Barkoding Untuk Virus dan Tumbuhan

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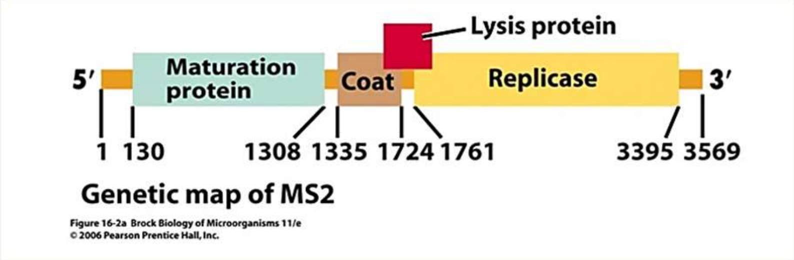
VIRUS

RNA bacteriophage



Genetic map of MS2

Figure 16-2a Brock Biology of Microorganisms 11/e
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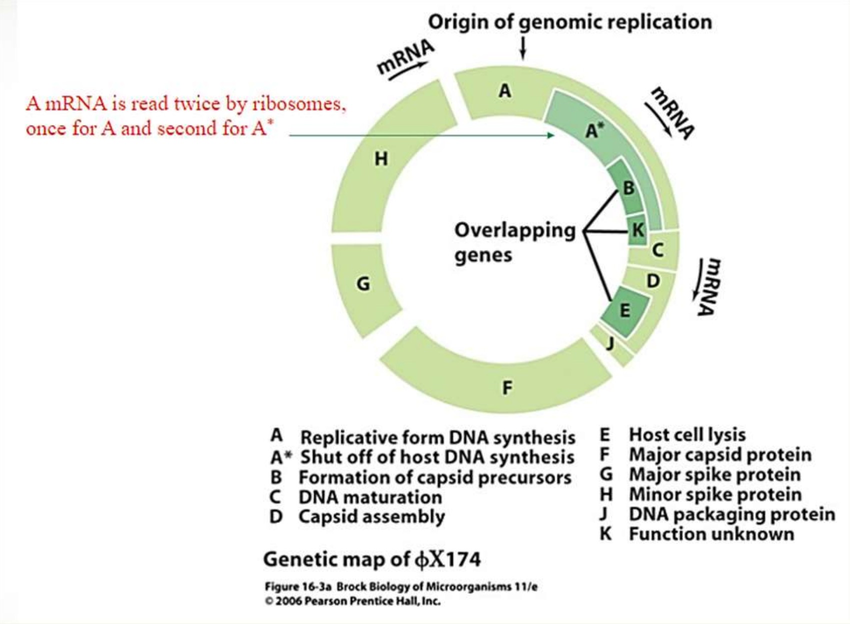
ssDNA bacteriophage



A	Replicative form DNA synthesis
A*	Shut off of host DNA synthesis
B	Formation of capsid precursors
C	DNA maturation
D	Capsid assembly
E	Host cell lysis
F	Major capsid protein
G	Major spike protein
H	Minor spike protein
J	DNA packaging protein
K	Function unknown

Genetic map of ϕX174

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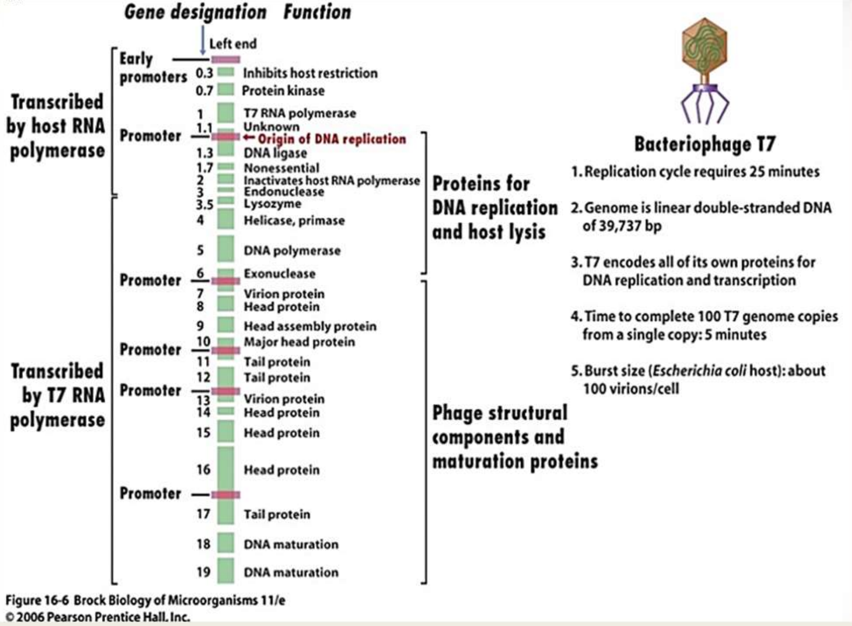
Bacteriophage T7



Gene designation	Function
0.3	Inhibits host restriction
0.7	Protein kinase
1	T7 RNA polymerase
1.1	Unknown
1.3	DNA ligase
1.7	Nonessential
2	Inactivates host RNA polymerase
3	Endonuclease
3.5	Lysozyme
4	Helicase, primase
5	DNA polymerase
6	Exonuclease
7	Virion protein
8	Head protein
9	Head assembly protein
10	Major head protein
11	Tail protein
12	Tail protein
13	Virion protein
14	Head protein
15	Head protein
16	Head protein
17	Tail protein
18	DNA maturation
19	DNA maturation

Bacteriophage T7

1. Replication cycle requires 25 minutes
2. Genome is linear double-stranded DNA of 39,737 bp
3. T7 encodes all of its own proteins for DNA replication and transcription
4. Time to complete 100 T7 genome copies from a single copy: 5 minutes
5. Burst size (*Escherichia coli* host): about 100 virions/cell

Figure 16-6 Brock Biology of Microorganisms 11/e
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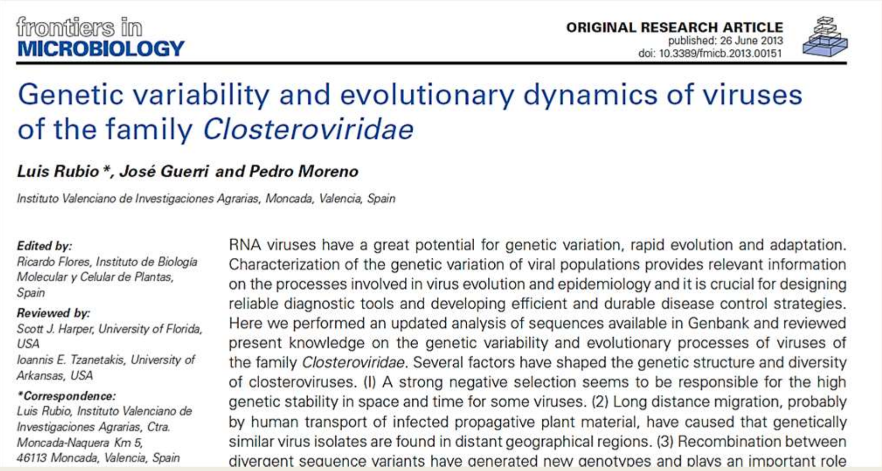

frontiers in
MICROBIOLOGY

ORIGINAL RESEARCH ARTICLE
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Genetic variability and evolutionary dynamics of viruses of the family *Closteroviridae*

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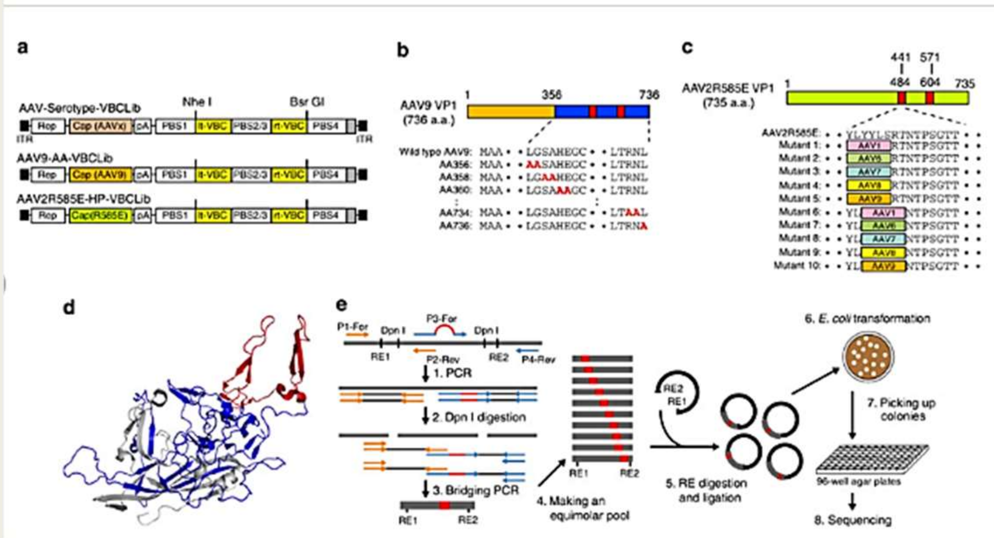
RNA viruses have a great potential for genetic variation, rapid evolution and adaptation. Characterization of the genetic variation of viral populations provides relevant information on the processes involved in virus evolution and epidemiology and it is crucial for designing reliable diagnostic tools and developing efficient and durable disease control strategies. Here we performed an updated analysis of sequences available in Genbank and reviewed present knowledge on the genetic variability and evolutionary processes of viruses of the family *Closteroviridae*. Several factors have shaped the genetic structure and diversity of closteroviruses. (I) A strong negative selection seems to be responsible for the high genetic stability in space and time for some viruses. (2) Long distance migration, probably by human transport of infected propagative plant material, have caused that genetically similar virus isolates are found in distant geographical regions. (3) Recombination between divergent sequence variants have generated new genotypes and plays an important role

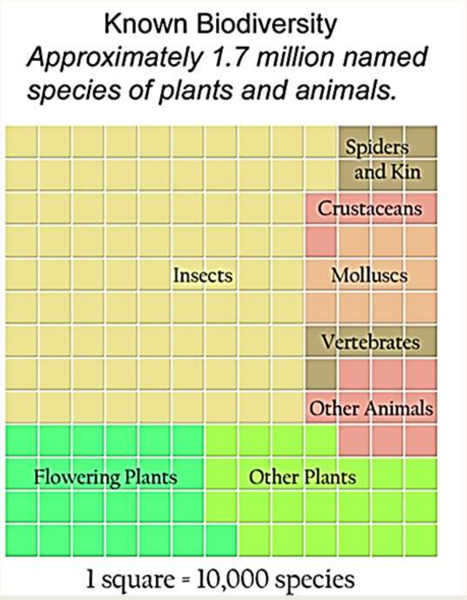
Phylogenetic trees of the coat protein genes of different viruses of the family Closteroviridae

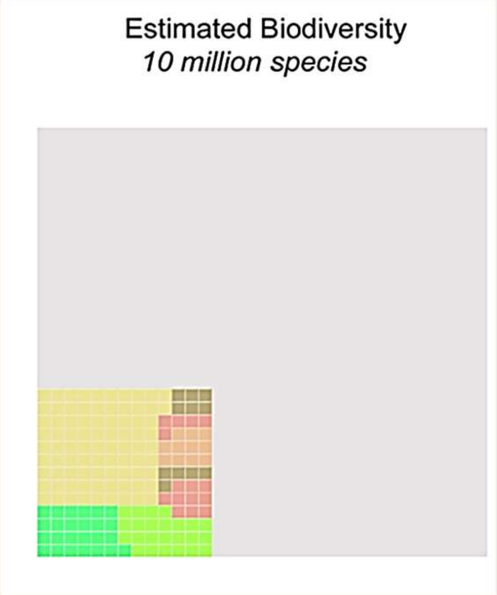


TUMBUHAN

Apa itu barkode DNA tumbuhan

dan
mengapa ada kebutuhan untuk itu?





Bagaimana cara kerja barkoding

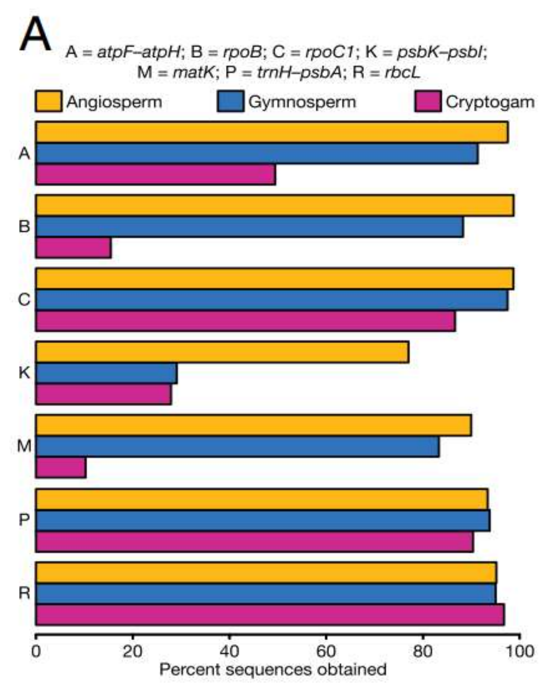
Tumbuhan disampel

DNA di ekstrak

Amplifikasi barkode

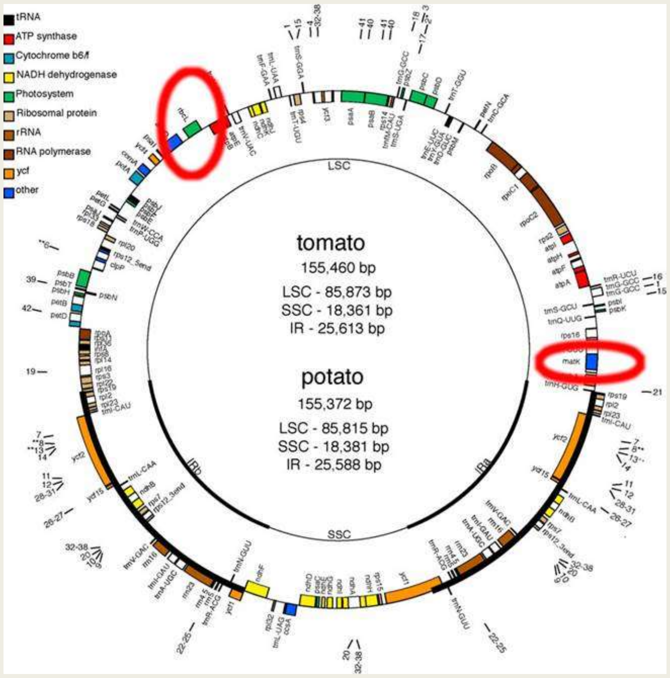
ACGAGTCGGTAGCTGCCCTCTGACTGCATCGAA
TTGCTCCCCTACTACGTGCTATATGCGCTTACGAT
CGTACGAAGATTTATAGAATGCTGCTACTGCTCC
CTTATTCGATAACTAGCTCGATTATAGCTACGATG

Hasil sekuensing DNA tumbuhan dibandingkan dengan sekuens di database barcode



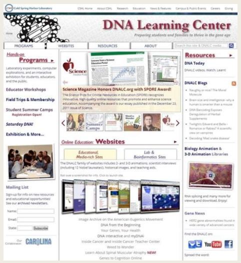
Konsorsium untuk Barcode of Life merekomendasikan penggunaan gen kloroplas *rbcL* dan *matK* sebagai barkode universal tumbuhan.

Peringatan:
Seperti barkode yang lain, *rbcL* dan / atau *matK* memiliki kemungkinan untuk gagal. Apabila kedua gen tidak bekerja maka memerlukan identifikasi baru lokus barkode yang sesuai.

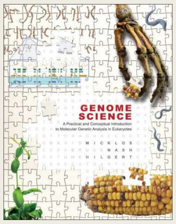


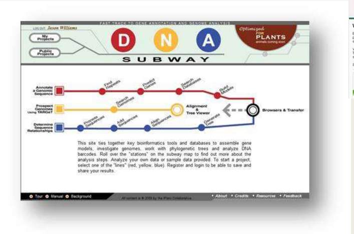
*Rbc*L
*Mat*K

DNA Barcoding: The Works



- DNA ekstraksi
- Amplifikasi gen
- Sekuensing barkode
- Analisis sekuens



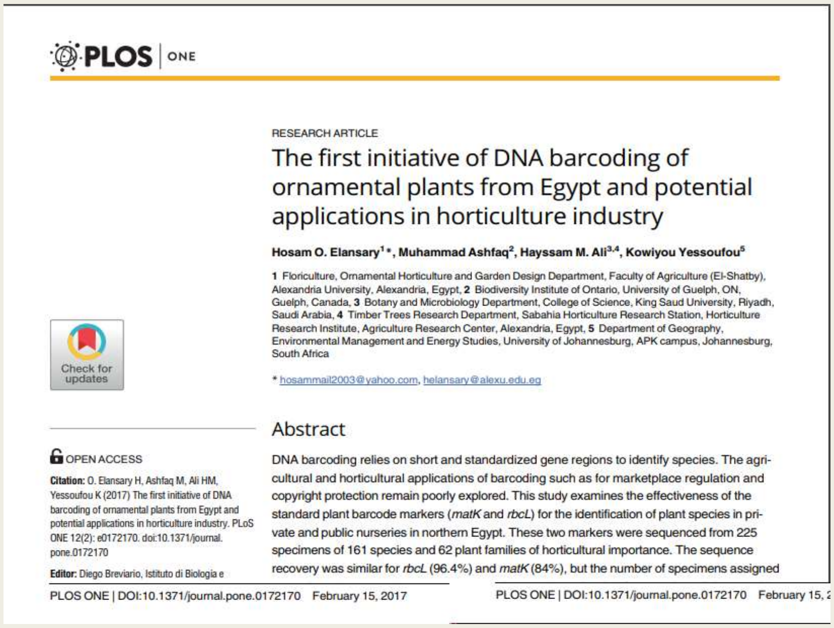


This site ties together key bioinformatics tools and databases to assemble gene models, investigate genomes, work with phylogenetic trees and analyze DNA barcodes. Roll over the "stations" on the subway map to find out more about the analysis steps. Analyze your own data or sample data provided. To start a project, select one of the "lines" (red, yellow, blue). Register and login to be able to save and share your results.

Potensi Aplikasi Barkoding

a) Mengendalikan hama pertanian - dengan cara mengidenfikasi hama pada berbagai fase kehidupannya, pengendalian sebelum terjadi kerusakan tanaman.
b) Identifikasi vektor Penyakit - memungkinkan identifikasi penyakit yang disebebkan vektor pada hewan dan manusia.
c) Mempertahankan sumber daya alam - dengan memantau perdagangan illegal produk yang terbuat dari sumber daya alam seperti kayu keras.
d) Melindungi spesies yang terancam punah.
e) Inspeksi authentifikasi produk kesehatan alami.
f) Biosekuriti

Untuk dipelajari !



PLOS | ONE

RESEARCH ARTICLE

The first initiative of DNA barcoding of ornamental plants from Egypt and potential applications in horticulture industry

Hosam O. Elansary[1]*, Muhammad Ashfaq[2], Hayssam M. Ali[3,4], Kowiyou Yessoufou[5]

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OPEN ACCESS

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Editor: Diego Breviario, Istituto di Biologia e

Abstract

DNA barcoding relies on short and standardized gene regions to identify species. The agricultural and horticultural applications of barcoding such as for marketplace regulation and copyright protection remain poorly explored. This study examines the effectiveness of the standard plant barcode markers (*matK* and *rbcL*) for the identification of plant species in private and public nurseries in northern Egypt. These two markers were sequenced from 225 specimens of 161 species and 62 plant families of horticultural importance. The sequence recovery was similar for *rbcL* (96.4%) and *matK* (84%), but the number of specimens assigned

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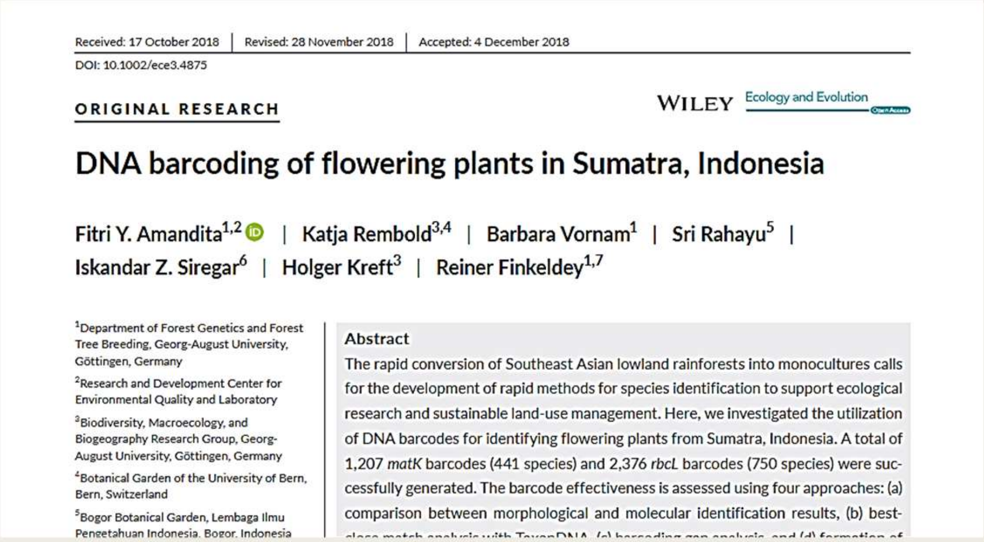

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ORIGINAL RESEARCH

WILEY Ecology and Evolution Open Access

DNA barcoding of flowering plants in Sumatra, Indonesia

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Abstract

The rapid conversion of Southeast Asian lowland rainforests into monocultures calls for the development of rapid methods for species identification to support ecological research and sustainable land-use management. Here, we investigated the utilization of DNA barcodes for identifying flowering plants from Sumatra, Indonesia. A total of 1,207 *matK* barcodes (441 species) and 2,376 *rbcL* barcodes (750 species) were successfully generated. The barcode effectiveness is assessed using four approaches: (a) comparison between morphological and molecular identification results, (b) best-

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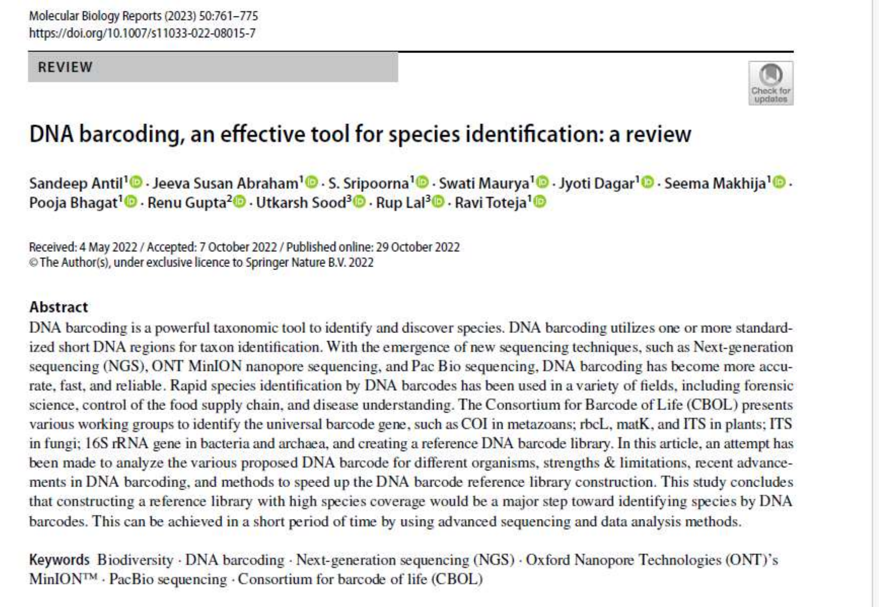

Molecular Biology Reports (2023) 50:761–775
https://doi.org/10.1007/s11033-022-08015-7

REVIEW

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DNA barcoding, an effective tool for species identification: a review

Sandeep Antil[1] · Jeeva Susan Abraham[1] · S. Sripoorna[1] · Swati Maurya[1] · Jyoti Dagar[1] · Seema Makhija[1] · Pooja Bhagat[1] · Renu Gupta[2] · Utkarsh Sood[3] · Rup Lal[3] · Ravi Toteja[1]

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Abstract

DNA barcoding is a powerful taxonomic tool to identify and discover species. DNA barcoding utilizes one or more standardized short DNA regions for taxon identification. With the emergence of new sequencing techniques, such as Next-generation sequencing (NGS), ONT MinION nanopore sequencing, and Pac Bio sequencing, DNA barcoding has become more accurate, fast, and reliable. Rapid species identification by DNA barcodes has been used in a variety of fields, including forensic science, control of the food supply chain, and disease understanding. The Consortium for Barcode of Life (CBOL) presents various working groups to identify the universal barcode gene, such as COI in metazoans; rbcL, matK, and ITS in plants; ITS in fungi; 16S rRNA gene in bacteria and archaea, and creating a reference DNA barcode library. In this article, an attempt has been made to analyze the various proposed DNA barcode for different organisms, strengths & limitations, recent advancements in DNA barcoding, and methods to speed up the DNA barcode reference library construction. This study concludes that constructing a reference library with high species coverage would be a major step toward identifying species by DNA barcodes. This can be achieved in a short period of time by using advanced sequencing and data analysis methods.

Keywords Biodiversity · DNA barcoding · Next-generation sequencing (NGS) · Oxford Nanopore Technologies (ONT)'s MinION™ · PacBio sequencing · Consortium for barcode of life (CBOL)