

Title: Phylogenetic analysis of the genus *Olinia* (Oliniaceae)

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Level: Masters

Additional information:

A revised classification of Oliniaceae was published by Sebola and Balkwill in 2013, providing a new circumscription of species and a morphological basis and justification and corroboration of Mujica and Cutler (19860)'s arguments of two possible sections based on the anatomical characters which were then considered arbitrary. The two sections are distinguishable on the basis of the pattern of leaf venation, shape of leaves and petals. Section *Olinia* comprises *O. capensis*, *O. emarginata*, *O. micrantha*, *O. ventosa*, *O. radiata* and *O. vanguerioides*; whereas Section *Rochetiana* includes *O. huillensis*, *O. rochetiana*, *O. ruandensis* and *O. usambarensis*. Species of section *Olinia* have leaves with secondary veins branching from midrib at acute angles (i.e. 30° – 44°) and looping once before the margins, tertiary veins not clearly visible on upper surface, whereas species of section *Rochetiana* have leaves with secondary veins branching from midrib at an obtuse angle (i.e. 45° – 60°) and looping more than once before the margins, tertiary veins clearly visible on upper surface. Section *Olinia* comprises species that occur largely in southern Africa, whereas section *Rochetia* comprises species that occur in tropical east Africa, respectively.

In a preliminary cladistics analysis based on morphological data, *Olinia* taxa formed a strongly supported monophyletic clade with two poorly supported subclades. Optimization of morphological characters on consensus trees revealed synapomorphic character states that support the subclade comprising the southern African species (*O. emarginata*, *O. radiata*, *O. capensis*, *O. micrantha*, *O. ventosa*, and *O. vanguerioides*), whereas the subclade comprising tropical east African species (*O. rochetiana sensu stricto*, *O. ruandensis*, *O. usambarensis*, *O. huillensis* subsp. *huillensis*, *O. huillensis* subsp. *burttdavii*, and *O. huillensis* subsp. *discolor*) is not supported by any synapomorphic character states. Morphological data alone have proved insufficient to fully resolve the species relationships in *Olinia*, more specifically the relationships among the taxa that form polytomies. The low internal support for some of the clades is indicative of the relatively high homoplasy level in the data set. An expanded data set of combined morphological and molecular characters is desirable in order to improve clade support as bootstrap values are strongly influenced by the number of characters. In this project the aim is to produce a phylogenetic hypothesis based on a combination of both molecular and morphological characters. Molecular data will be generated and analysed to clarify the infrageneric circumscriptions and assess the robustness of morphology-based clades within *Olinia*, and improve on the classification of genus.

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