

Phylogenomic analyses of large-shelled cones from Cabo Verde, West Africa

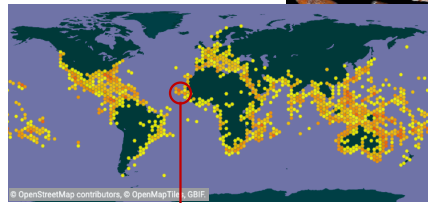
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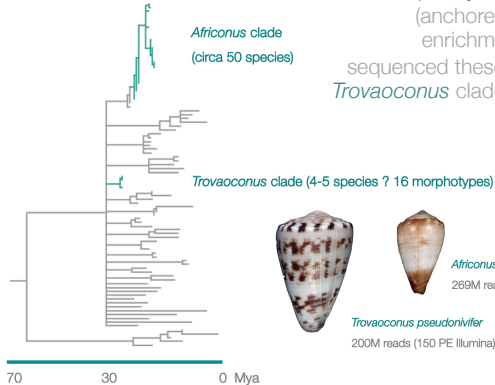
1. Genus *Conus* harbours huge species diversity and local “radiations” but most data validating species ID is morphology and mtDNA alone



from Abalde S, 2019: PhD Thesis

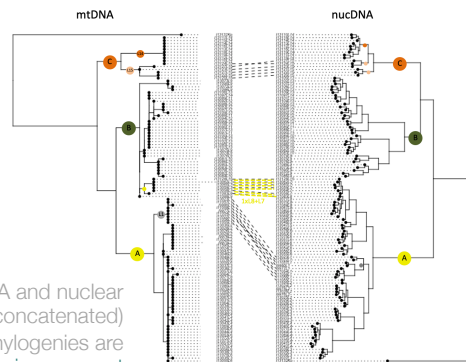


2. Focusing on Cabo Verde species, we generated probes for 1750 (anonymous) loci (anchored hybrid enrichment) and sequenced these for the *Trovaconus* clade (target capture)

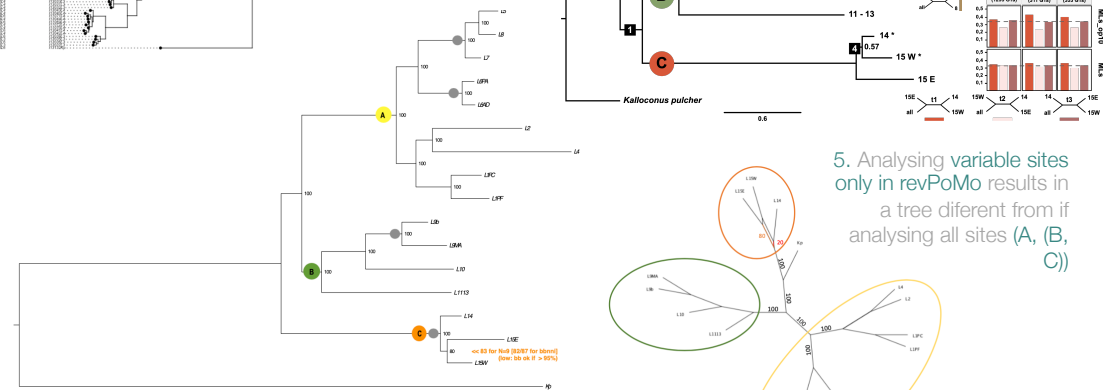


70 30 0 Mya

3. mtDNA and nuclear (concatenated) phylogenies are incongruent



4. Using as tips “populations” defined by STRUCTURE analyses of loci biallelic SNPs, species-tree methods ASTRAL (above) and revPoMo (below) also result in incongruent trees



Why these differences ??

breaking model assumptions (non-independent sites) in revPoMo ?
non-adequacy of the root for PoMo analyses (1 sequence) ?
existence of (ancient) gene-flow influencing differently the different methods?
is it correct to analyse all sites of many long loci with PoMo models ?

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5. Analysing variable sites only in revPoMo results in a tree different from if analysing all sites (A, (B, C))

