

The advent of DNA sequencing has had a profound impact, affecting all of us in innumerable ways. From the now popular ancestry research (available for humans, cats or dogs!), to establishing paternity, developing medical gene therapies, improving agricultural crops and catching criminals, DNA sequencing is a widely applied tool that has become both accessible and relatively inexpensive. Perhaps most impactful is the use of DNA sequencing in biological research, where it has found a place in virtually all fields, including species and population ecology, conservation biology, environmental surveys, and taxonomy. Scientists at the Department of Biodiversity, Conservation and Attractions (DBCA) are adopting molecular techniques to reveal hidden biodiversity that only a few decades ago would have remained mysteries.

Taxonomy, the science of recognising, characterising, and naming species, has been revolutionised by the use of DNA sequencing. Traditionally based on detailed observations of a species' morphology and comparisons with the morphology of related species, this task is most challenging for species with limited morphological features or where good specimens are lacking. The adoption of DNA sequencing in taxonomy now allows a view of the underlying 'blueprints' that govern that morphology, without the often confounding intrusion of environmental conditions, and greatly improves our understanding of species and their evolutionary relationships in the tree of life.

If we look at the seaweeds as an example, in the latter part of the 20th Century there was a general belief that many species were widely distributed, and many of the earlier-named species in different locations were no longer recognised as unique. When DNA sequencing became common and scientists around the world generated DNA sequences from their local specimens, three things became clear: firstly, that there are considerably more



## Red seaweed (*Hypnea* sp.)

species than previously thought, secondly that in many cases species are not widely distributed, and thirdly the importance of generating DNA sequence data from an 'authentic' specimen to be able to link the genetic entities identified with the correct species names.

These outcomes have recently been re-iterated during the course of molecular research at DBCA. Just as DNA sequencing has revealed that there are many distinct species that in appearance are indistinguishable from one another but are clearly different based on their DNA sequences, so called 'cryptic' species, our research has recently detected a new cryptic species of a seaweed found in the Perth region. For several years this red seaweed at Point Peron has been known as *Hypnea musciformis*, being an excellent match based on morphology, but our molecular data reveal that it does not belong to that species or indeed any other named species. True *Hypnea musciformis* was first described from Trieste in Italy

and in the past has been regarded as widely distributed. A cryptic species, also for many years identified as *Hypnea musciformis* but recently named as the new species *Hypnea caraiibica*, is regarded as a pest in the Hawaiian islands, where it forms extensive blooms that foul the local beaches. Fortunately, our local entity has never shown a propensity to act similarly and it is a relief that we can now regard it as a native seaweed, albeit one that is yet to be named!

With ongoing global efforts to share sequence data and properly document authentic type specimens, DNA sequencing of seaweeds and other morphologically challenging groups will only continue to reveal more of the unique and wonderful biodiversity of the natural world.

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**Above** Hiding in plain sight, a new species of red seaweed (*Hypnea* sp.).  
Photo – John Huisman