

The limitations and shortcomings of DNA barcoding as a sole taxonomic tool

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The biodiversity of our planet remains inadequately documented, despite the longstanding history of modern taxonomy, which spans over 260 years. It is estimated that there are up to 15 million extant eukaryotic species on Earth, yet only around 2 million of them have been identified and formally described. Taxonomists are in a race against time to discover and describe the vast unknown portion of Earth's biodiversity before it is lost as a result of the Anthropocene mass extinction. Each year about 18,000 species are described as new to science, with the annual species loss similar to, or even higher than, the rate of new species discoveries, which is known as the taxonomic impediment. Given that the current average time between species discovery and formal description stands at about 21 years, it is evident that we urgently require revolutionary approaches to expedite the discovery and description of species. Traditionally, morphology has served as the primary method for delineating species, despite a growing trend in integrative studies that encompass a variety of data types. Since the introduction of a standardized fragment of mitochondrial cytochrome oxidase I (COI) fragment as a molecular 'barcode' for identifying known animal species in 2003, DNA barcoding has played a crucial role in biological sciences. DNA markers, especially barcodes, have significantly facilitated the discovery of new species when combined with morphology, as well as other molecular and ecological data, made possible by the availability of DNA barcodes from previously documented species. However, even though proponents of DNA barcoding have acknowledged its limitations as a sole taxonomic tool for describing new species, a 'revolutionary' protocol for the description of understudied hyperdiverse taxa was proposed in 2019, with the premise of providing only DNA-barcode-based species descriptions, which in theory would dramatically increase the rate of description and provide a 'human-readable record in the literature' that can later be supplemented with additional information. This presentation reviews the primary criticisms directed at this protocol.

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