



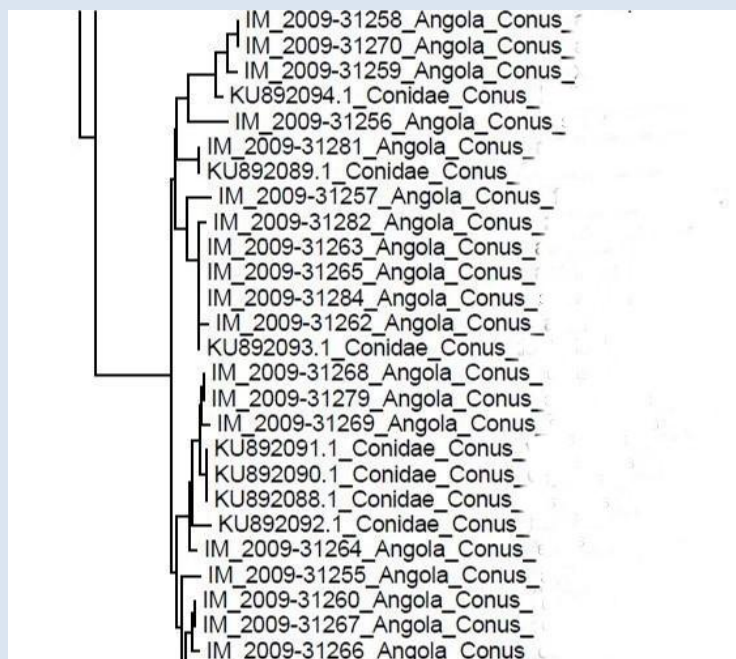
DNA analysis of Angolan cones 2019

No report has yet been published which specifically addresses phylogenetic relationships among Angolan cones. However, as part of wider DNA studies of worldwide Conidae led by the Paris Museum (MNHN - Nico Puillandre et al) and of West African cones led by the Madrid museum (MNCN - Rafael Zardoya et al), a number of sequences for Angolan species are recorded in Genbank. These sequences are based on the mitochondrial COI gene.

No specimens of the West African species *C. ermineus*, *C. pulcher*, *C. tabidus*, *C. genuanus*, collected in Angola, have been tested to check how closely they are related to conspecific specimens from Senegal and the western edges of their distribution. The current DNA data set contains several species of the endemic cones from Luanda, Namibe and Benguela provinces which are found in the *Lautoconus* group. No specimen of *C. carnalis*, thought to be in a separate genus *Pseudonoduloconus*, has been tested.

Genetics studies have tended to require that a species name is given to each specimen before analysis. It is unclear whether the radula was evaluated as part of the identification process of these specimens. So some of the attributed names used for the DNA specimens are based on identification of non-typical forms using shell morphology and are open to error.

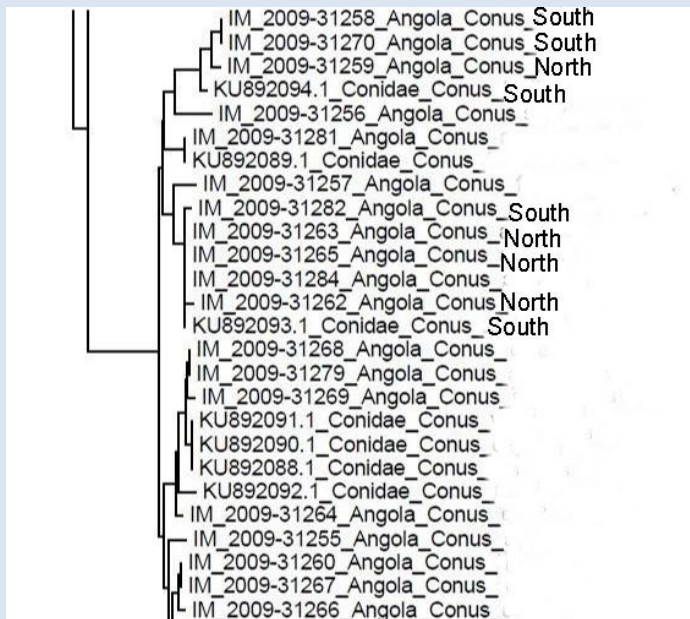
Below is the 2019 COI tree of the endemic species from Luanda and Benguela/Namibe with the species names removed.



The species all cluster together in a phylogenetic clade now named as the genus *Lautoconus*. No specimens of these endemic species were to be found elsewhere in the tree. The genetic distances found between specimens are quite small, which makes it very difficult to use such a tree to investigate species boundaries.

Note: The difference in the structure of the COI gene between each specimen is represented by the length of the two horizontal branches of the tree, back to their common point. The vertical distance between entries has no genetic significance.

Given the geographical gap in cone distribution, where no cone specimens are reported between Luanda in the north and Benguela in the south, we could expect perhaps a split in the tree between northern and southern species.



The COI results show that the one specimen of *C. xicoi* from the north is nearest to the two specimens of *C. allaryi* from the south. The 3 specimens of *C. aemulus* from the north do not have a close alignment with *C. xicoi* but are closest to 2 specimens of the southerly species *C. zebroides*.

C. allaryi is unique among currently recognised Angolan cones in being the only species reported from San Antonio and it is only found in that bay. The other species are found in several bays, normally living sympatrically with several other species.

The lower half of the tree is difficult to interpret, with specimens of *C. micropunctatus*, *C. chytreus* and forms of *C. variegatus* all showing similar DNA. *C. lineopunctatus* and *C. trovai* have a significantly different radula from the other species in *Lautoconus*. Their specimens in the DNA set are closely related to the other species; however they are non-typical specimens and open to interpretation of identity.

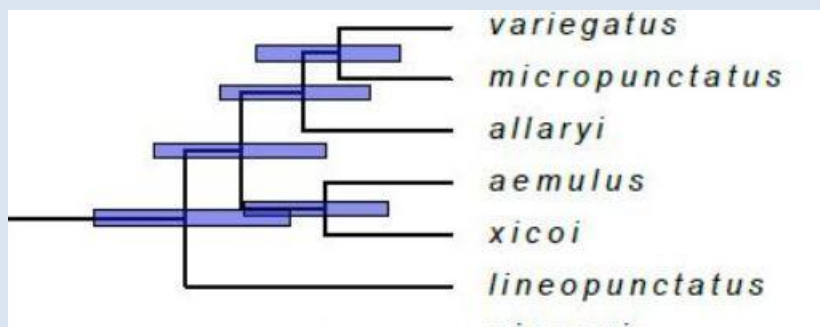
This situation is succinctly summarised by Nicolas Puillandre and Loic Limpalaer in their article published within the book “Taxonomic Iconography of Living Conidae” by Monnier et al, 2018.

“...species that have diverged recently may still have identical sequences for a given gene, leading to the erroneous conclusion that they belong to the same species. These examples correspond to situations where the species are still in the “grey zone”, the zone of the speciation process in which species started to diverge, but did not reach a step where all their characters are fully differentiated. Some characters will need more time to develop and establish differences between the species, and conversely other genes will more quickly accumulate and establish differences between populations that still belong to the same species.

The strategy to overcome these issues is theoretically simple. First, increasing the number of sequenced specimens and populations sequenced can help to detect such cases. However, ... collecting many specimens from different populations for all the species of a given species complex is a difficult task. Second, sequencing not only one gene but several independently evolving genes may also help. Discrepancies between the pattern observed with one gene and the species limits (often referred to as the “gene tree/species tree” conflict) are generally detected with other genes, because these other genes will evolve faster or slower than the first one, and will thus not necessarily have the same erroneous “gene tree”. The more independent genes that are sequenced, the easier it is to infer the correct species delimitation.”

In 2019, Phoung et al published a phylogeny of worldwide cones, based on multiple genes associated with the production of venoms.

Their derived basic phylogenetic trees showed small differences between the Angolan species, which were all in one subclade. The trees lack sufficient resolution to draw any conclusions on species boundaries and evolution at the species level. However their time tree begins to show some of the evolution events that we might expect.



C. lineopunctatus with its different radula is in a separate lineage; the Luandan endemic species from the north, *C. aemulus* and *C. xicoi*, are together and separated from the southerly species. *C. allaryi*, which is found only in one bay, is in a separate lineage.

To get more meaningful results at the species level for the Angolan cones will require testing with a wider set of genes, a common standard for identification including radula tests, a better set of typical specimens for the existing species and samples of different forms and different populations of selected species.

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