ISSN: 2155-9597
Journal of Bacteriology & Parasitology

OPEN ACCESS Freely available online

Opinion Article

# DNA Barcoding: An Obligatory Tool for Species Detection and Specimen Identification

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## DESCRIPTION

Bacteria are everywhere and have unlimited power. Since ancient times, scientists have studied bacterial infections in an effort to stop epidemics, food spoilage, losses in agricultural production, and fatalities. Consideration is given to contemporary methods of species identification using DNA. Hence, learning an easy and quick identification method is necessary. Thus, the effectiveness of DNA barcoding for bacteria is covered in this review study. Regular DNA barcoding entails the creation of PCR amplicons from specific regions in order to sequence them. The sequence data are then used to identify, or barcode," that organism in order to distinguish it from other species.

DNA barcoding is now an acceptable approach for evaluating patterns in global biodiversity and enabling nontaxonomists to identify recognized species. By utilizing short DNA sequences, DNA barcoding provides a quick, precise, and consistent method for species-level identification.

The uniform methodology of DNA barcoding makes it easier to conduct biodiversity research like species discovery and identification. By combining molecular, morphological, and distributional data, this method aids in the understanding of genetic and evolutionary links. DNA barcoding is typically used to identify species at the level of the genome by recovering a brief DNA sequence from a typical region of the genome.

Each unknown specimen's barcode sequence was then compared to a database of reference barcode sequences collected from people with known identities. For the purpose of identifying specimens and species, DNA barcoding is a necessary tool. The mapping of all species on Earth benefits greatly from the use of uniform identification methods, especially now that DNA sequencing technology is widely accessible and reasonably priced. According to the idea behind the phrase "DNA barcode," standardised DNA sequences can identify taxa in a similar manner to how the 11-digit Universal Product Code identifies goods sold in stores. The Barcode of Life Data System (BOLD) is a workbench for informatics that facilitates the acquisition, examination, preservation, and dissemination of DNA barcode information. By gathering morphological, molecular, and distributional data, it opens a conventional bioinformatics door. Any researcher with knowledge of DNA barcoding has free access to BOLD. The goal of the Quarantine Barcoding of Life (QBOL) project is to collect DNA barcode information from significant bacterial species and other organisms in order to provide an analytical tool for quarantine. The composition of an insect's bacterial symbionts and how they change over time are all investigated by species quantification using the entire DNA barcode. Also, new bacterial diseases of insect pests, and the hidden biodiversity of soil samples are evaluated and examined.

Life is meant to be catalogued through DNA barcoding. This cutting-edge approach uses brief but precise DNA identifiers, or "barcodes," to identify different species. In the case of bacteria, the majority of species are cryptic; therefore, barcoding might provide important information to assess ecological sequences and determine conservation priorities.

The study of bacterial pathogens gives us a picture of how populations of bacteria behave as groups, but it lacks the resolution to show how individual germs behave, so we cannot tell how few microbes are necessary to cause infection at a specific organ location. So, throughout a prolonged infection, it is essential to generate markers that distinguish between clones in a mixed population. For the behaviour of pools of altered bacteria, signature-tagged mutagenesis was proposed. This method entails creating a bank of individual mutants with transposon insertions, each of which has a distinct oligonucleotide barcode, allowing the fate of individual mutants to be tracked. With multiple bacterial pathogens, this technique has been widely employed to pinpoint the virulence components necessary for various stages of infection.

Six sequenced genomes of the genus *Xanthomonas*, which contains numerous significant phytopathogens, were compared to generate a DNA marker that distinguishes plant-associated

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**Received:** 02-Jan-2023, Manuscript No. JBP-23-20537; **Editor assigned:** 04-Jan-2023, Pre QC No. JBP-23-20537 (PQ); **Reviewed:** 18-Jan-2023, QC No. JBP-23-20537; **Revised:** 25-Jan-2023, Manuscript No. JBP-23-20537 (R); **Published:** 02-Feb-2023, DOI: 10.35248/2155-9597.23.14.445

**Citation:** Kress D (2023) DNA Barcoding: An Obligatory Tool for Species Detection and Specimen Identification. J Bacteriol Parasitol. 14:445.

bacteria at the species level and below. A fragment of the DNA, a Replication Initiation Factor (RIF) makes up this DNA marker. In contrast to the rRNA genes, DNA is a single-copy gene in the vast majority of sequenced bacterial genomes, and genus-specific primers are required for RIF amplification. The RIF marker has a higher sequencing success rate than the Internal Transcribed Spacer (ITS) and more sequence barcodes than the ITS, making it suitable for the meaningful grouping and classification of strains. Most bacterial genera should be adaptable to the RIF marker system, including *Pseudomonas* and *Xylella*.

To stop epidemics and the loss of lives, novel ways to swiftly, perfectly, and highly sensitively identify tiny levels of infectious microorganisms are constantly in demand. It is essential to identify these pathogens early in order to stop the spread of illnesses and treat them. These requirements are met by adaptable biofunctionalized engineered nanomaterials, which are used to diagnose infections in clinical samples, blood, and food. Focusing on the advancements in metallic nanostructures, superparamagnetic nanoparticles, and fluorescent nanoparticles is beneficial for bioimaging, the detection of infectious microorganisms, and the capture of infectious viruses and bacteria in solutions, food, or biological samples *in vitro* and *in vivo*.

Bacterial DNA barcoding has only recently been studied and is still in its infancy. So, further research in this area is necessary for the next investigation. For the purpose of identifying bacterial illnesses in both plants and animals, bacterial DNA barcoding will be helpful.