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ABSTRACTS

Paper Number: 2462

Evidence for ancestry in taxonomic studies: Lessons from mid-Cretaceous biserial planktonic foraminifera

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The *TimeScale Creator* visualization suite accesses an extensive database to draw a wide range of Earth-history events against standard global and regional time-scale charts. It is the prime vehicle for incorporating updates to the International Geologic Time Scale. An evolutionary-tree function has recently been added to *TimeScale Creator*, allowing trees to be seamlessly scaled against the entire event suite, and to employ built-in visualization features such as continuous zoom to desired levels of precision. Stratigraphic ranges of taxa on the trees can be graded by abundance, color coded by taxonomic or other criteria, and easily recognized by thumbnail images magnified relative to actual size. For each taxon a mouse-over pop-up can display diverse user-chosen text and visuals such as hot-links to external sites, taxonomic information, and labeled images ordered by, e.g., stratigraphic position. This content can be generated from a back-end relational database, which becomes a valuable resource in itself. So, what have been static, stand-alone evolutionary trees, published as text-figures or derived from phylogenetic programs, can become a living resource and knowledge base of evolution and stratigraphy.

As part of the on-going development of the *TimeScale Creator* evolutionary-tree function, a taxonomic study of extraordinarily well-preserved Cenomanian-Coniacian biserial planktic was chosen to assess the relevance of the visualization tool. As the published tree was presented against an up-to-date time scale, conversion to the *TimeScale Creator* could provide only relatively minor overall improvements to the tree. These included: explicit correlation to other zonations relevant to range determinations referred to in the study; automated labeling of origins of genera; and display of entire stratigraphic ranges for taxa extending higher than the scope of the published tree.

The visualization includes several features that provide flexibility for presentation of varying degrees of certainty and access to extra information. Conjectured range extensions are shown to identify stratigraphic intervals that should be targeted for follow-up investigations

of species whose ancestor-descendent relationships are not understood. Mouse-over pop-up windows provide quick access to more nuanced stratigraphic information, including detailed comments and references to the relevant literature. Illustrated specimens are displayed in order of location and stratigraphic level within their species pop-up, providing a powerful illustration of infra-specific variation observed up-section. Also, thumbnail images selected for the tree can be magnified relative to actual size; given that size was an important element of the evolution of lineages in this group, this providing a much more pertinent means of display for the tree.

Categorization of the evidence for the ancestor–descendant proposals in the visualized tree provided added insights into the published study’s reconstruction of phylogeny. Of more general significance, such an approach could prove to be the beginnings of a template for standard documentation in taxonomic studies employing stratophenetic methods and encourage their incorporation into project planning. Given that e.g. cladistic approaches to phylogeny provide a highly explicit approach to presentation and analysis of evidence, the raising of this issue could prove timely for contemporary biostratigraphic studies wanting to employ stratophenetic approaches.



Evidence for ancestry in taxonomic studies: Lessons from mid-Cretaceous biserial planktic foraminifera

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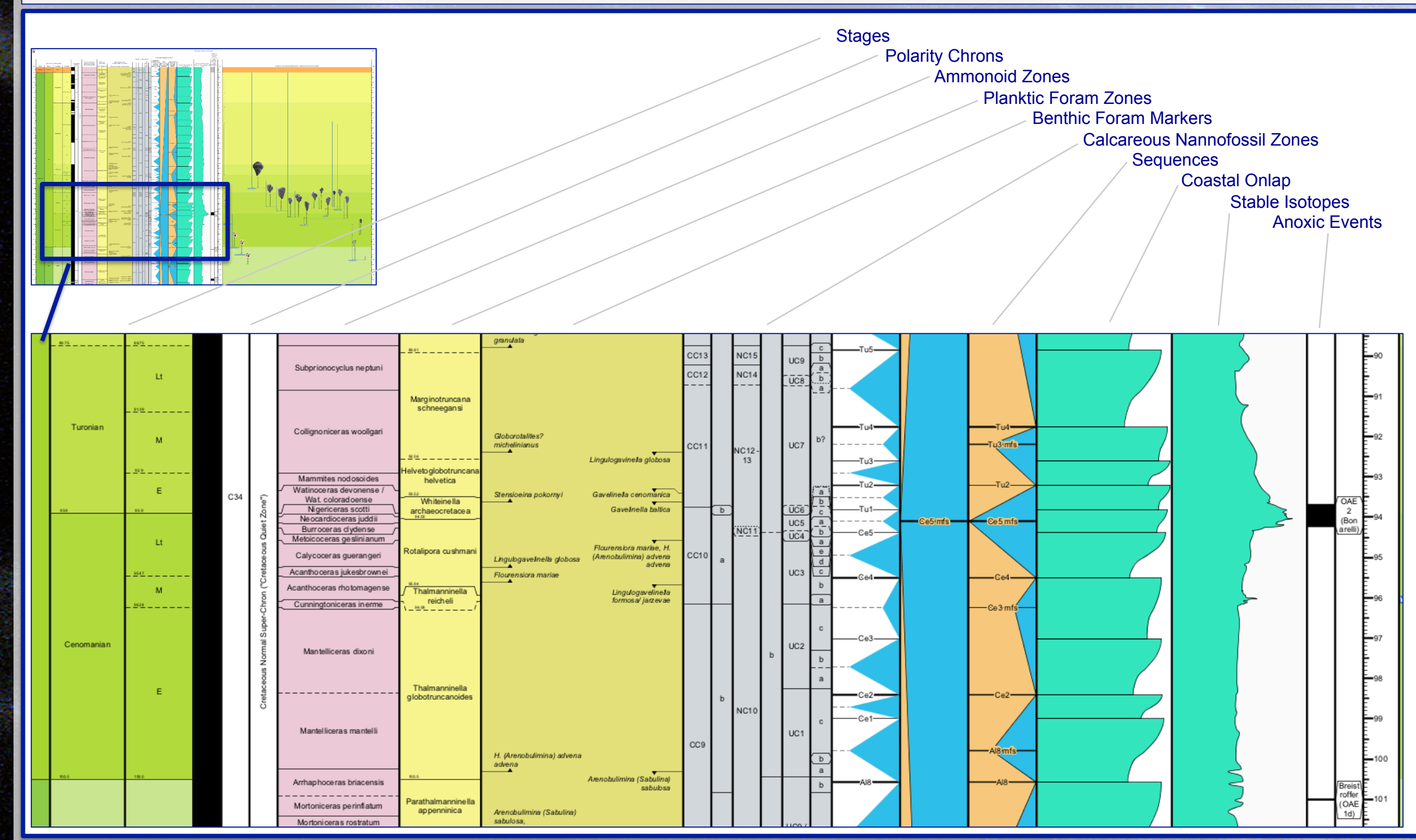
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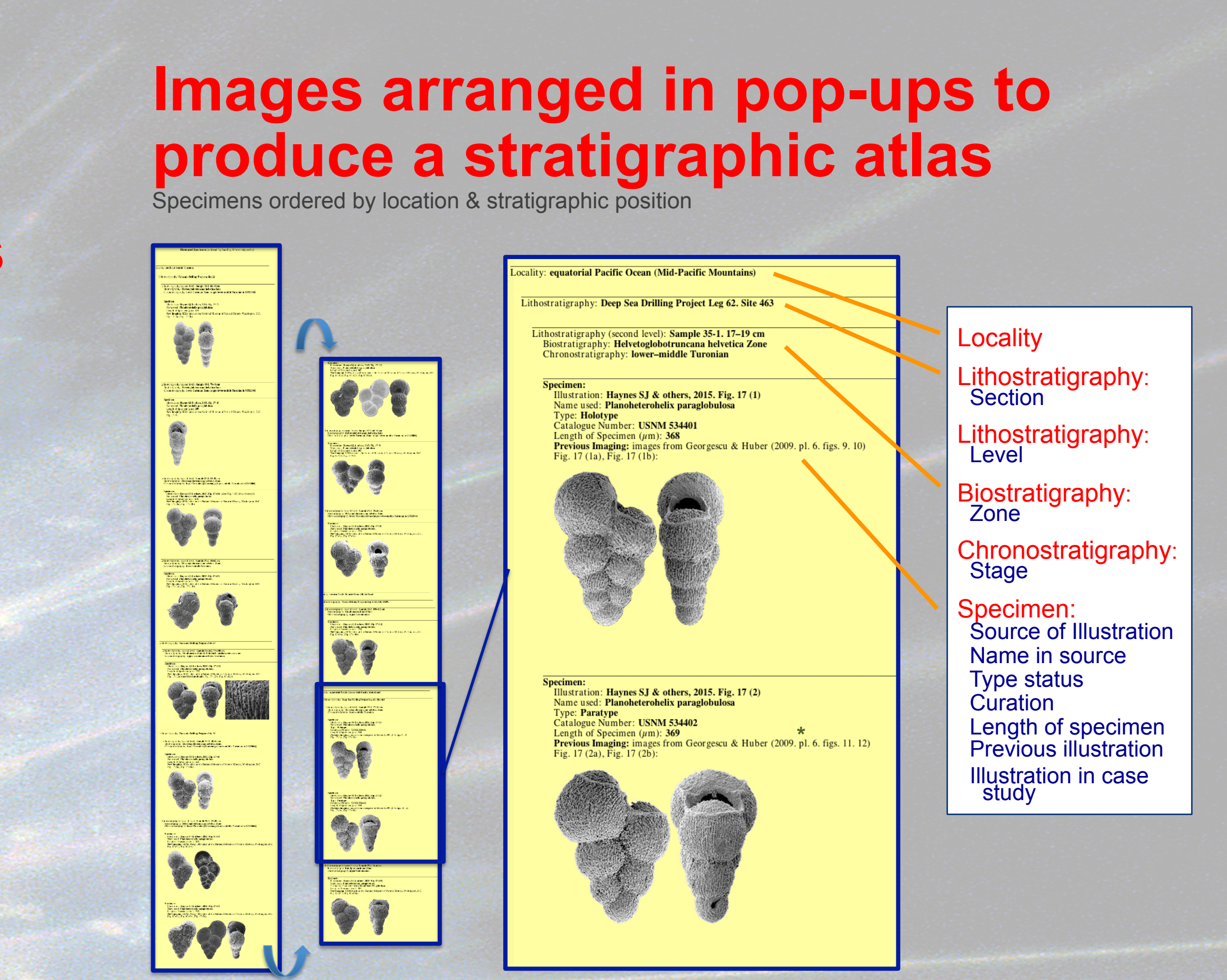
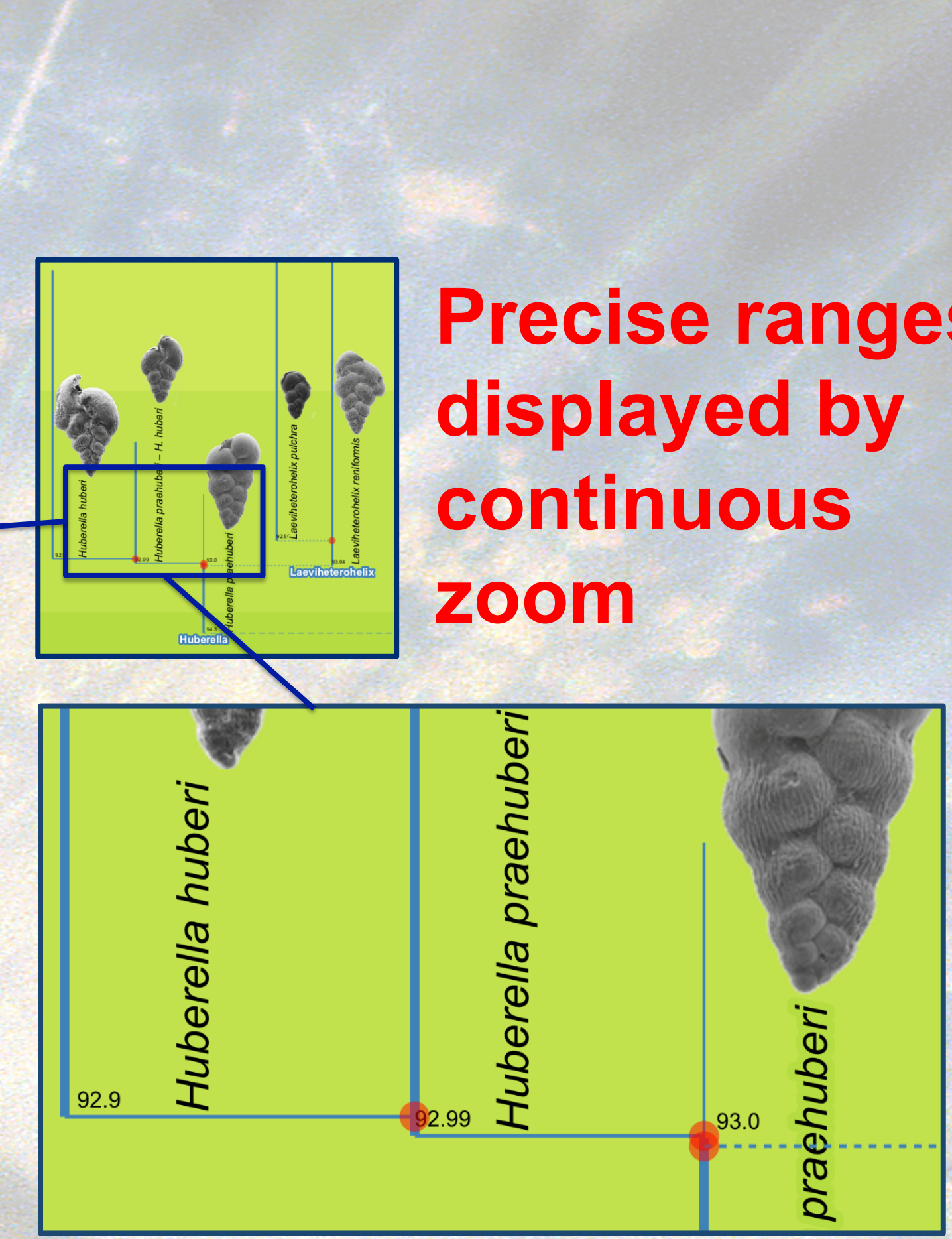
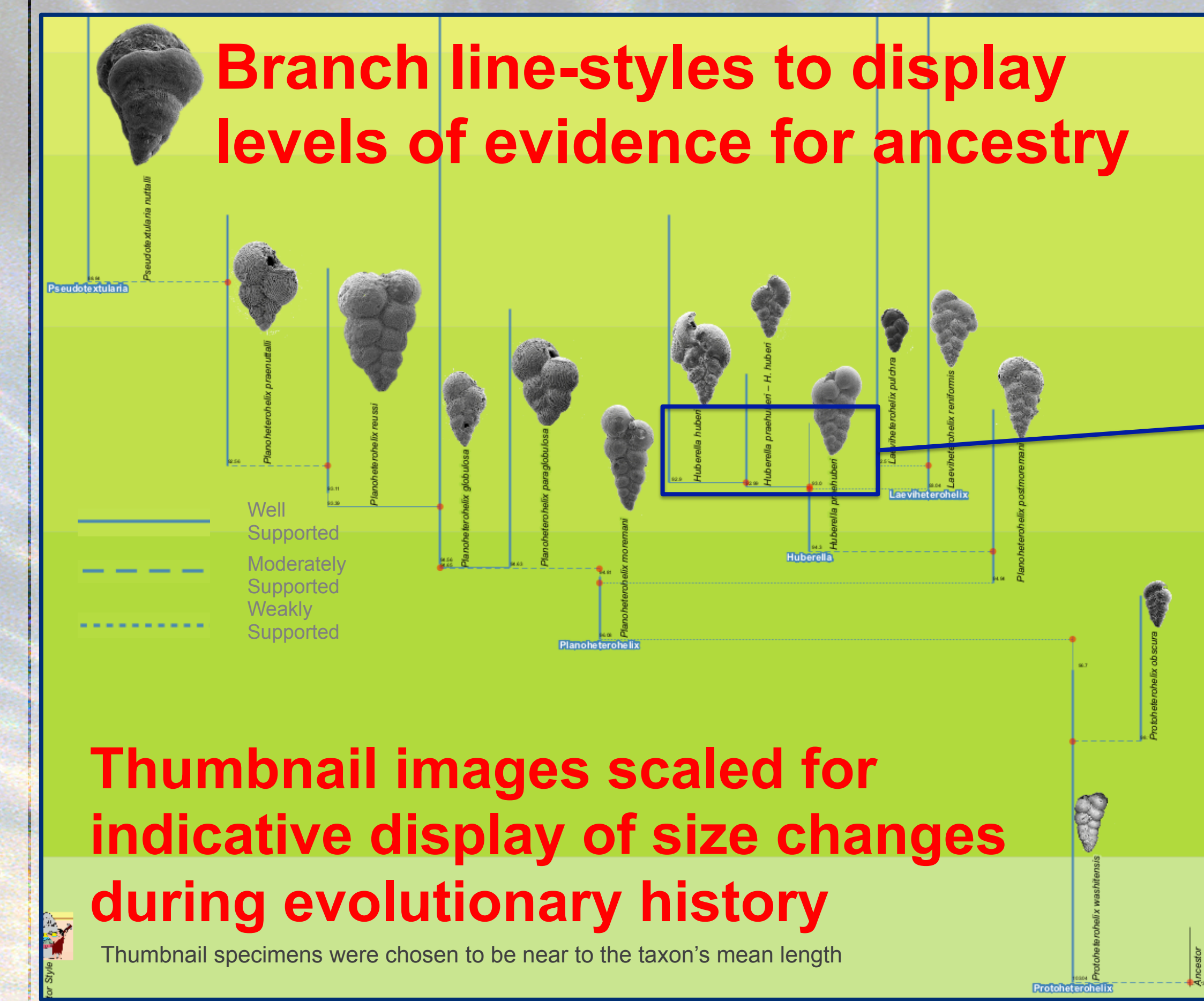
Poster for Theme:
Phanerozoic Earth History, Stratigraphy
and the Geologic Time Scale
35th International Geological Congress
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Town, South Africa

TimeScale Creator & Evolutionary Trees:

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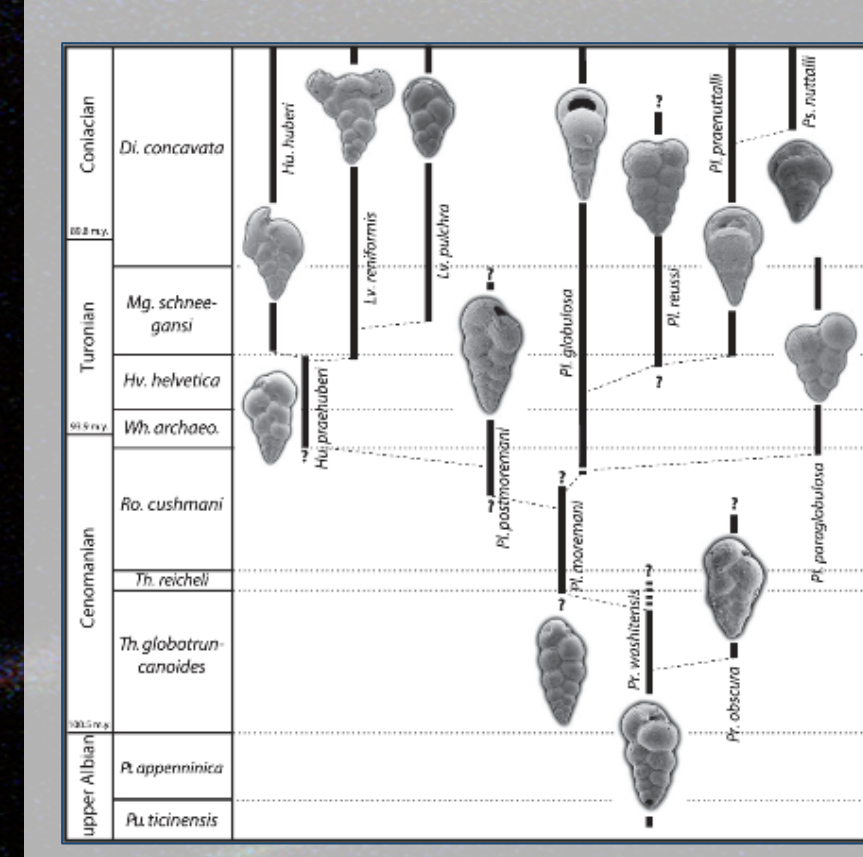


Adding Value to the Tree:



The Case Study:

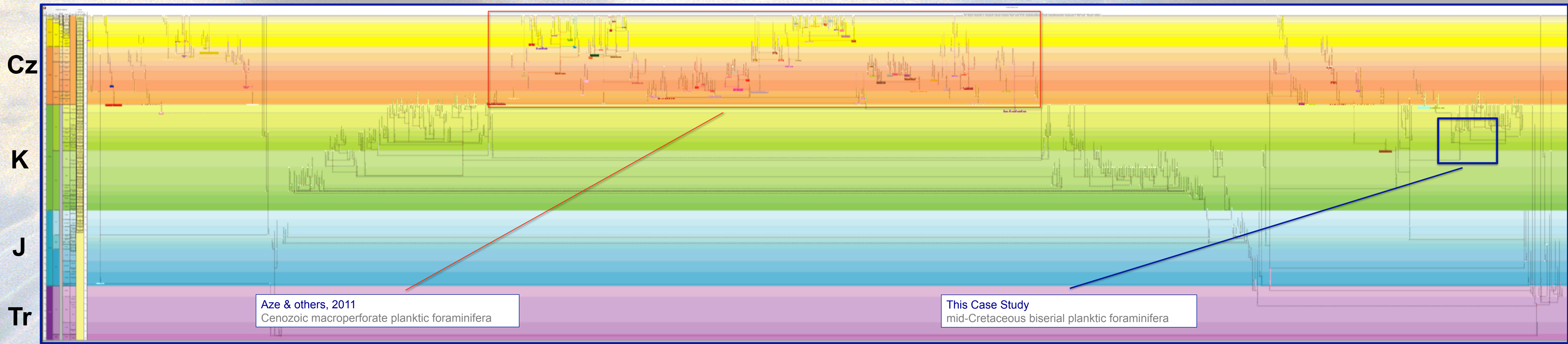
Haynes, Huber, & MacLeod, 2015
Evolution and phylogeny of mid-Cretaceous (Albian–Coniacian) biserial planktic foraminifera. *Journal of Foraminiferal Research*, 45: 42–81.



Taxonomic revision of mid-Cretaceous biserial planktic forams:

- Hemiplegic sediments of southeast Tanzania
- Detailed sampling through Turonian–Coniacian
- Exquisite preservation
- SEM imaging & X-ray
- Interspecific & intraspecific variability
- Detailed biometrics, including primary types
- Revised phylogeny

TimeScale Creator trees against a mock-up phylogeny of all planktic foram lineages from their early-Mesozoic origins



Putting Ancestry Information into Pop-ups:

Stratophenetics: presenting evidence
Studies making use of stratophenetics:

- Usually do not have the resources needed for focussed and sophisticated approaches such as those of Gingerich, Knappertsbusch, Pearson & Ezard, etc.
- A more systematic/structured approach to documenting the evidence would encourage:
 - more-effective stratophenetic analysis
 - closer dialogue with approaches to phylogeny reconstruction employing explicit methodologies e.g., cladistics, molecular phylogenies

An Evidence Template

Main Headings:

- Summary, Related Info
- Taxonomic Categorisation Employed
- Potential for Undetected Cryptic Taxa
- Density of Sampling
- Documentation of Samples
- Continuity between Samples
- Paleogeographic Plausibility
- Plausibility of Adaptations implied by Morphologies

Summary section:

Phylogeny Method & Level For Stratophenetic — Speculative or Supported: Weakly, Moderately, Well, Very Well, Strongly

Branching Type: Budding or Bifurcating

Summary: Brief justification for Phylogeny Method and its Level

Example section: Documentation of Samples

Overall: Overall documentation of taxa accomplished by the case study at the sample level

Qualitative Categorization: Taxa or informal categories employed

Quantitative Documentation: Counts taken, such as abundances of taxa or informal categories

Documentation of Samples - Overall: Samples not described individually, but detailed description of morphological variation of species taxa compiled from all samples.

Qualitative Categorization: Formal species taxa only.

Quantitative Documentation: Counts are given for ancestor and descendant in TDP 31: %'s for the ancestor are typically high throughout the section, and for the descendant are typically moderate to high in the Helvetoglobotruncana helvetica Zone and lower in the overlying Marginotruncana schneegansi Zone. Occurrences in other sections are presence/absence only.

Morphometrics - Variables: Multiple variables: many measurements, both overall and per chamber.

Specimens per Sample: Only one, or at most a few (type series), specimens in any sample (so published plots of fields of variability for either taxon represent compilations from multiple samples).

Fields of Variability: For both species taxa, compiled from all samples.

Identification of Specimens: Measured specimens individually identified, including, where relevant, links to name-bearing types (and their catalogue numbers) and illustrations.

Quantity: A dozen or so specimens of each species taxon.

Variation: Illustrated specimens depict some key morphological variation; one specimen transitional between ancestor and descendant illustrated.

Future Links: PF@Mikrotax

