LARGE SCALE SPECIES DELIMITATION METHOD FOR HYPERDIVERSE GROUPS

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Species delimitation: the easy way

Most species already known, characters and criteria congruent

\[\text{intra-interspecific limit deduced from the other species}\]
Problem I: "The grey zone"

- The characters do not differentiate at the same rhythm
- All the criteria will not lead to the same species hypotheses

Species = hypotheses validated or rejected with the addition of new data:

- Criteria: Similarity, Biological (direct and indirect), Phylogenetic
- Characters: DNA, Morphology, Ecology, Geography...
- Methods: Cross tests, Morphospecies, Trees/networks, Genetic structure, Distances
Problem II: Hyperdiverse and largely unknown groups

Conoidea

4,000 described species, probably more than 15,000
Problem II: Hyperdiverse and largely unknown groups

Lophiotoma acuta

Turris garnonsii
Problem III: The shell

- Convergence
- Phenotypic plasticity

Puillandre et al. 2010 Syst. & Biodiv.
Problem I: "The grey zone"
Problem II: Hyperdiverse and largely unknown groups
Problem III: The shell

How to propose species hypotheses in this context?

DNA sequences
Exploratory method (without a priori hypotheses)
A new method based only on DNA sequences:

ABGD, Automatic Barcode Gap Discovery
Prior threshold $p$

$\downarrow$

Estimated $\theta$

$\downarrow$

Look for "next peak"

$\downarrow$

Posterior threshold $P$

$\downarrow$

N groups

$\downarrow$

Final partition

Recursive approach

# of groups

http://wwwabi.snv.jussieu.fr/public/abgd

Application to the Turridae

- Sequencing of the COI gene (Barcode fragment)
- Analysis with ABGD and GMYC (Pons et al. 2006)
ABGD
GMYC

85-103 PSH

Phylogeny COI
Phylogeny 28S
Genetic structure
Bathymetry
Locality
Morphology

87 SSH

PSH = Primary Species Hypotheses
SSH = Secondary Species Hypotheses

INTEGRATIVE TAXONOMY
Application to the Turridae
ABGD, for hyperdiverse and unknown groups: easy, fast and reproducible

But...

- Problems in the grey zone: overlap coalescent/speciation
- Several a priori thresholds can lead to several species partitions

Recursive approach to take into account variation in evolutionary rates

INTEGRATIVE TAXONOMY:
Need to turn Primary Species Hypotheses into Secondary Species Hypotheses
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