

Bar coding



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A taxonomic method that identifies the species of an organism by using a small genetic marker in the mitochondrial DNA of the organism is DNA bar coding. The mitochondrion of most eukaryotes contains the mitochondrial DNA, and the rate of mutations is faster than those responsible for a significant variation in the DNA sequences of the mitochondria between the species. The identification of the species via DNA bar coding relies entirely upon the short fragment of mitochondrial DNA.

Recently interest is increasing to use a short sequence of tags namely bar codes for identifying and documentation of the species. (Blaxter, 2003, Hebert and Gregory, 2005). The standard sequence of the DNA used as a bar code is the mitochondrial gene cytochrome c oxidase I or COI. A number of studies show that utilizing barcode gives accuracy in the classification of the species. (Kerret. et. al, 2007). The chitons live near the edge of the ocean they are mollusks.

The chitons of the north pacific region are diverse comprising around 80 species, and all these species belong to the genus *Mopalia*. (Eernisse). The present paper discusses on identification of the species of the genus *Mopalia* from the extremely diverse community of chitons of the north pacific region using the DNA bar coding. DNA bar coding: To characterize the species of the organisms a novel technique exists termed “ DNA bar coding”, and the technique uses a short sequence of DNA on the standard position of the genome.

Obtaining the DNA sequences is quick as they comprise a very short sequence in comparison with the whole genome. The cytochrome oxidase subunit 1 of the mitochondrial region is the standard bar code region that

contains a length of 648 nucleotide base pairs. There is a variation of the DNA bar codes among the individuals of the same species, but it is little. The effectiveness of the DNA bar code is directly dependent on the minor variation within the species, which is smaller than the differences between the species.

(Consortium). Genus *Mopalia*: Fauna and flora of the north pacific region is diverse with long coastline and cool temperatures. Many species of the chitons play an important role in the ecology of the rocky shorelines. The *Mopalia* group has its recent origin with an interesting morphological similarity that attracts case study for DNA bar coding. DNA bar coding using the genus *Mopalia*: Up to now focus of the studies on DNA bar coding was mainly with the collection of the species within the geographical areas. (Hebert et. al, 2003a).

Studies in DNA bar coding with reference to the monophyletic groups is less leaving the ambiguity whether this technique is useful in distinguishing the closely related species. (Moritz and Cicero, 1994) The present study uses the genus *Mopalia*, a challenging case study for the DNA bar coding methodology. The genus *Mopalia* is a recently originated; monophyletic that has a wider geographical occurrence. (Kelly et. al, 2007). Kelly et. al studied 19 species of the genus *Mopalia*, and six closely related species that out group the 131 individuals of the total of the 25 species used.

The character-based assessment referred to as the characteristic attribute organizations system is fast, that avoids the false-positive data and it also retains the information on evolution that is in the character-state data. (Desalle et. al, 2005). This approach gives a new perspective to the methods

of DNA bar coding. This kind of information is more like a traditional taxonomy. (Desalle et. al, 2005). The CAOS method or the character based method gives clear information, and getting the information is faster, and there is accuracy in the identification of the query sequences of the given data set.

The CAOS method is sensitive that distinguishes the taxa of the monophyletic group of the closely related species with a very short sequence of the mitochondrial DNA. The advantage in this method is that it preserves the evolutionary information in the form of character data that avoids the false-positive identification of the query sequences. The number of diagnostics that supports the placement of a query sequence in a clade also used as a confidence value. The bar coding group has no relevance with the CAOS method; this is because the diagnostic character distinguishes monophyletic groups.

While distinguishing the monophyletic groups, reference is not a requirement about the relative degree of divergence within and between the taxa. The additional advantage with the CAOS approach is its use as a means of cataloguing the diagnostic molecular characteristics used to distinguish the species. These diagnostics complement the traditional taxonomy. (De Salle et. al, 2005). Even though the description of the species depends on the multiple lines of evidence, the CAOS approach is a good tool to identify significant intraspecific divergences.

Additional evidence that includes morphological, geographical, ecological, and behavioral that is diagnostic for the new taxon. The CAOS method preserves the character state information, reports diagnostic differences for

each node. This method helps the taxonomists to identify and describe divergent organisms that require further scrutiny. (Blaxter, 2004). In this method threshold values for the species level are not necessary, which addresses the critical issues in other methods. (Meyer and Paulay, 2005). This method of DNA bar coding corrects some pitfalls of the distance based approaches.

The inclusion of the evolutionary and taxonomic information in this method gives a context in which there is interpretation of the sequence data and gives a real promise to the DNA bar coding. The CAOS method gives a way to the researchers' confrontation to identify and make the sense of diversity. Conclusions: The distance based methods for DNA bar coding lack the accuracy that largely depend on the degree of disparity between the intra and site-specific variation that is the bar coding gap. (Meyer and Paulay, 2005).

Insufficiency in sampling the taxon will increase the disparity that increased the apparent accuracy. CAOS method of DNA bar coding addresses the problems associated with the distance based methods of bar coding.

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