

## Investigating evolution of closely related, sympatric cryptic species using complete mitochondrial DNA

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Cryptic species are organisms with very similar morphology but distinct genetic make-up. They can be found in many animal groups, but typically in organisms for which chemical recognition is more important than visual recognition for mating. If the cryptic species are living in sympatry (in the same area), reproduction could, in theory, still be possible and hence, gene flow will occur. Gene flow will inhibit further differentiation of the species and thus speciation. Why speciation does or does not occur, is not always clear and investigating the genes that are under selection will provide more insights in the speciation process.

Genetic differences can be detected by comparing the genomes of the species. These genetic differences can be as large as those observed in species with clear morphological distinctions. The position of the gene in the genome or alteration in the genes by mutation, are a few examples of these genetic differences. Four cryptic species of the marine nematode *Litoditis marina* species complex are held in monospecific cultures. Recent research found that these four species cannot interbreed, but they do co-occur. Therefore reproductive barriers must exist between the different subspecies. Next-generation sequencing allows to sequence complete genomes instead of a few genes and enables to differentiate between the nucleotides and the position of the genes in the genome. By comparing the mitochondrial genomes of closely related species, we can investigate which genes are under selection and which are important for the speciation and evolution of the cryptic species.