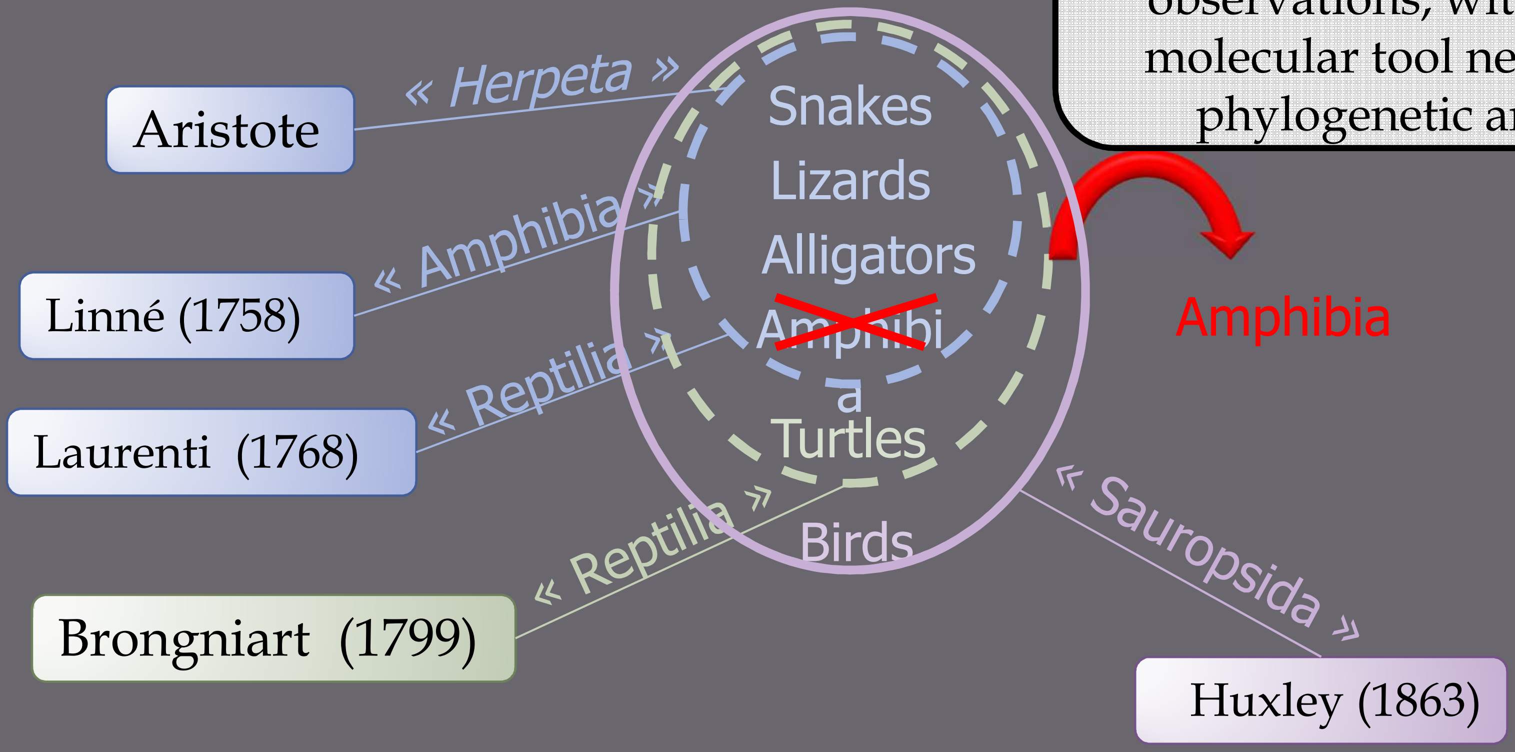
Latreille (1825)

Reptilia ≠ Amphibia

Don’t underestimate traditional taxonomic works!

- A example with ”reptiles”

All these groupings were proposed based on direct morpho-anatomic observations, without any molecular tool neither any phylogenetic analysis



Aristote
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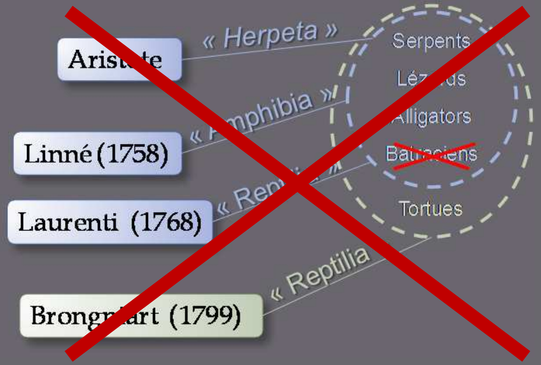
Snakes
Lizards
Alligators
~~Amphibia~~
Turtles
Birds

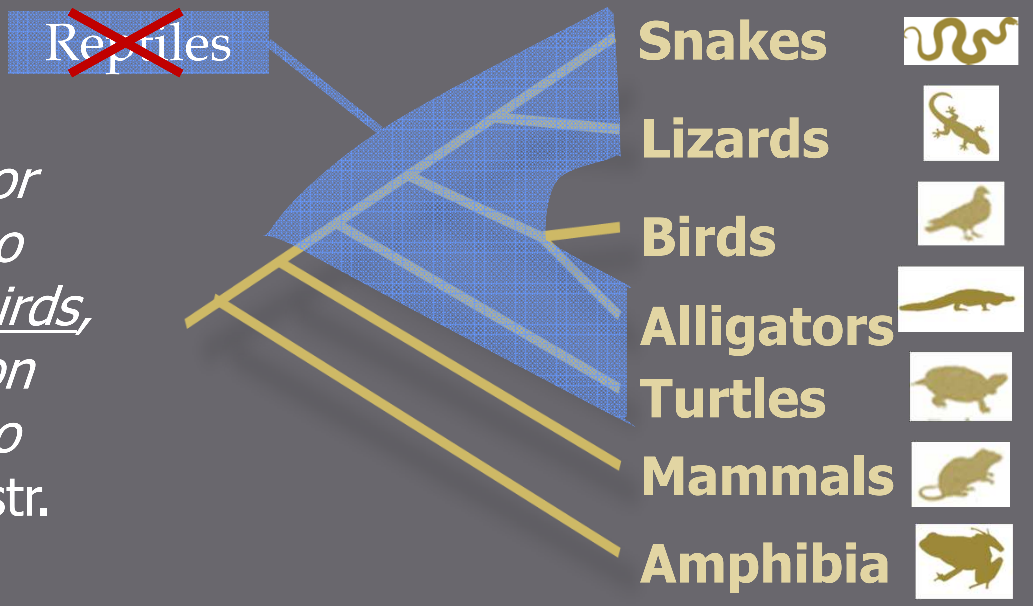
« Sauropsida »
Huxley (1863)

Amphibia

Don't underestimate traditional taxonomic works!

- A example with "reptiles"





~~Reptiles~~

Snakes

Lizards

Birds

Alligators

Turtles

Mammals

Amphibia

An ancestor common to <u>reptiles+birds</u>, no common ancestor to reptiles s.str.

XXe century

Phylogenetic analysis

Morphological characters + DNA

Don’t underestimate traditional taxonomic works!

- A example with ”reptiles”


Serpents
Lézards
Alligators
Tortues
Oiseaux
« Sauropsida »
Huxley (1863)


Huxley’s Sauropsida do have a common ancestor

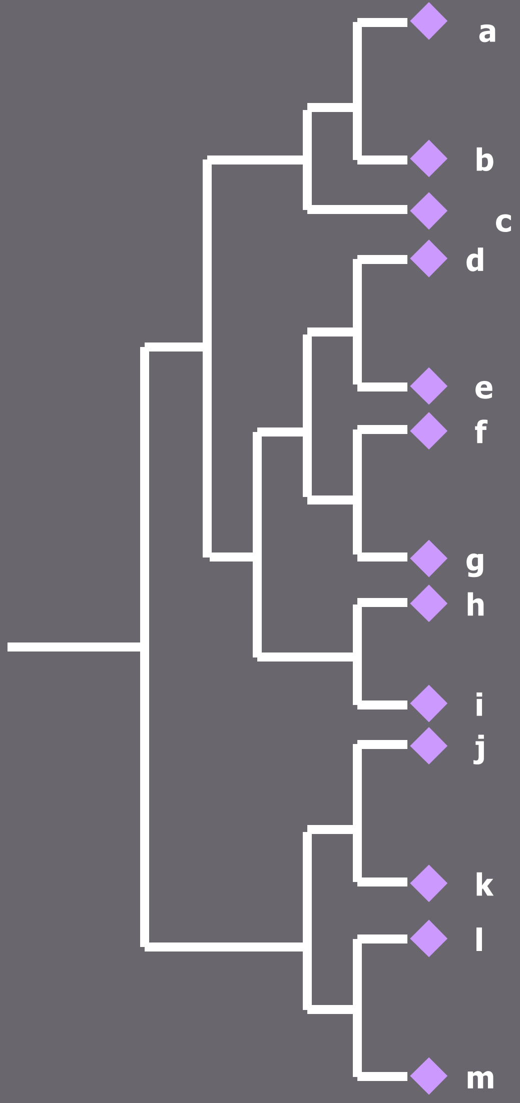
Snakes
Lizards
Birds
Alligators
Turtles
Mammals
Amphibia

Phylogenetic analysis

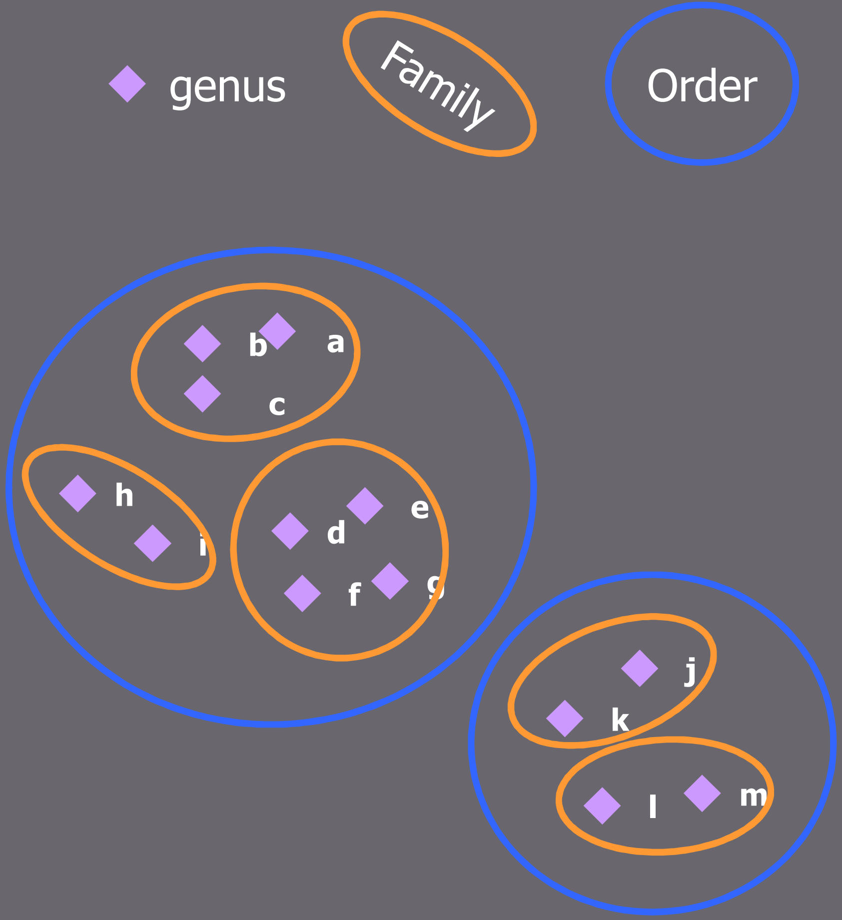
Morphological characters + DNA

Confirmation of Huxley’s proposal by phylogenetic studies

Supra-specific levels not evident on phylogenetic tree

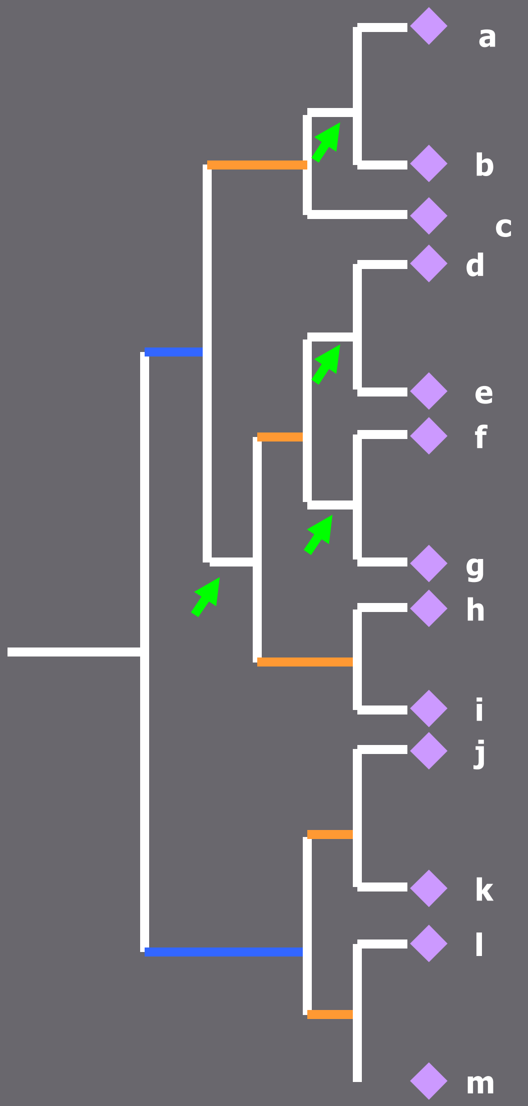


Phylogenetic relationships

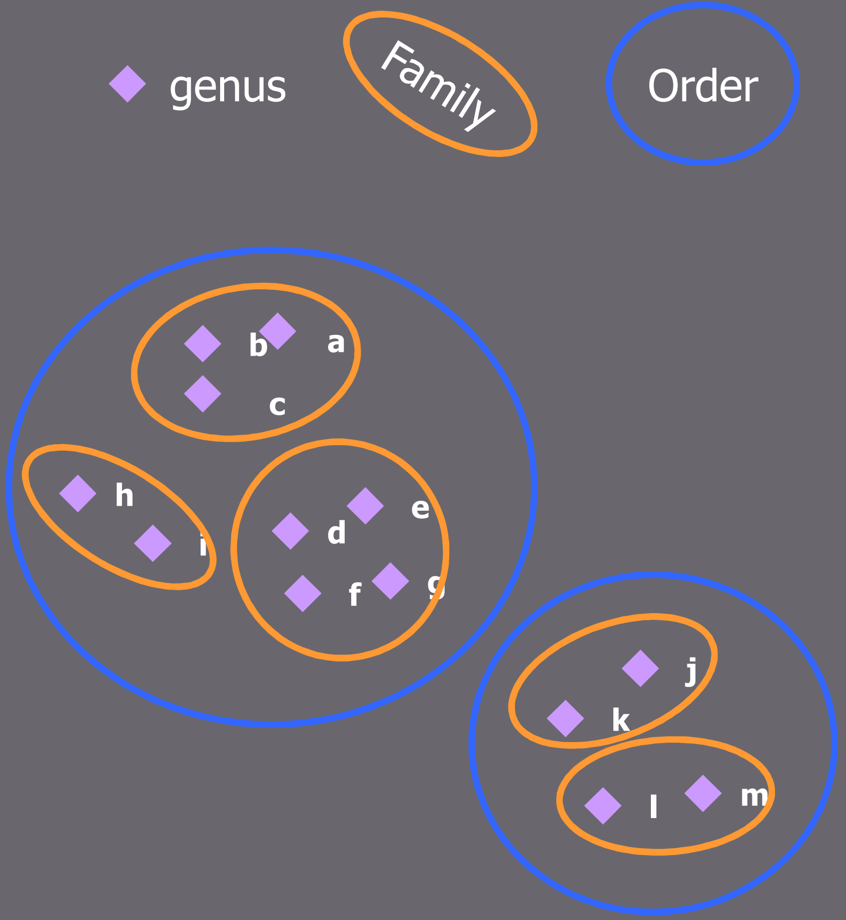


Linnean classification

Supra-specific levels not evident on phylogenetic tree



Phylogenetic relationships



Linnean classification

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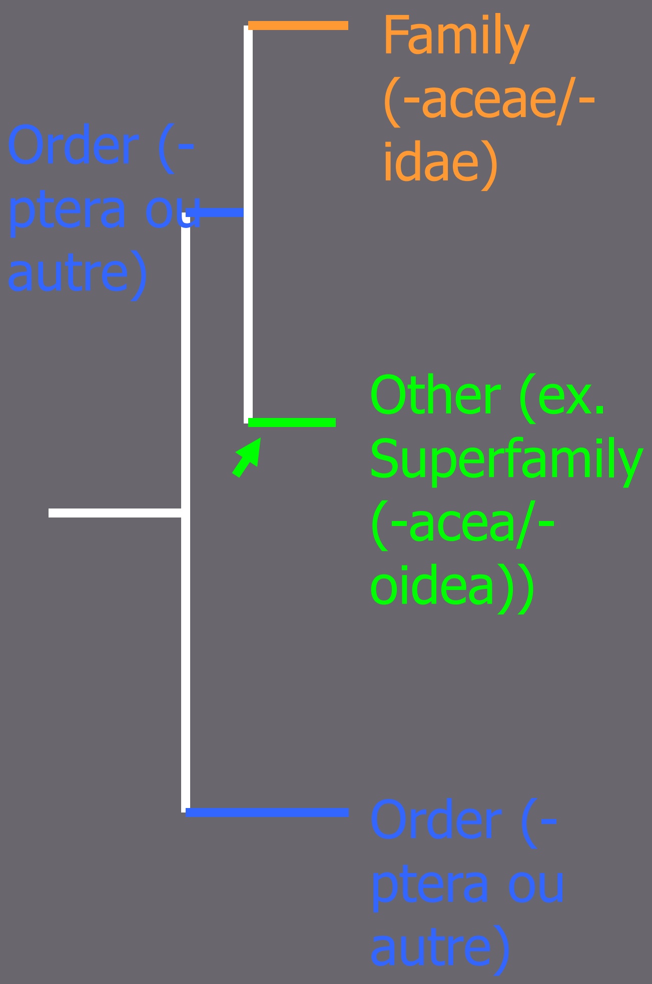
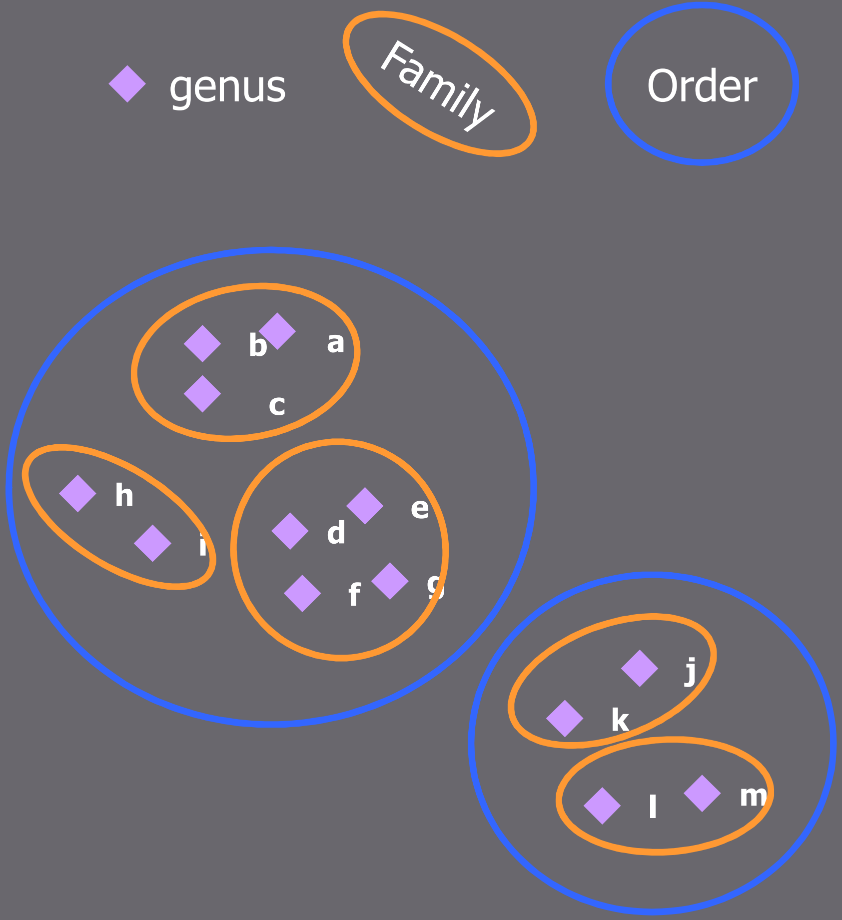


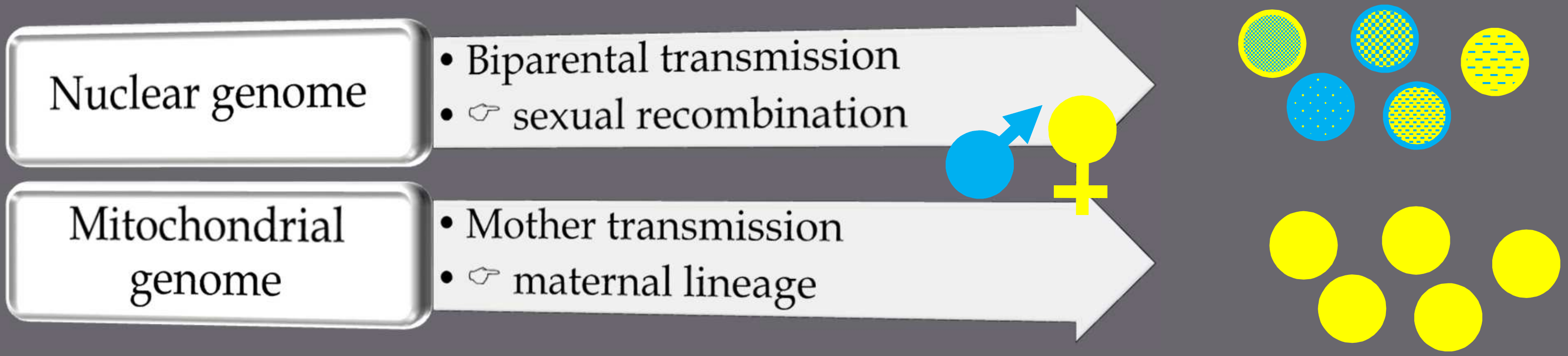
Phylogenetic relationships



Linnean classification

/!\ Warning!
Getting a tree is not a result in itself

- Any gene region allows getting a tree
  - Individual gene tree ≠ species tree
  - Evolution of a locus, not of the populations
- Network-like structure detected using different tools
  - Confrontation between several gene trees

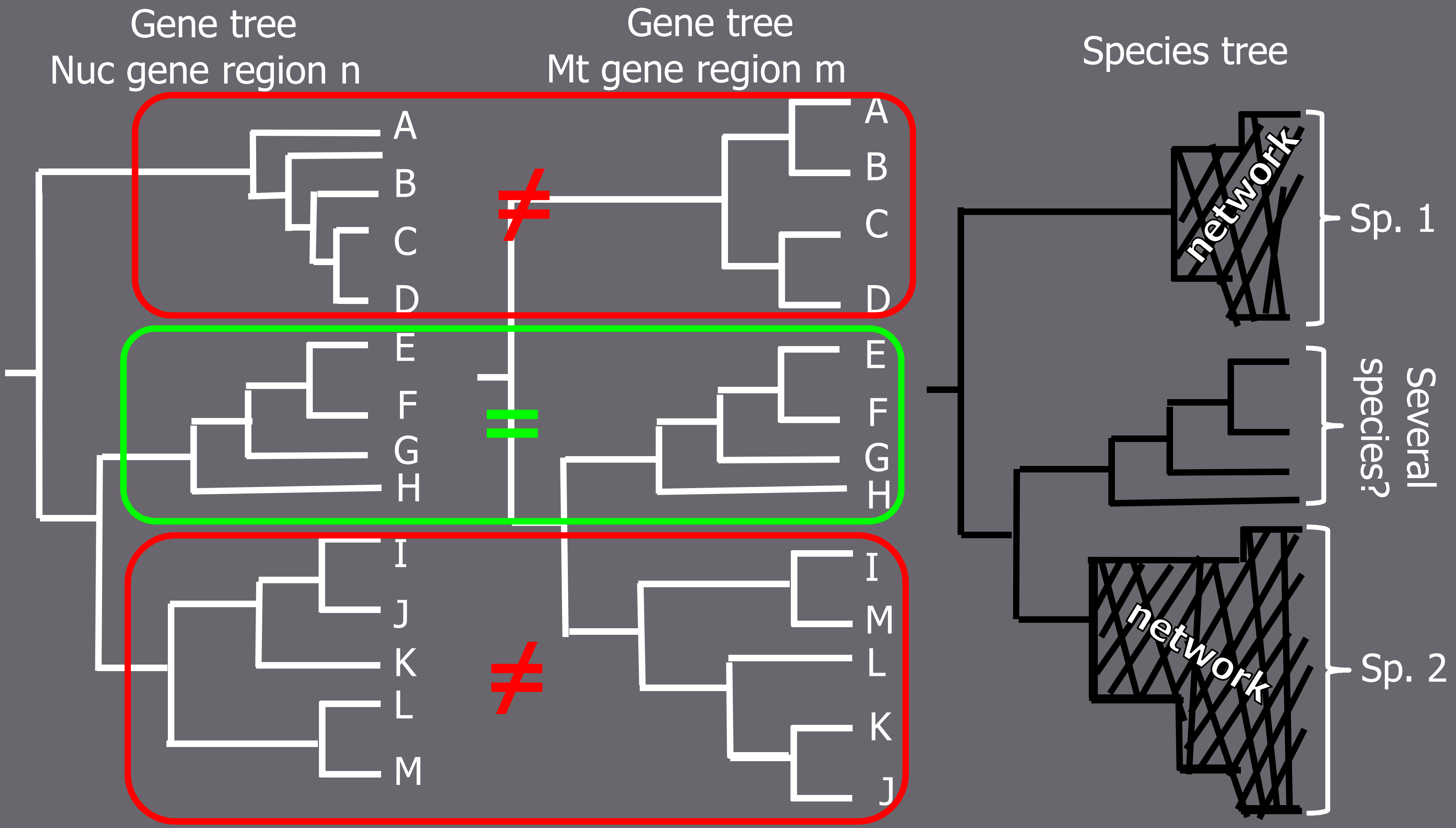


Nuclear genome
- Biparental transmission
- ☞ sexual recombination

Mitochondrial genome
- Mother transmission
- ☞ maternal lineage

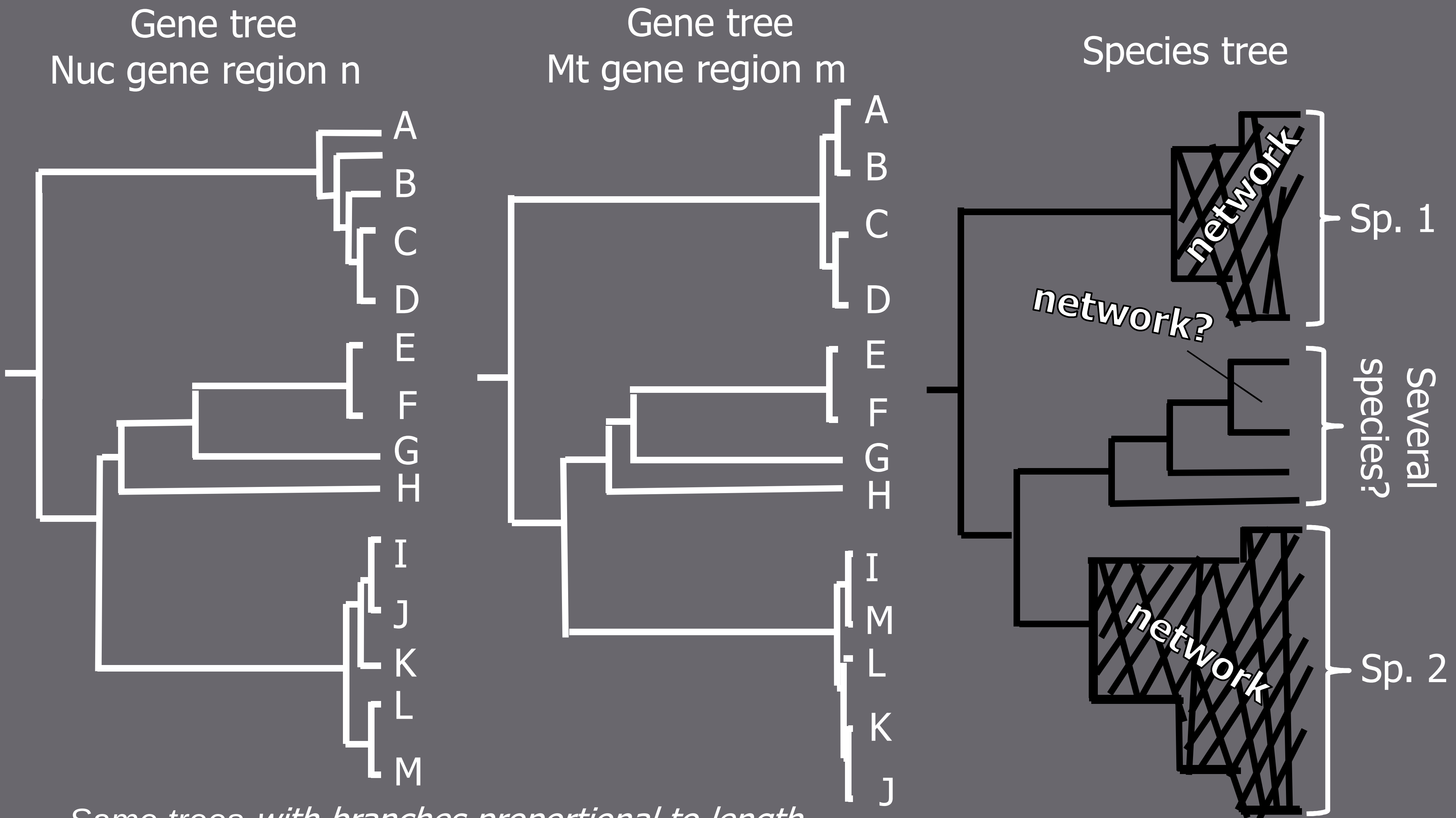
  - Population genetics analyses (statistics)

Confrontation nuclear vs mitochondrial DNA



Intra-distal clade incongruence → network

Confrontation nuclear vs mitochondrial DNA

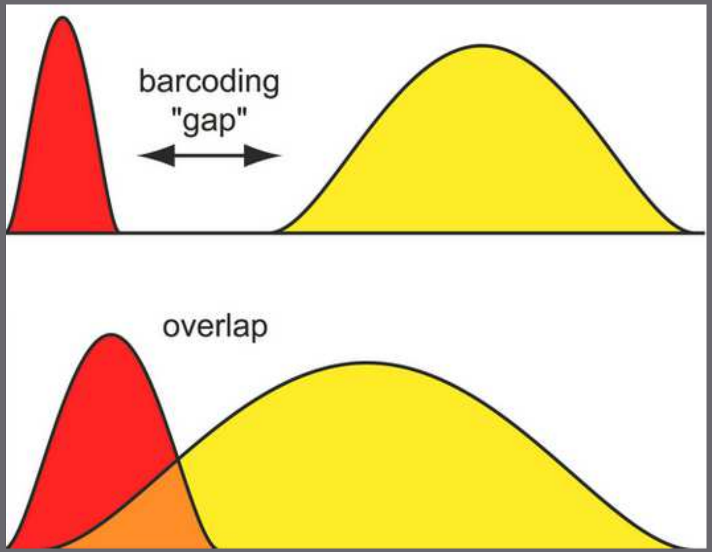


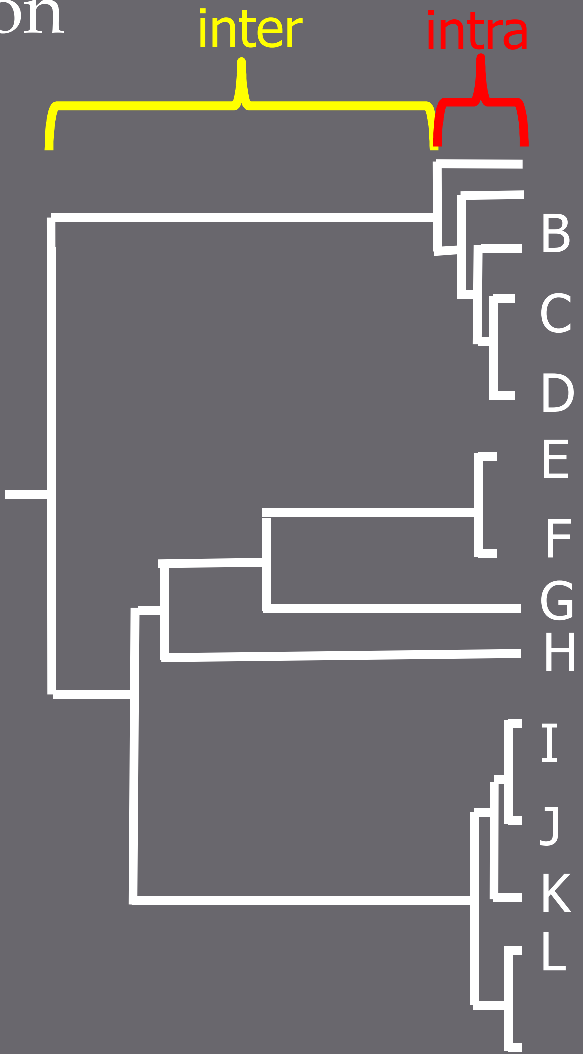
Same trees with branches proportional to length
(amount of character change)

⇘ relative branch lengths bring information

Nucleotidic variability very different from one gene to another one

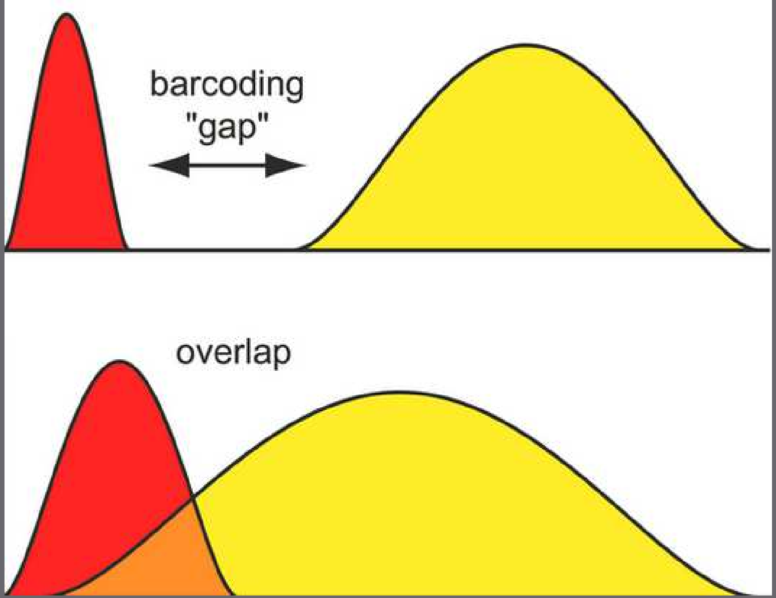
- Interspecific delineation require enough interspecific and not too much intraspecific variation
  - Barcoding “gap”
  - Mt Co1 = a good candidate with most Metazoa





Nucleotidic variability very different from one gene to another one

- Interrelationships between higher-level taxa require less fast evolving genes
  - If too much fast evolving → homoplasies due to saturation (reverse mutations consecutive to multiple changes with only 4 possibilities A-C-T-G)
  - Mt Co1: usually basal interrelationship unresolved or wrong



Different variability-levels makes generalisation of diagnostic characters difficult

- Instraspecific molecular and morphological variability not equivalent in each group of species

→ traditional characters as mostly applied to large mite groups may be misleading

Some characters may be informative in the one species group not in the other one
→ need for new characters – phylogeny may help

Example with genus *Dermanyssus*

- High intraspecific variation in leg chaetotaxy among Mesostigmatid parasitic mites (Evans 1963)
- Highest morphological variability within *Dermanyssus* (Moss 1978)

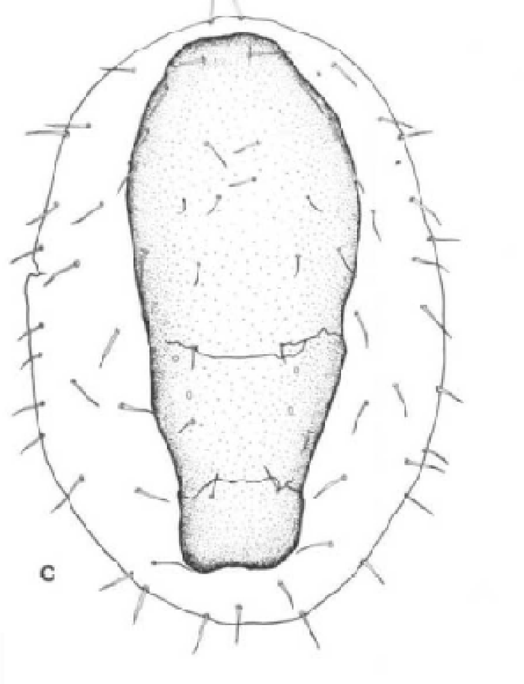
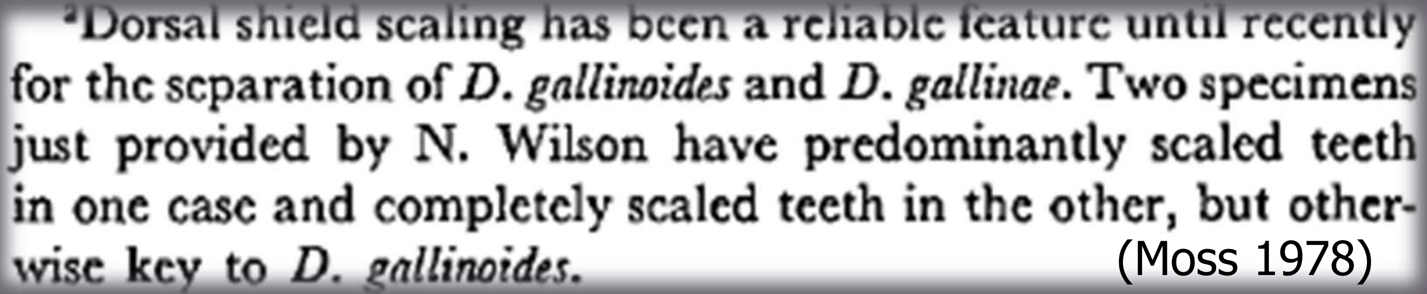
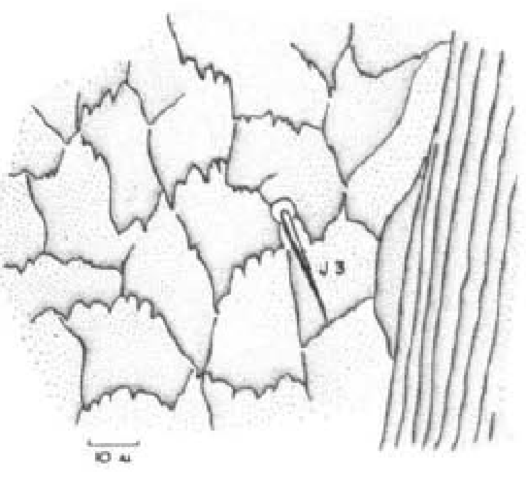


FIG. 5. *Dermanyssus faralloni* Nelson & Furman, shield scaling; D, ventral view. dha=dorsal hexag



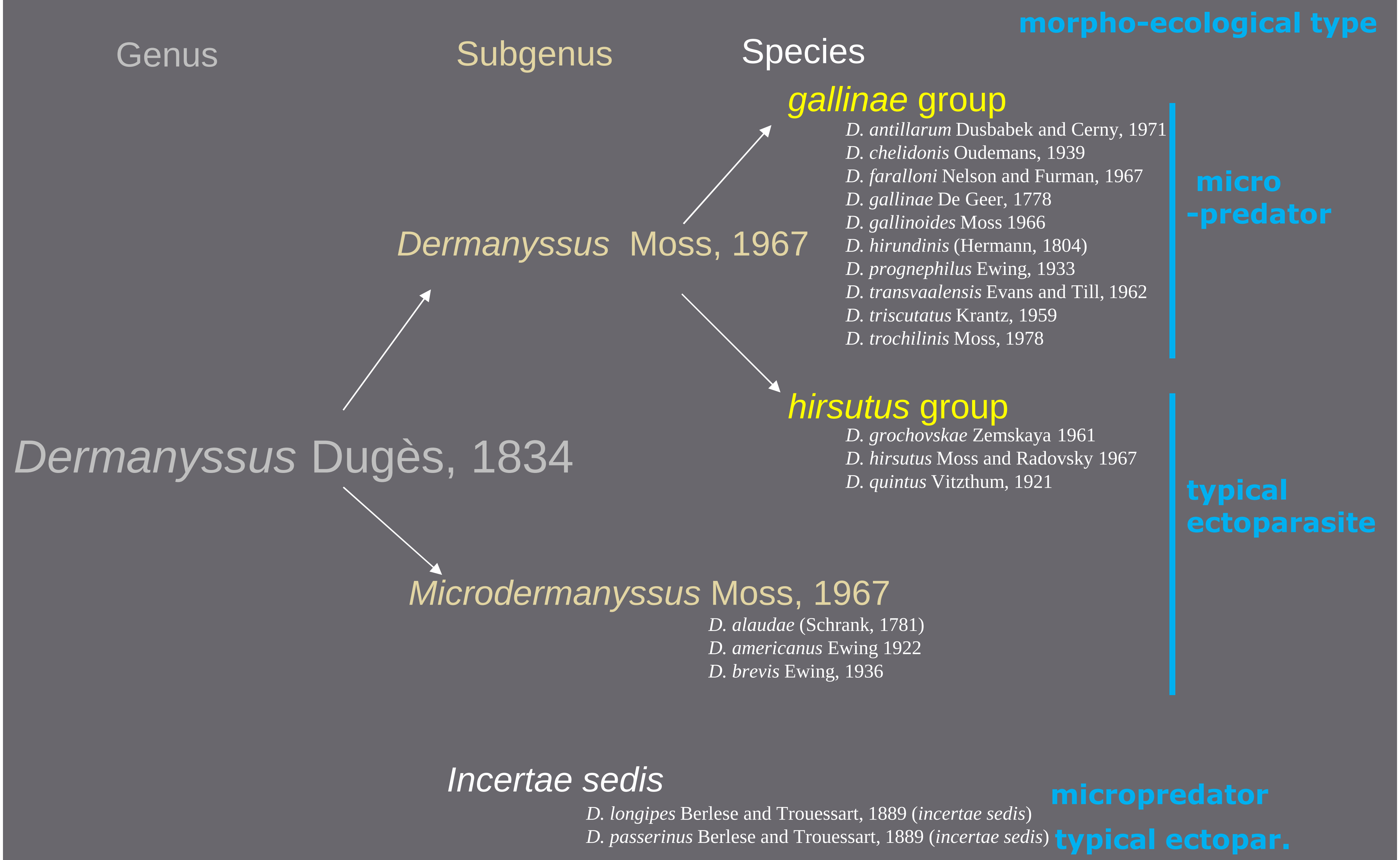
[a]Dorsal shield scaling has been a reliable feature until recently for the separation of *D. gallinoides* and *D. gallinae*. Two specimens just provided by N. Wilson have predominantly scaled teeth in one case and completely scaled teeth in the other, but otherwise key to *D. gallinoides*.

(Moss 1978)



Evans G.O., 1963. Ann. Mag. Nat. Hist. 13, 513–527
Moss W.W., 1978. J. Med. Entomol. 14, 627–640

Composition of Dermanyssus sensu Moss 1978



morpho-ecological type

Genus

Subgenus

Species

gallinae group

D. antillarum Dusbabek and Cerny, 1971
D. chelidonis Oudemans, 1939
D. faralloni Nelson and Furman, 1967
D. gallinae De Geer, 1778
D. gallinoides Moss 1966
D. hirundinis (Hermann, 1804)
D. prognephilus Ewing, 1933
D. transvaalensis Evans and Till, 1962
D. triscutatus Krantz, 1959
D. trochilinis Moss, 1978

micro -predator

Dermanyssus Moss, 1967

hirsutus group

D. grochovskae Zemskaya 1961
D. hirsutus Moss and Radovsky 1967
D. quintus Vitzthum, 1921

Dermanyssus Dugès, 1834

typical ectoparasite

Microdermanyssus Moss, 1967

D. alaudae (Schrank, 1781)
D. americanus Ewing 1922
D. brevis Ewing, 1936

Incertae sedis

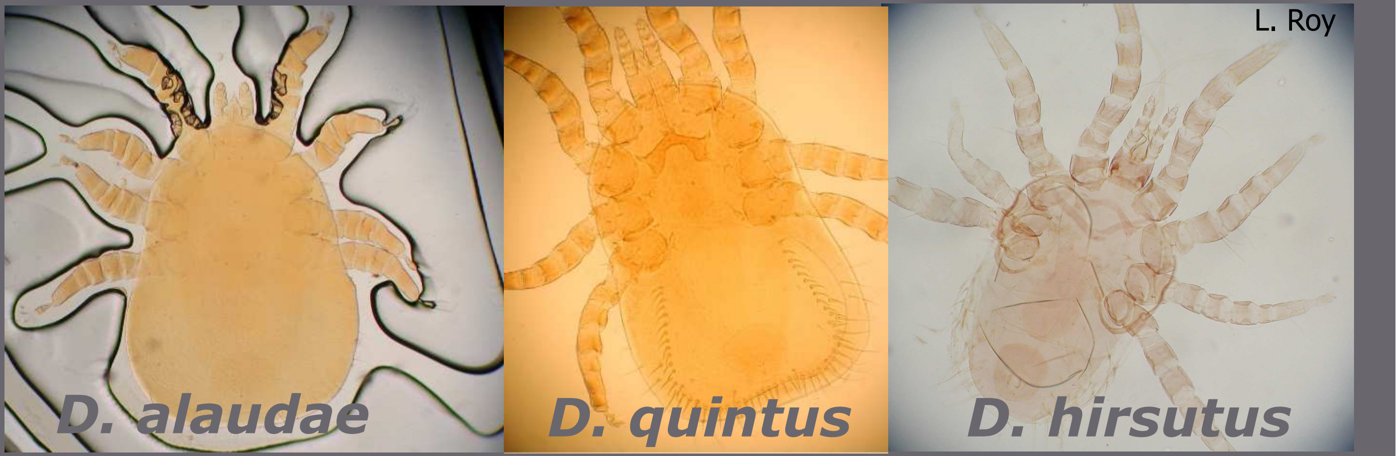
D. longipes Berlese and Trouessart, 1889 (*incertae sedis*) **micropredator**
D. passerinus Berlese and Trouessart, 1889 (*incertae sedis*) **typical ectopar.**

Fuzzy morphology in micropredators

Typical ectoparasites

9 species

Sharply characterized from each another

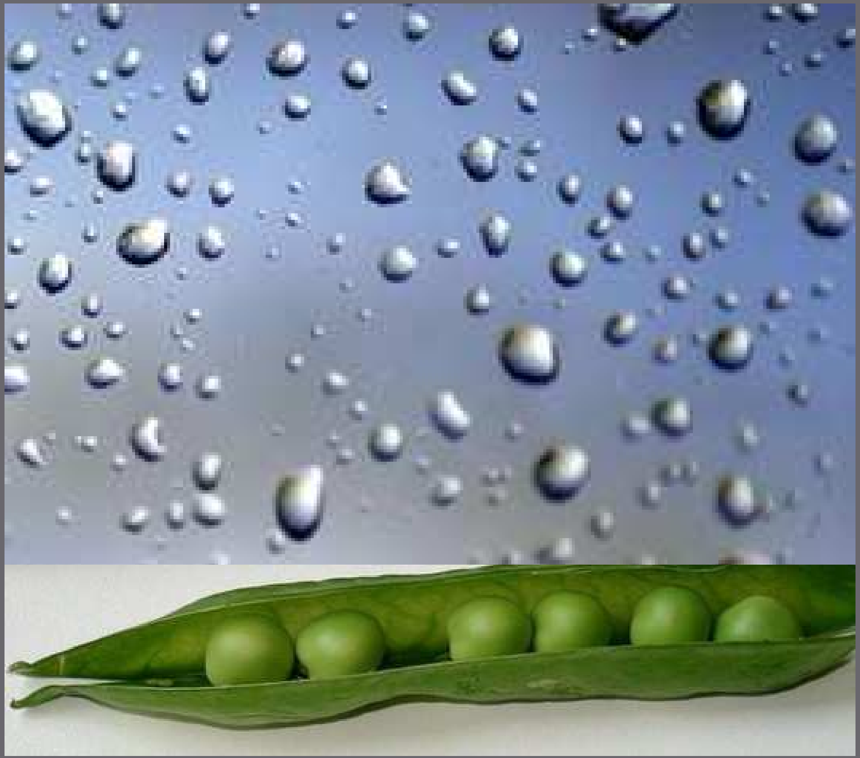


Micropredators

14 species

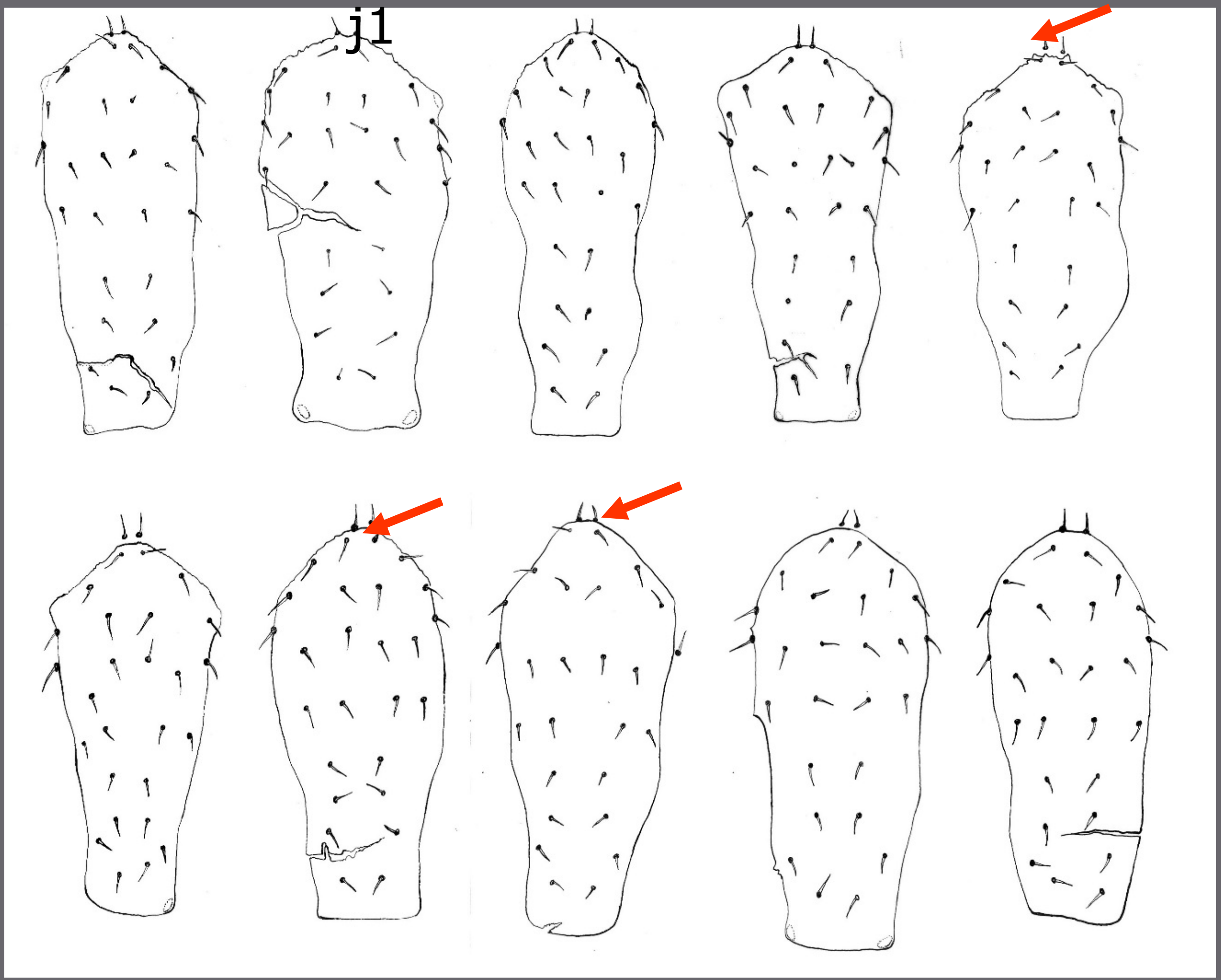
➔ High inter-individual variability within populations of a single sp.
➔ Overlap between species

Two micropredator species are as alike as two peas in a pod…



Example with genus *Dermanyssus*

- Traditionally used characters weakly informative for specific diagnostics

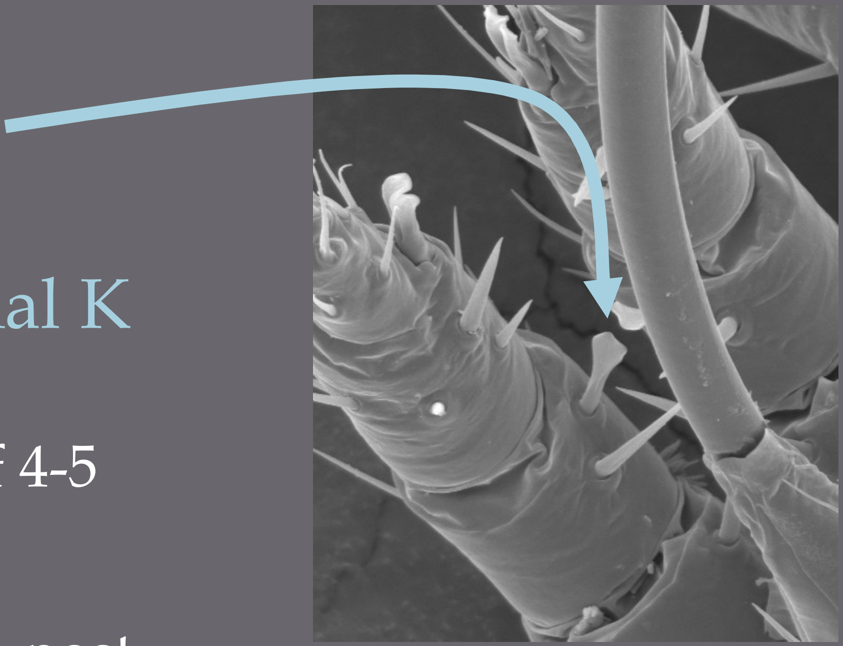


E.g. Dorsal shields of 10 among 20 randomly selected adult females in a single isolate of *D. gallinae* cultured at lab

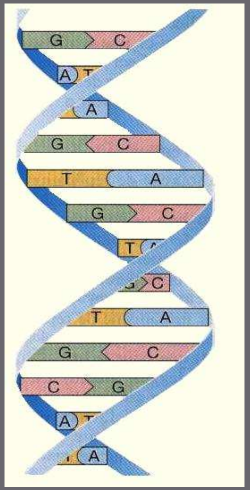
L. Roy, ICA 2006

« New » or re-encoded characters

- 1 new K in Moss (1968)
  - shape of the *al1* seta of palp genu
- Re-encoding of certain traditionnal K
  - ex: relative length of the peritrema / stigmate diameter, 2 states instead of 4-5
- Several additional new K
  - ex: shape of the principal pore on the post-stigmatic element



- DNA sequences
  - mitochondrial 16S rRNA, Co1
  - nuclear ITS1+2, EF-1α, Tropomyosin



Some taxonomic novelties from LR PhD

Genus

Species

morpho-ecological type

A species complex to be further explored ←

D. antillarum Dusbabek and Cerny, 1971
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D. triscutatus Krantz, 1959
D. trochilinis Moss, 1978
D. wutaiensis Gu and Ting, 1992
D. nipponensis Uchikawa and Kitaoka, 1981
D. carpathicus Zeman, 1979
D. longipes Berlese and Trouessart, 1889
D. apodis Roy, Dowling, Chauve & Buronfosse, 2009

Micro -predator

Dermanyssus Dugès, 1834

Intra-genus phylogenetic patterns consistent with morpho-ecological types, not with previous subgenera

D. grochovskae Zemskaya 1961
D. hirsutus Moss and Radovsky 1967
D. quintus Vitzthum, 1921
D. brevirivulus Gu and Ting, 1992
D. rwandae Fain, 1993
D. alaudae (Schrank, 1781)
D. americanus Ewing 1922
D. brevis Ewing, 1936

Typical ectopar.

D. diphyes Knee, 2008

?

Nomen dubium

D. passerinus Berlese and Trouessart,
1889 (*incertae sedis*)

Micropredator

Take home message

- DNA sequence alignments are much easier to be analyzed than morphology
  - Morphological skills require time to be developed, as opposed to molecular biology
  - Molecular tools fast and easy to be used ≠ morphological analyses time-consuming

- Correct species delineation requires confrontation of several lines of evidence
  - Morphology alone or single DNA sequence alone insufficient
  - Better coupling morphological analyses, molecular phylogenetics and ecological information (habitat, host spectrum)

Time-consuming & expensive