# DNA Barcoding

Shilpa Deshpande Kaistha
Department of Biotechnology
School of Life Sciences & Biotechnology
CSJM University Kanpur

# Introduction

- DNA barcoding is a taxonomic method of species identification using a short section of DNA from a specific gene or genes
- DNA barcoding, or sequence-based specimen identification, was developed by Paul Hebert in 2003 to identify a broad range of taxa by sequencing a standardized short DNA fragment, the “DNA barcode”
- Several loci have been suggested in different species, eg 16SrDNA, mitochondrial cytochrome oxidase 1 (COX1) gene. Mitochondrial genes are preferred over nuclear genes because of their lack of introns, their haploid mode of inheritance and their limited recombination. In plants mt not used as low mutation rates- RUBISCO, ITS (ribosomal intertranscribed spacer region)

# DNA barcode properties

- To be used as a barcode, a gene/genomic region—

  i) should be universal and contain enough phylogenetic information

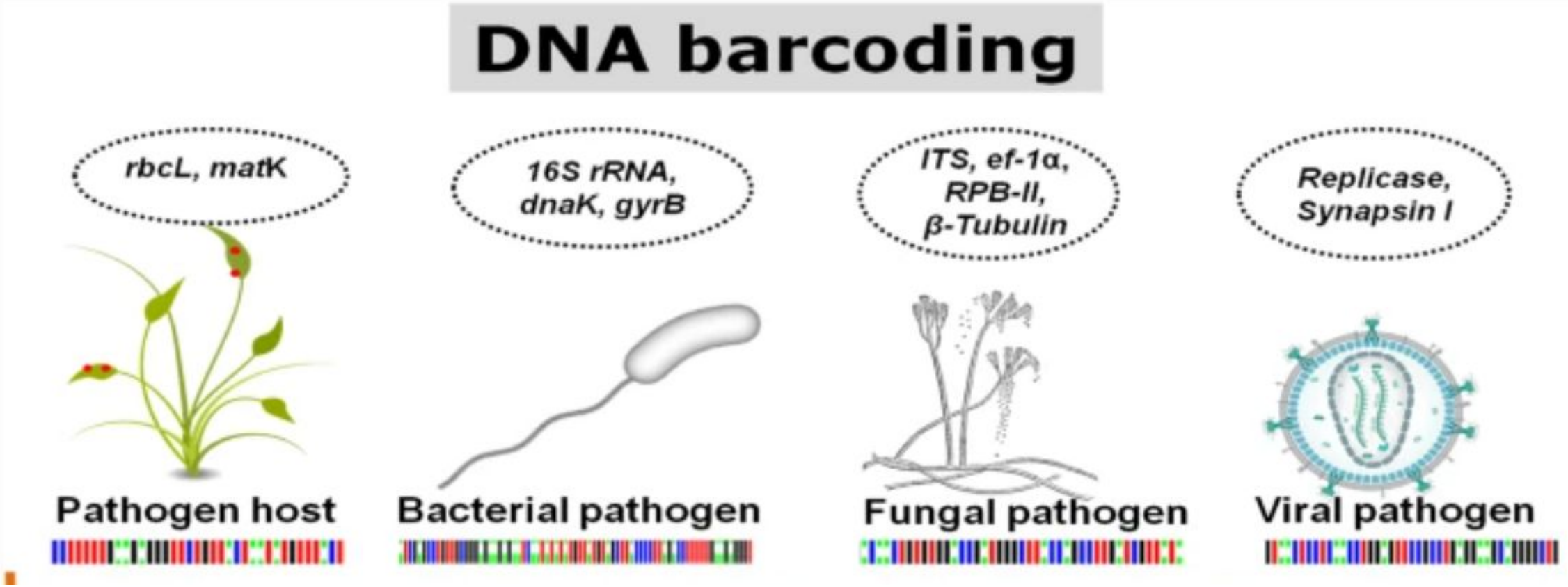
  ii) should have sufficient sequence variability

  ii) must possess sufficient sequence conservation in the regions flanking the variable sequences

  iii) should not be too long to amplify, sequence or analyze

# Building DNA barcode reference libraries

- There are a number of DNA barcode reference libraries.
- The International Barcode of Life Project (iBOL) completed the BARCODE 500K program. Research organisations from 25 countries barcoded 500,000 species. Building on this success, iBOL has launched BIOSCAN, which will extend barcode coverage to 2.5 million species by 2026
- Launched in 2007, the Barcode of Life Data System (BOLD) is one of the biggest databases, containing about 780 000 BINs (Barcode Index Numbers) in 2022.



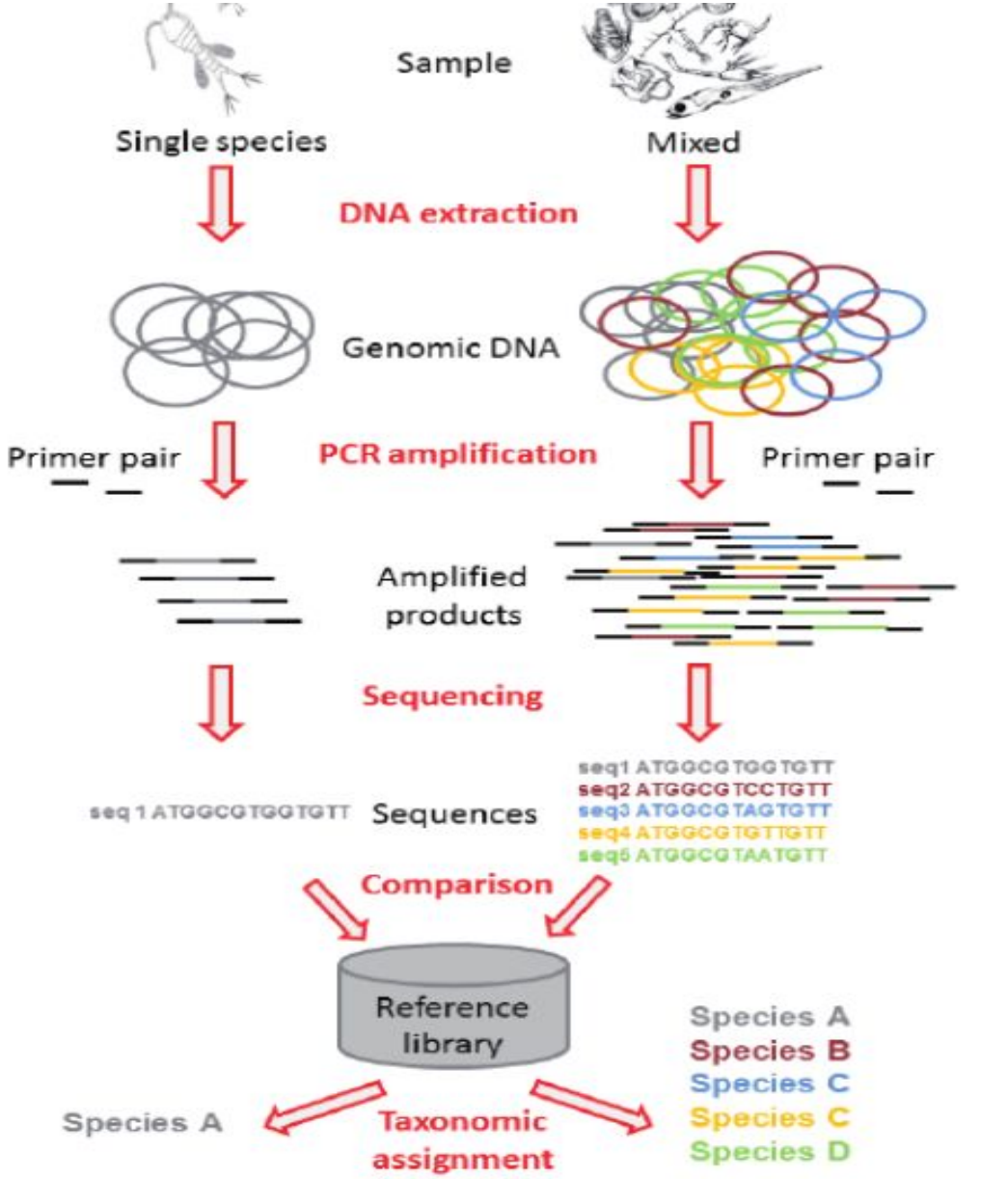

Choudhary, P., Singh, B.N., Chakdar, H. *et al.* DNA barcoding of phytopathogens for disease diagnostics and bio-surveillance. *World J Microbiol Biotechnol* **37**, 54 (2021). https://doi.org/10.1007/s11274-021-03019-0

# DNA barcoding

- **The process of DNA barcoding entails two basic steps:**
- (1) building the DNA barcode library of known species and
- (2) matching the barcode sequence of the unknown sample against the barcode library for identification.
- **Steps of DNA barcoding**

1. Extracting DNA from the sample specimen ·
2. Copying the DNA ·
3. Checking the DNA ·
4. DNA sequencing ·
5. Comparing **DNA barcodes**

# DNA meta barcoding




Schematic representation of the processes of DNA barcoding (left) and metabarcoding (right). Coloured circles represent extracted genomic DNA, which is composed of multiple copies of the same genome (barcoding) or of multiple copies of the genomes of the species composing the samples (metabarcoding). Amplified products are identical in barcoding, whereas a mixture of amplified products from the different genomes is obtained in metabarcoding. Once the amplified products have been sequenced, taxonomic assignment is preformed based on comparison of the obtained sequences with a reference database.


- Corell, Jon & Rodriguez-Ezpeleta, Naiara. (2014). Tuning of protocols and marker selection to evaluate the diversity of zooplankton using metabarcoding. Revista de Investigación Marina. 21. 19-39.

# Applications of DNA barcoding (wiki)

- identification of new species, safety assessment of food, identification and assessment of cryptic species, detection of alien species, identification of endangered and threatened species, linking egg and larval stages to adult species, securing intellectual property rights for bioresources, framing global management plans for conservation strategies, elucidate feeding niches, and forensic science.
- DNA barcode markers can be applied to address basic questions in systematics, ecology, evolutionary biology and conservation, including community assembly, species interaction networks, taxonomic discovery, and assessing priority areas for environmental protection.