

The assessment of the Ph.D. thesis by Mgr. Kristýna Hlavatá

The thesis "Phylogenomics, genome size evolution, and repeat dynamics in the genus *Amomum* Roxb. (Zingiberaceae)" by Kristýna Hlavatá delves into the complex taxonomy, phylogenomics, and evolutionary dynamics of genome size and repetitive DNA sequences within the genus *Amomum*. It investigates the genus's phylogenetic relationships and identifies three new genera, alongside resurrecting three and merging the genus *Elettariopsis* into *Amomum*. Through extensive molecular and morphological analyses, the study reveals the existence of four main clades within *Amomum*, highlighting significant genome size variation driven by repetitive element dynamics and ancient hybridization events. These findings contribute to the understanding of genome evolution in tropical plants and provide a revised taxonomical framework for *Amomum*, facilitating future studies and conservation efforts.

Three of the four papers that form the basis of the thesis have been published in reputable journals. I am confident that the fourth paper, which offers an extensive analysis of *Amomum*'s repeatome, will soon be accepted for publication. Reading the thesis was a pleasure, and I found it inspiring. It applies several methods, such as using tandem repeat analysis to detect hybridization events, which were new to me. Considering the variety of applied methods, I must admire the breadth of Kristýna's skills. Overall, I view the thesis as the work of a highly competent scientist.

Questions and topics for a discussion:

- 1) The thesis concentrates on establishing order within the chaos of the *Amomum* genus, elucidating its biogeography, and unraveling the evolution of its genome size. Now that this groundwork, described as a 'stepping stone for more comprehensive studies' in the conclusions, has been established, I wonder: What potential does *Amomum* hold as a model system for investigating more general questions and hypotheses?"
- 2) Throughout the thesis, the evolution of genome size in *Amomum*, whether as a factor influencing species habitats or as a trait resulting from transposable elements activity, is considered in the context of natural selection (referring to, e.g., large-genome-constraint hypothesis). However, natural selection (the adaptationist view) is not the only evolutionary mechanism behind genome size evolution. How would the interpretation of the results change if they were considered also in the context of genetic drift?
- 3) If I understand correctly, Pagel's lambda, which was used to measure the phylogenetic signal (in Papers III and IV), assumes Brownian motion of trait evolution. Can the Brownian motion really be universally assumed in the case of repeatome and genome size evolution in the genus *Amomum*?

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