विकसित भारत

Plant-Biotic Interactions and Sustainable Development

सुदेष्णा मजूमदार लेइटों

smazumdar@botany.du.ac.in

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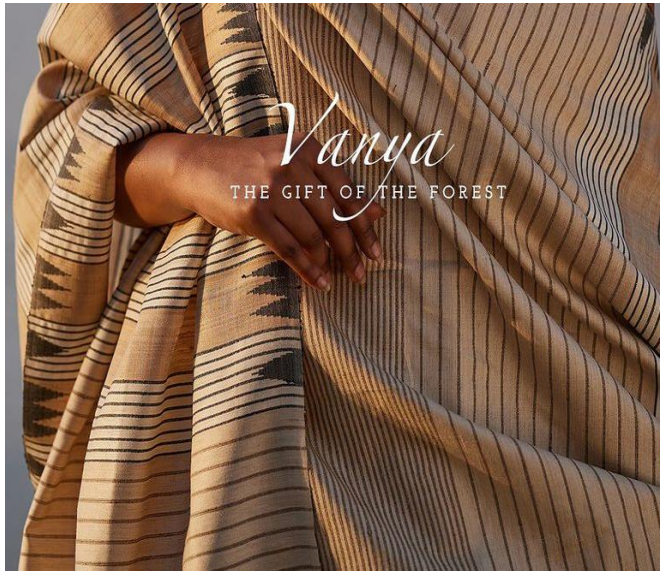
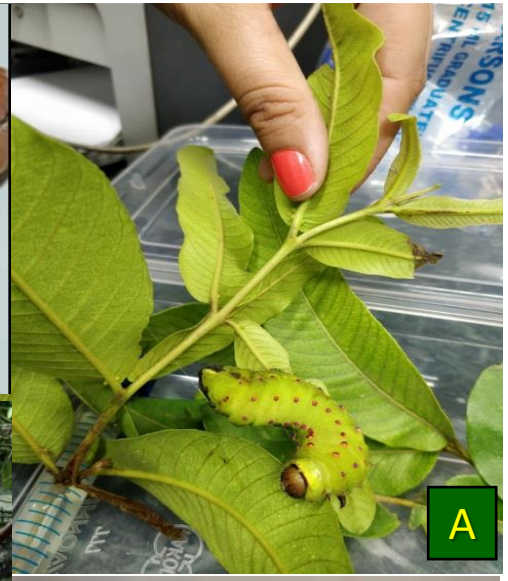
Vanya Cocoon Silks: Fiber, Feed, & Food



Vanya (Non-Mulberry) silkworms

(A & B) Eri moth & larvae (*Samia ricini* Anderson);
(C & D) Muga moth & larvae (*Antheraea assamensis* (Helfer))



(A) Tasar larva, (B) Tasar cocoons, (C), (D) Male and Female moth (*Antheraea mylitta* Drury)

Host plants of Non-mulberry silkworms

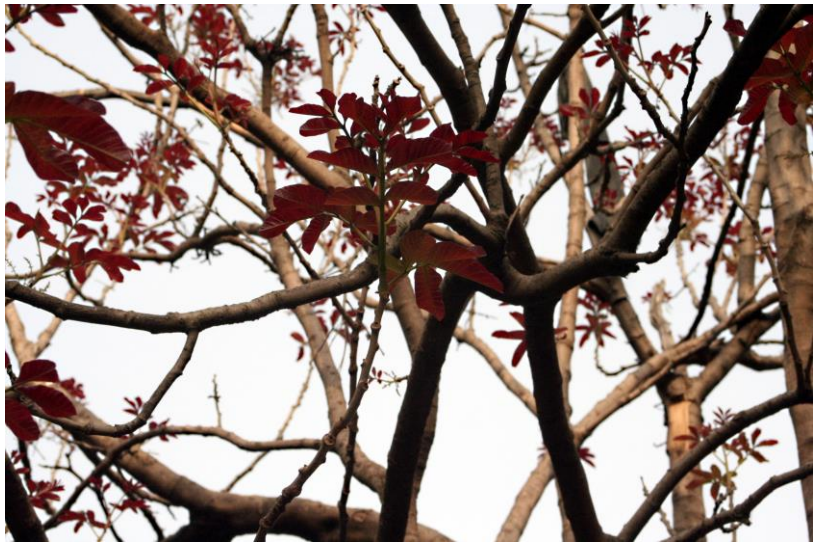
Ricinus communis L. (Castor)
Image source: nationaalherbarium.nl

Persea bombycina (Som)
Image source: researchgate.net

Terminalia arjuna (Arjun)

Ailanthus excelsa Roxb. (Tree of heaven)
Image source: indiabiodiversity.org

Litsea monopetala (Sualu)
Image source: researchgate.net



Schleichera oleosa (Kusum)

Low Production of Non-mulberry silks

Silk sector	2003-4	2004-5	2005-6	2006-7	2007-8	2022-23	2023-24 Price Per kg
Mulberry (*B. mori*)	13970	14620	15455	16525	16245	23896	25818 Rs. 3,421
Tassar (*A. mylitta*)	315	322	308	350	428	2689	1466 Rs. 4,000
Eri (*S. ricini)*	1352	1448	1442	1485	1530	6946	7364 Rs. 731
Muga (*A. assamensis*)	105	110	110	115	117	239	255 Rs. 27,000

- Current Silk Production Statistics of India (Metric tons), Employs 87.8 lakh people, 248.56 million $ (2024)
- In comparison to mulberry silk, the indigenous silk production has shown less perceptible improvement in recent years www.indiansilk.kar.nic.in

Diversity of Non-Mulberry Silkworms & Host Plants: Sustainable Livelihood for Diverse Tribal communities

Picture: (from left: The author, Mr. Sudhir Rabha and his family at Jorhat, Assam, 2004; photo courtesy: Mr. Jogesh Deuri, Goalpara)

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GOVERNMENT OF INDIA

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- United Nations Permanent Forum On Indigenous Issues (UNPFII)

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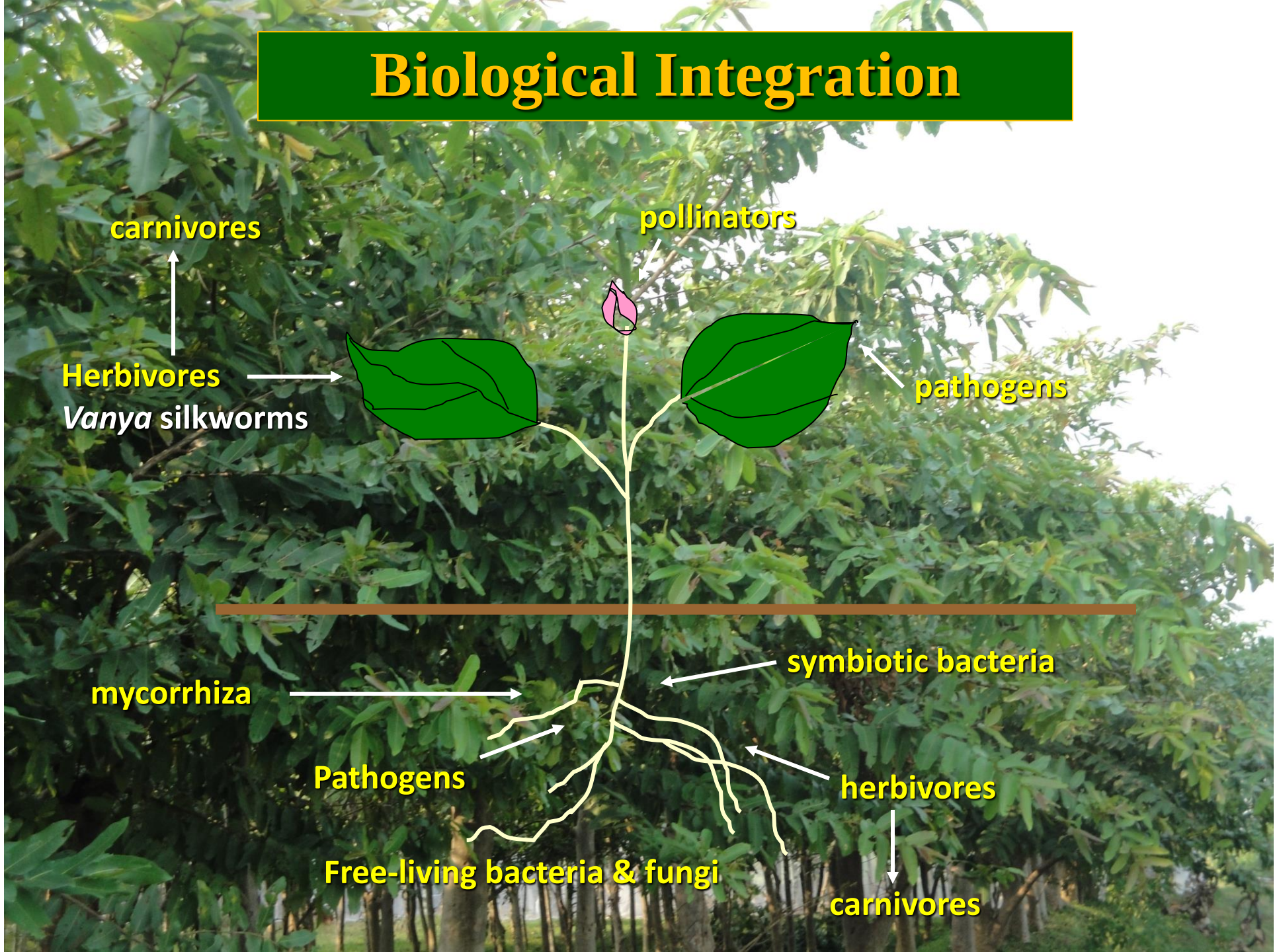
Rs 24,000 crore scheme for tribal welfare

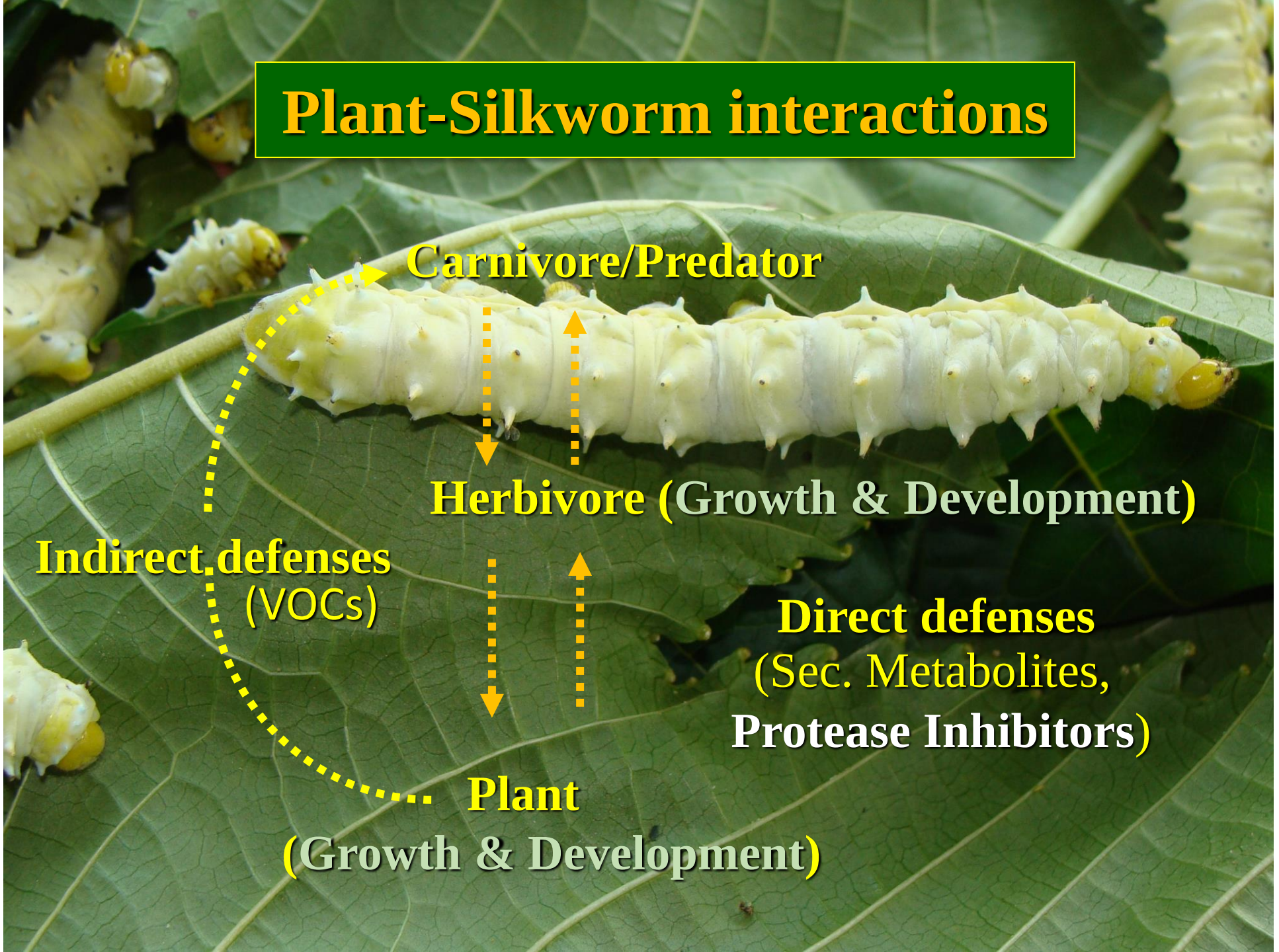
Pradhan Mantri Particularly Vulnerable Tribal Groups Development Mission's mandate is Inclusive development, social welfare (health and livelihood) to 75 tribes across 22,544 villages that require special attention and support by the government.

Host-plant Choice & Consequences for Non-Mulberry Silkworms reared by tribal communities in North-east and Central India

- Monophagy, Oligophagy and Polyphagy: **Biology** needs to be understood
- Plant defense responses to herbivory affects silkworm *growth & development*
- Dietary choice influences insect defense and *immunity*
- Anthropogenic rearing practices impacts silkworm domestication
- Populations of silkworms and host plant trees species need *in situ* conservation

Biological Integration




Plant-Silkworm interactions
Carnivore/Predator
Herbivore (Growth & Development)
Indirect defenses
(VOCs)
Direct defenses
(Sec. Metabolites,
Protease Inhibitors)
Plant
(Growth & Development)

Functional Co-evolution of Plant & Insect

Plant protease inhibitors - Insect digestive proteases

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Muga silk

Genetic Variation within Native Populations of Endemic Silkmoth *Antheraea assamensis* (Helfer) from Northeast India Indicates Need for *In Situ* Conservation

Y. Tunginba Singh, Sudeshna Mazumdar-Leighton, Mahaswetta Saikia, Prashant Pant, Sochanngam Kashung, Kartik Neog, Rajen Chakravorty, Suresh Nair, Javaregowda Nagaraju, Cheerukeri Raghavendra Babu

Published: November 21, 2012 • https://doi.org/10.1371/journal.pone.0049972

Abstract

A. assamensis is a phytophagous Lepidoptera from Northeast India r
Lauraceae family for its characteristic cocoon silk. Source of these c
farm stocks that crash frequently and/or wild insect populations that
need to reduce dependence on wild populations for cocoons neces
genetic diversity in cultivated and wild populations. Molecular mark
simple sequence repeats (ISSR) and simple sequence repeats (SS
populations of wild insects and eleven populations of cultivated ins
high genetic diversity estimates (H_I=0.25; H_S=0.28; H_E=0.42) an
contained private alleles. Both marker systems indicated that ger

Insect Molecular Biology

Royal Entomological Society

Expression of diverse midgut serine proteinases in the sericigenous Lepidoptera *Antheraea assamensis* (Helfer) is influenced by choice of host plant species

M. Saikia, Y. T. Singh, A. Bhattacharya, S. Mazumdar-Leighton

First published: 21 September 2010 | https://doi.org/10.1111/j.1365-2583.2010.01048.x | Citations: 15

Abstract

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frontiers | Frontiers in Insect Science

TYPE Original Research
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Guy Smagghe,
Vrije University Brussels, Belgium
Yiping Li,
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*CORRESPONDENCE
Sudeshna Mazumdar-Leighton
smazumdar@botany.du.ac.in

†PRESENT ADDRESSES
Sochanngam Kashung,
Department of Botany, Manipur College, Department of University and Higher Education, Imphal, State Government of Manipur, India
Mahaswetta Saikia,

Midgut serine proteinases participate in dietary adaptations of the castor (Eri) silkworm *Samia ricini* Anderson transferred from *Ricinus communis* to an ancestral host, *Ailanthus excelsa* Roxb

Sochanngam Kashung†, Parul Bhardwaj, Mahaswetta Saikia† and Sudeshna Mazumdar-Leighton*

Plant-Biotic Interactions Lab, Department of Botany, University of Delhi, Delhi, India

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Results-Tasar host trees and Rearers

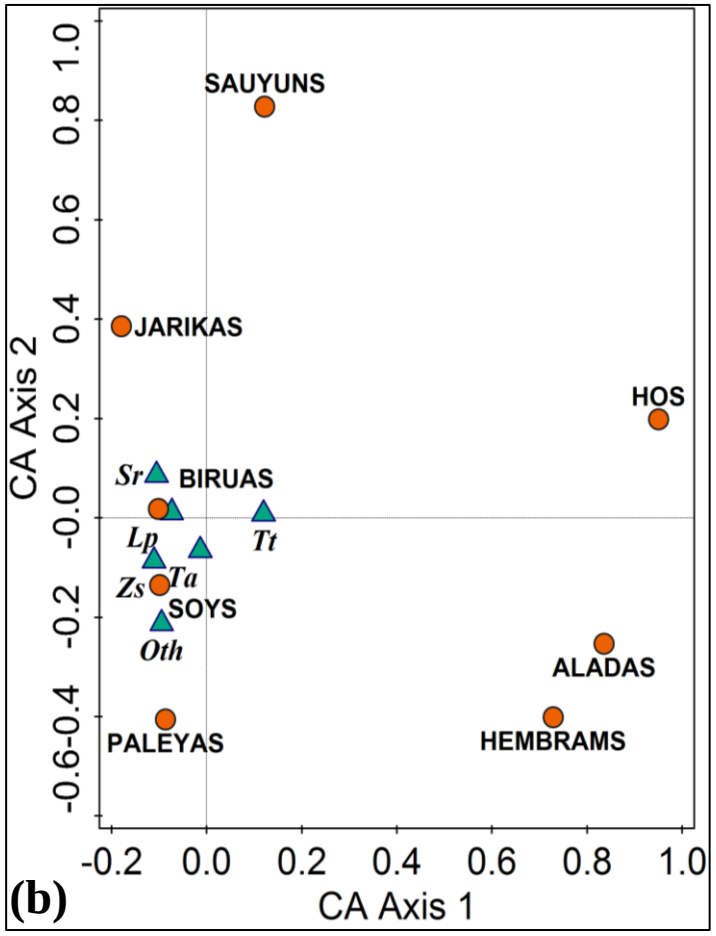


Figure 2.2: (a) Interactions with Tasar rearers in Bihar, Odisha and Chhattisgarh; (b) **Ordination plot of Canonical correlation analysis (CCA) of tribal communities and the host plants of the Tasar silkworms owned by the tribal families.** Blue triangles represent host plants (primary and secondary) and orange circles represent the different families who contributed to the survey. Key: Sr: *S. robusta*, Tt: *T. tomentosa;* Ta: *T. arjuna*; Lp: *Lagerstroemia parviflora*, Zs: *Zizyphus* and Oth: other species

Different families owned different numbers and types of Tasar host plant species. Therefore NTFP generated per village may be mixed or dominated by type(s) of host tree as well as insect genotype(s). More quantitative data (including host tree surveys) is needed to correlate NTFP type, host plant and rearer communities in the country. Monitoring for disease status in wild populations is **Urgently Needed**.

Results: Tasar sericulture in *T. arjuna* plantations, Banka, Bihar

Figure 2.1: **Plantations are composed of only one or two tree species and are well-maintained.** (d) *T. arjuna* plantations; (e) Tasar silkworm rearing under nylon nets; (f) Early instars of the commercial "Daba" ecorace feeding on *T. arjuna* leaves.

Results: Diversity of host tree species in tribal lands

Figure 2.1: **A rich diversity of host trees are available for tasar sericulture in forest fringe villages**. (a) ***Shorea robusta*** dominated forest in Chhattisgrah, Central India (b) A forest in Odisha, Central India with **mixed species** of host plants. (c) ***Anogeissus latifolia***, a secondary host plant of the insect in forests of Odisha

Nosema : Major caveat to yield realization in Tasar sericulture

Healthy Tasar female moth

Pébrinised Tasar female moth

Results: Map showing disease incidence in wild and cultivated populations of silkmoths

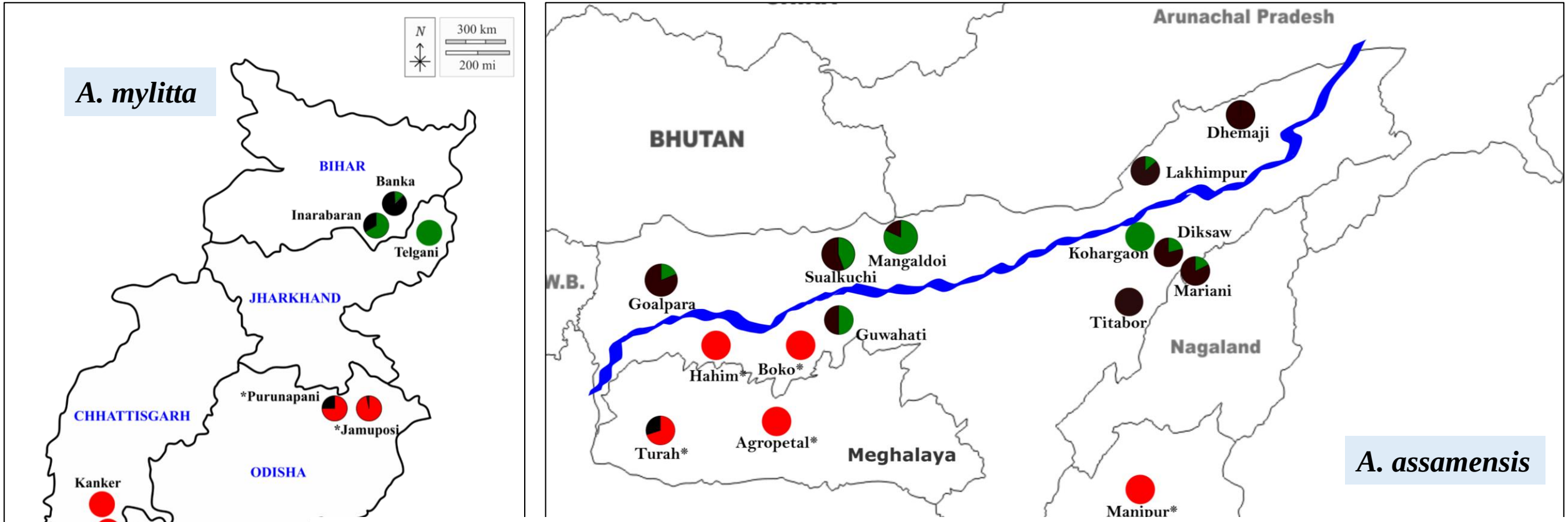
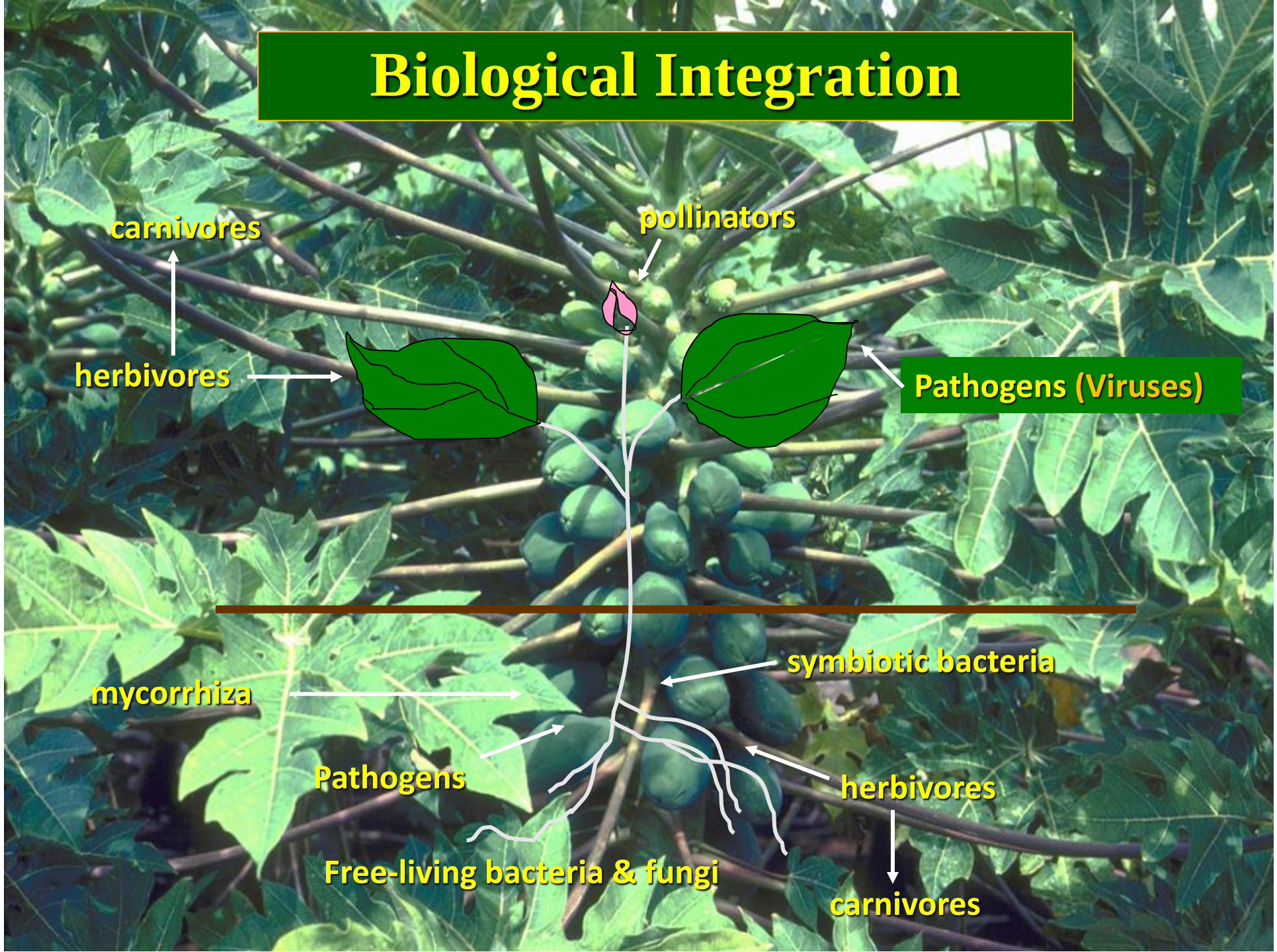


Figure: A map of (a) central India and (b) north-eastern India showing pie charts with % healthy and infected moths in sampled wild (marked with an asterisk *) and cultivated populations.

Results with both *A. mylitta* and *A. assamensis* clearly indicated that **wild populations had fewer individuals that were PCR positive for *Nosema* and hence, lower levels of Pébrine disease** ($\chi^2 = 91.413$, $p \leq 0.05$). However, the presence of even one insect in any wild population that is *Nosema* positive raises alarm bells, and **indicates that conservation of wild populations *in situ* as well as nil introduction of infected, highly susceptible commercial stocks is paramount to preserve low disease levels in forest/wild silkmoth populations.**


Biological Integration
carnivores
pollinators
herbivores
Pathogens (Viruses)
mycorrhiza
symbiotic bacteria
Pathogens
herbivores
Free-living bacteria & fungi
carnivores

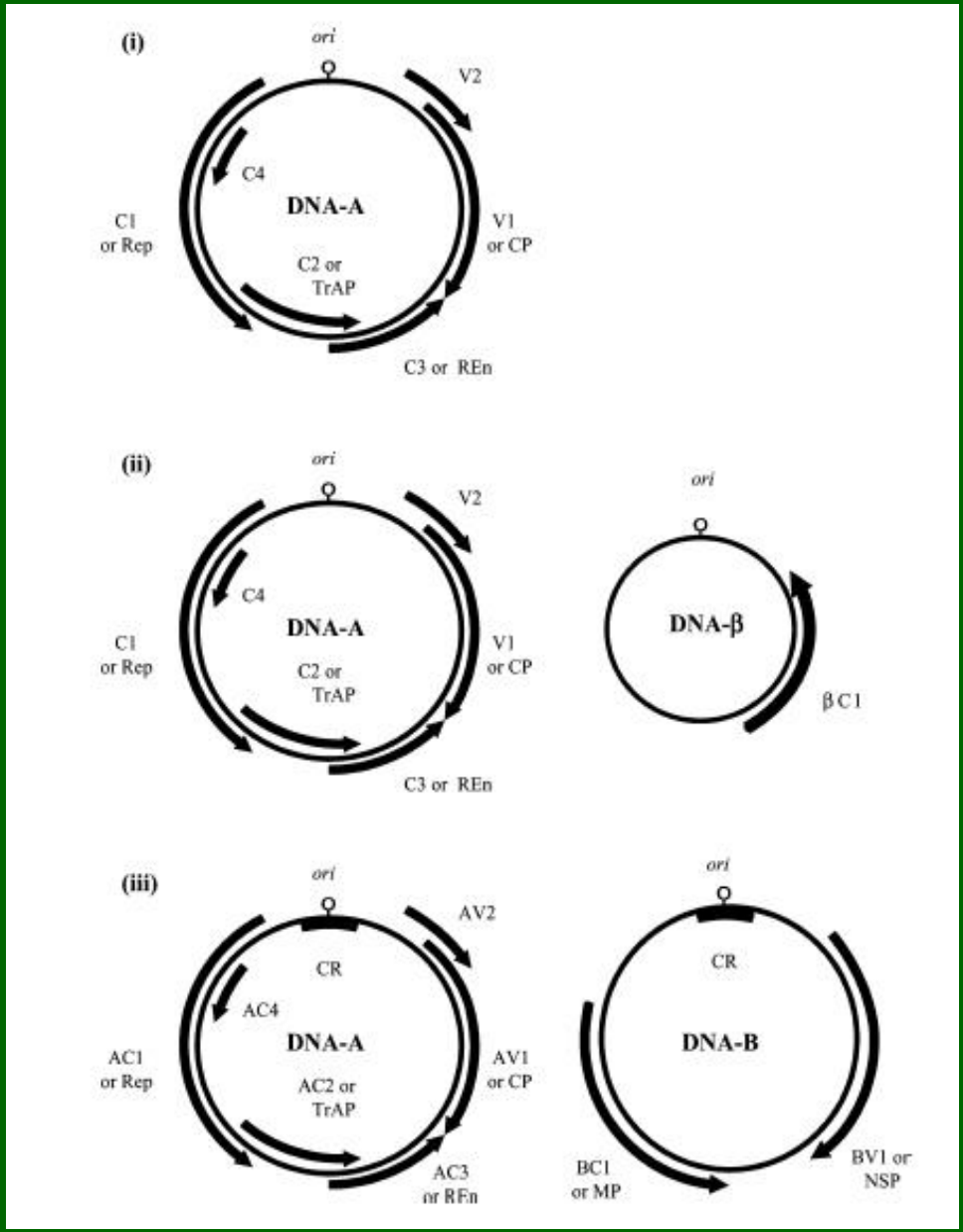
C. papaya has been grown in tropics since 1800s. Introduced from central America. Recent trends show preference for smaller, seedless, red-flesh fruit varieties

- No resistance
- Transmitted by insects
- Worldwide problem

Papaya viruses in India

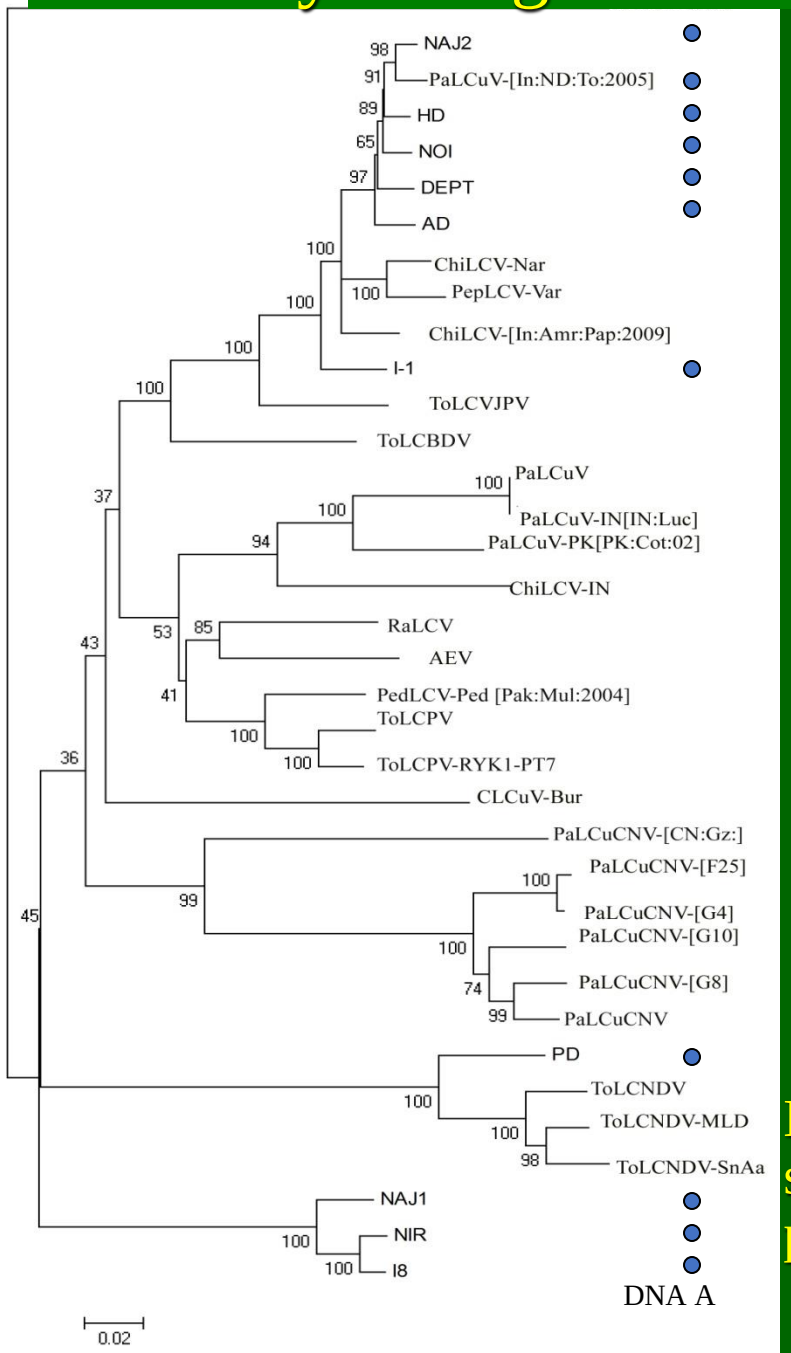
- PRSV & PaLCuV
- PaLCuV: DNA virus
- Transmitted by whiteflies (Begomovirus)
- No Resistance
- Symptomatic plants in fields has been rising
- Severe epidemic of Cotton Leaf curl Disease in Pakistan in 1990s.
- Recent LCD outbreak in Punjab, in 2015

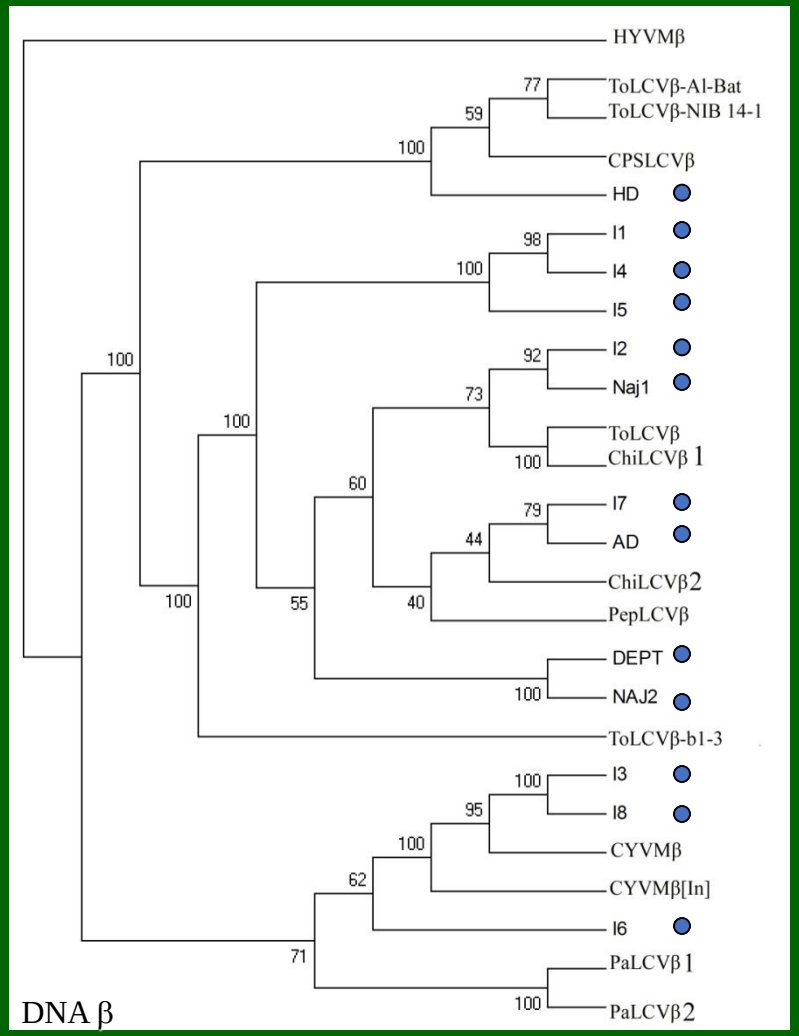
Amplification, cloning and sequencing



- Primers (Briddon et al., 2003)
- Diverse old-world mono-partite begomoviruses associated with DNA β
- Papayas infected with ChiLCuV, ToLCuNDV, and variants of a novel virus (PaLCrV)
- Persistent. No temporal/ spatial pattern of distribution.
- GenBank #DQ98925-6, HM140364-HM1403671, EU126825-6, HM143901-HM143911, DQ376036-39, EU126822-24, HM13420-37

Diversity of begomoviruses infecting papayas





Bootstrapped ML Trees drawn using PAUP showing relatedness of begomoviruses infecting papaya ( ), vegetables and weeds.

Mixed infections & Recombination

Various recombinational events were detected between the begomovirus DNA-A from papaya and their close relatives using RDP3 package. The parental sequences are represented with following colors:

U15016	AM712436
Najafgarh-1	DQ673859
EU939533	

Recombinational breakpoints were confirmed by GARD analysis.

Implications for transgenic strategies

- Papaya leaf curl disease is caused by infection of diverse begomoviruses associated with satellites.
- Host range expansion of viruses from Chilli, and tomato is evident. Recombination is implicated.
- Hence transgenic resistance need to be **broad-based**, targeting multiple viruses in the field.
- Selection of transgene for PDR is not straight-forward like PRSV.
- Genomic regions that are non-recombining, non-silencers of host plant defense and show low levels of variation should be used.
- Management-based virus control needs to be explored

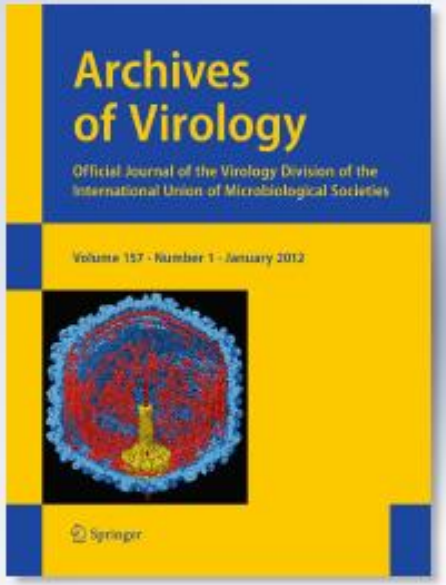
Spatial and temporal diversity of begomoviral complexes in papayas with leaf curl disease

P. Singh-Pant, P. Pant, S. K. Mukherjee & S. Mazumdar-Leighton

Archives of Virology
Official Journal of the Virology Division of the International Union of Microbiological Societies

ISSN 0304-8608
Volume 157
Number 7

Arch Virol (2012) 157:1217-1232
DOI 10.1007/s00705-012-1287-x



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Monitoring leaf curl disease complexes associated with whitefly-transmitted Begomoviruses infecting Papaya in Delhi NCR, India: Results from a long-term survey

K Tingneivah Mate[1], Aashima Mehra[1], Parul[1], Mansi Bansal[1] ,Tabasum Akhter[1], Pratibha Singh-Pant[1], Prashant Pant[1], Sunil Mukherjee[2], Sudeshna Mazumdar-Leighton[1*]
[1] Plant Biotic Interactions Group, Department of Botany, University of Delhi, Delhi-110007, India; [2]Department of Plant Pathology, IARI, New Delhi, India *Email: smceres21@yahoo.co.in, smazumdar@botany.du.ac.in

Abstract: Ongoing work initiated in 2004 indicated that cultivated commercial varieties and feral plants of papaya were susceptible hosts for highly divergent Begomoviruses causing leaf curl disease. In addition to DAS-ELISA based serological detection of Begomoviruses related to Tomato leaf curl disease, PCR-based screens were used to determine virus incidences in symptomatic and non-symptomatic plants from the region. While mono-partite Begomoviruses like *Chilli leaf curl virus* and *Papaya leaf crumple virus* were found to be persistent, *Tomato leaf curl New Delhi virus* was also prevalent among the sampled plants. Several Begomovirus
plants displayed a wi
satellites in the survey

Introduction: Papay
among tropical fruits i
is known to be infec
including *Papaya ring*
Begomoviruses that

Understanding Persistence and Evolution of Begomoviruses infecting Feral Papaya and Solanaceous weeds by Epidemiological Screenings.

S.Hamsa[1*], Tabasum Akhter[1*], Parul Bhardwaj[1*], Aashima Mehra[1*], Sunil Mukherjee[2], Sudeshna Mazumdar-Leighton[1*]
[1]Plant Biotic Interactions Lab, Department of Botany, University of Delhi, Delhi-110007; [2]NER-BPMC, Department of Biotechnology, Government of India.
*Authors SH, TA, PB, and AM contributed equally to this study.

Detection of Begomoviruses and associated satellites in viruliferous whiteflies for surveys of leaf curl disease in feral papaya and non-papaya hosts

K. Tingneivah Mate[1*], Mansi Bansal[1], Paula Tennant[2] & Sudeshna Mazumdar-Leighton[1]
[1]Plant Biotic Interactions Lab, Department of Botany, University of Delhi, Delhi-7, India; [2]Department of Life Sciences, The University of the West Indies, Mona, Kingston-7, Jamaica *Email: tingneivahmate08@

Abstract Papaya is an important horticultural crop in the tropics. It is host to various debilitating plant viruses that cause reduced crop yields and economic loss to farmers. Papaya leaf curl disease in India is caused by whitefly-transmitted single-stranded DNA viruses of family *Geminiviridae*. Papaya leaf curl disease can also co-occur with Papaya ringspot disease caused by the positive stranded RNA potyvirus; *Papaya ringspot virus* (PRSV) transmitted by aphids showing typical symptoms, a large diversity of Begomoviruses was detected (Singh-Pant et al., Arch. Virol., 2012). Continuation of the survey over a decade since of an area about 827 square kilometres complexes in symptomatic papaya and neighbouring, non-papaya plants. It can be assumed that the distribution and abundance of these Begomoviruses is related to viruliferous whiteflies in the we report standardization of PCR-based methods to detect genomic components (viral DNA A, DNA B, and/or satellite molecules) in iso-female lines of *Bemisia tabaci* derived from by their mitochondrial cytochrome oxidase gene sequences, are available as GenBank accessions OM365985, OM365983, OK236818, ON054966, OM365980, OP490

Keywords Vectors of papaya viruses, local whitefly populations, alternate host plants, single insect diagnostics, Begomovirus genomes, leaf curl disease

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An improved plant regeneration protocol for a popular Indian Madhubindu variety of papaya (*Carica papaya* L.) via somatic embryogenesis

Rathi Utkarsha, Gupta Alisha, Pradhan Priyanka Joshiya, Choudhury Aparajita, Patil Basavaprabhu L., Mazumdar-Leighton S., Rajam Manchikatla V.

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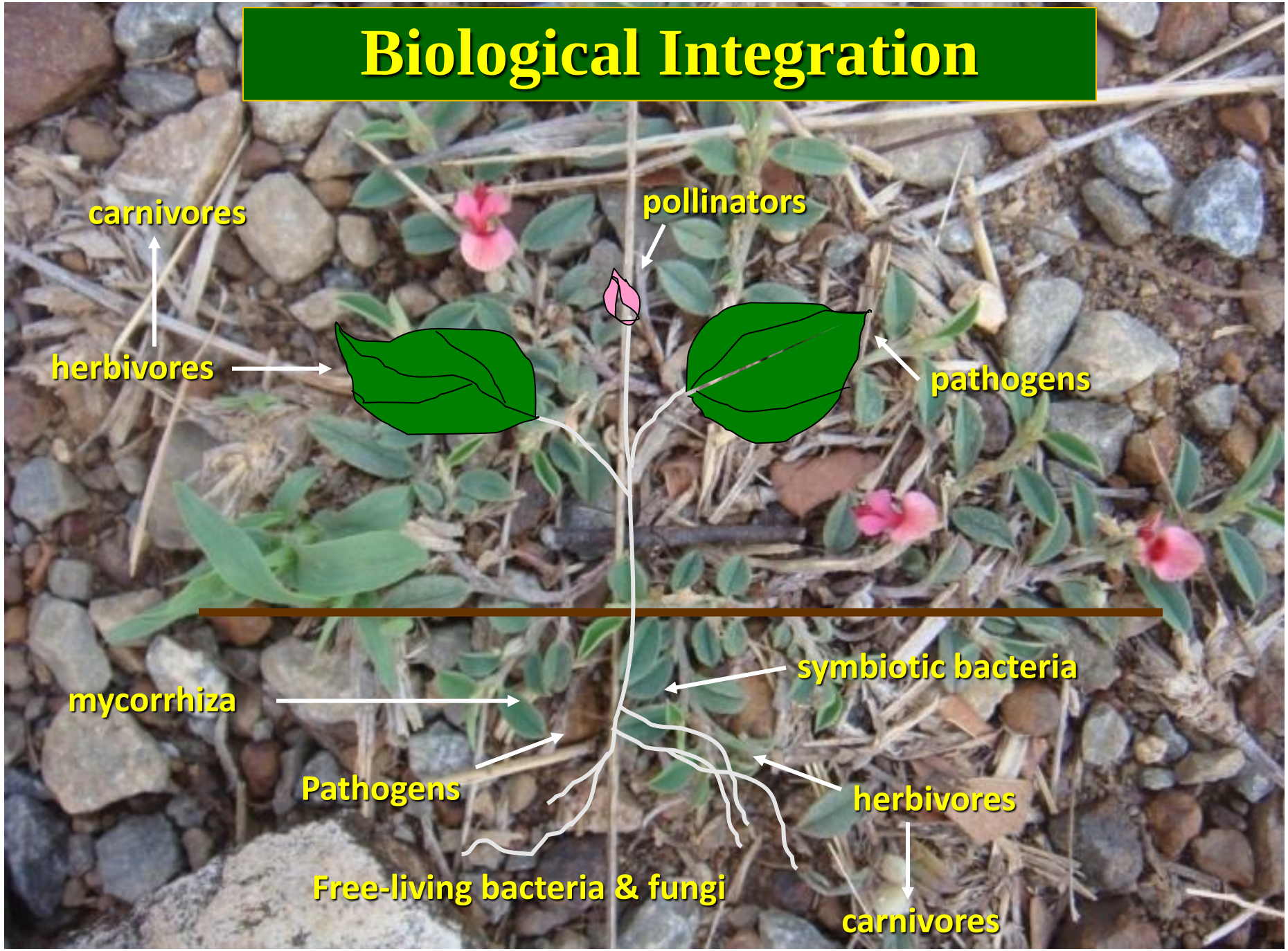
Pub Email: contact@vegetosindia.org

DOI: 10.1007/s42535-024-00971-8
First Page: 250
Last Page: 259
Views: 1745

Keywords: n Carica papayan , Plant hormones, Seed germination, In vitro plant regeneration, Somatic embryogenesis

Abstract

Papaya (*Carica papaya* L.) is an important fruit crop, and it is highly nutritive and has several medicinal properties. In the present study, we have developed an improved protocol for in vitro plant regeneration through somatic embryogenesis. A high seed germination rate was achieved, when the seeds were treated with 600 ppm of gibberellic acid to break the seed


Biological Integration
carnivores
herbivores
pollinators
pathogens
mycorrhiza
symbiotic bacteria
Pathogens
herbivores
Free-living bacteria & fungi
carnivores

Funding: DBT Program support on Restoration Ecology to Prof. CR Babu

2005 BEFORE RESTORATION, Purnapani, Odissa

Funding: DBT Program support on Restoration Ecology to Prof. CR Babu

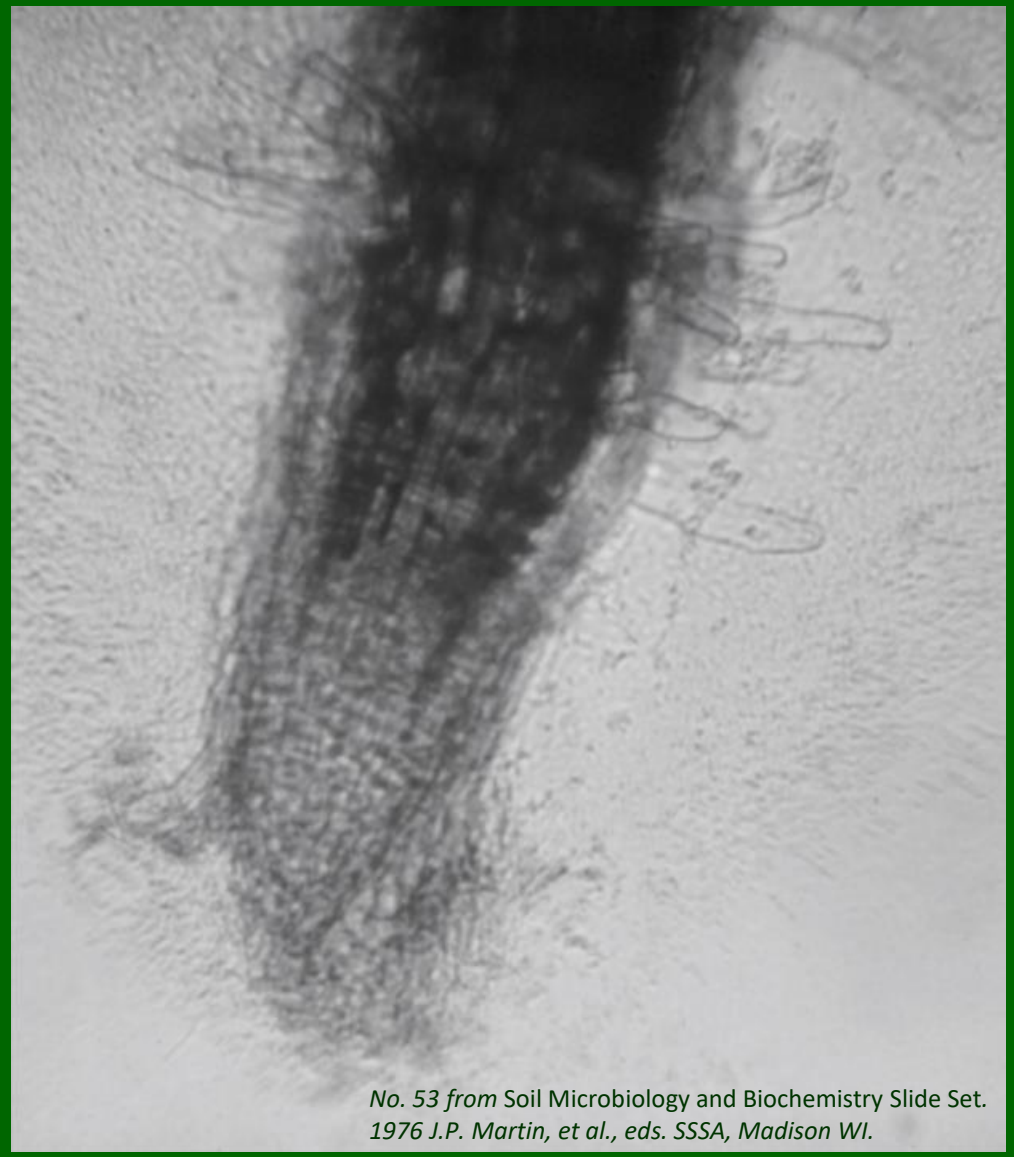
2011 AFTER RESTORATION, Purnapani, Odisha

Soil Microbial Diversity

The Rhizosphere

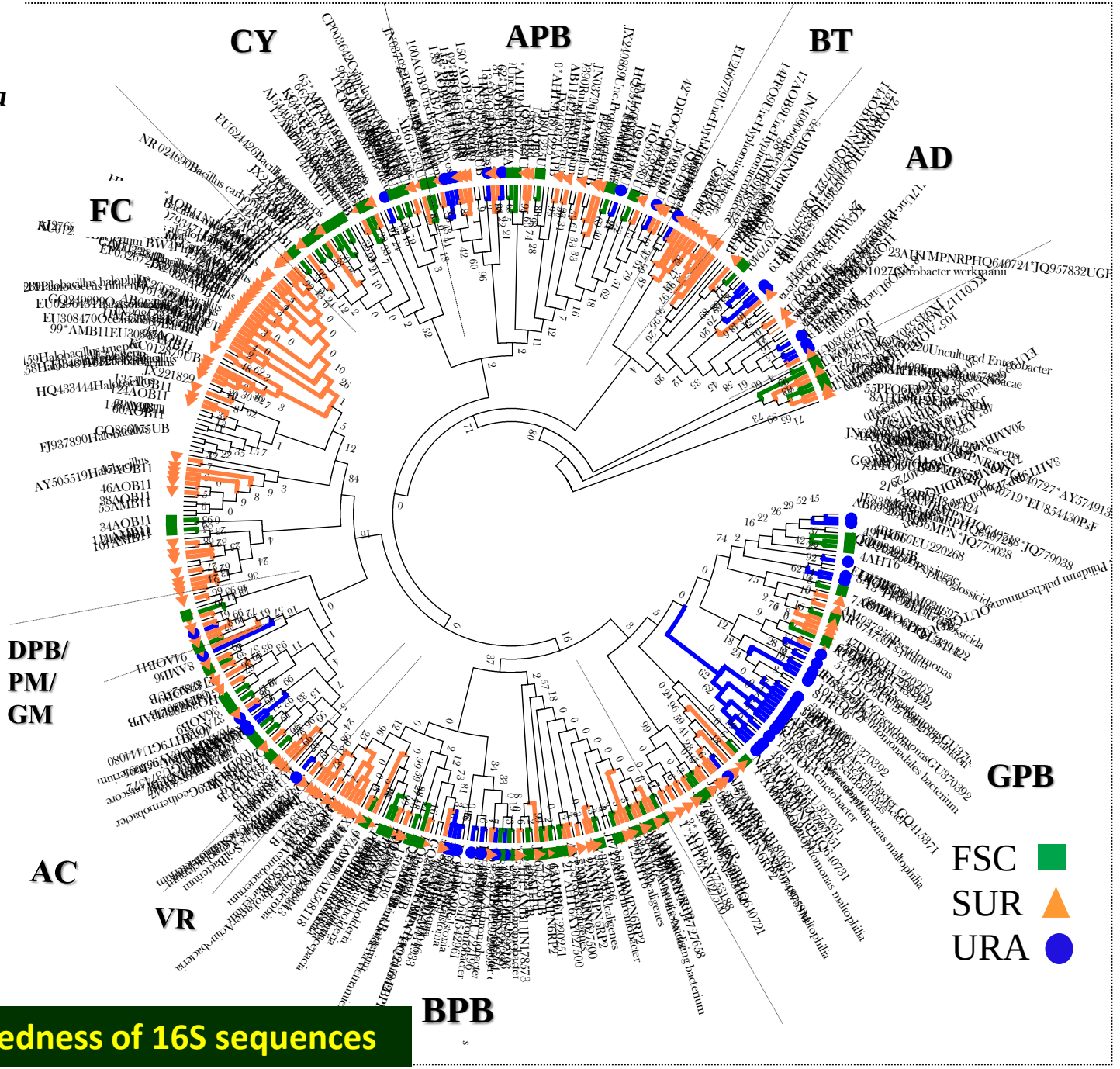
"rhizo" = root

"sphere" = zone



No. 53 from Soil Microbiology and Biochemistry Slide Set.
1976 J.P. Martin, et al., eds. SSSA, Madison WI.

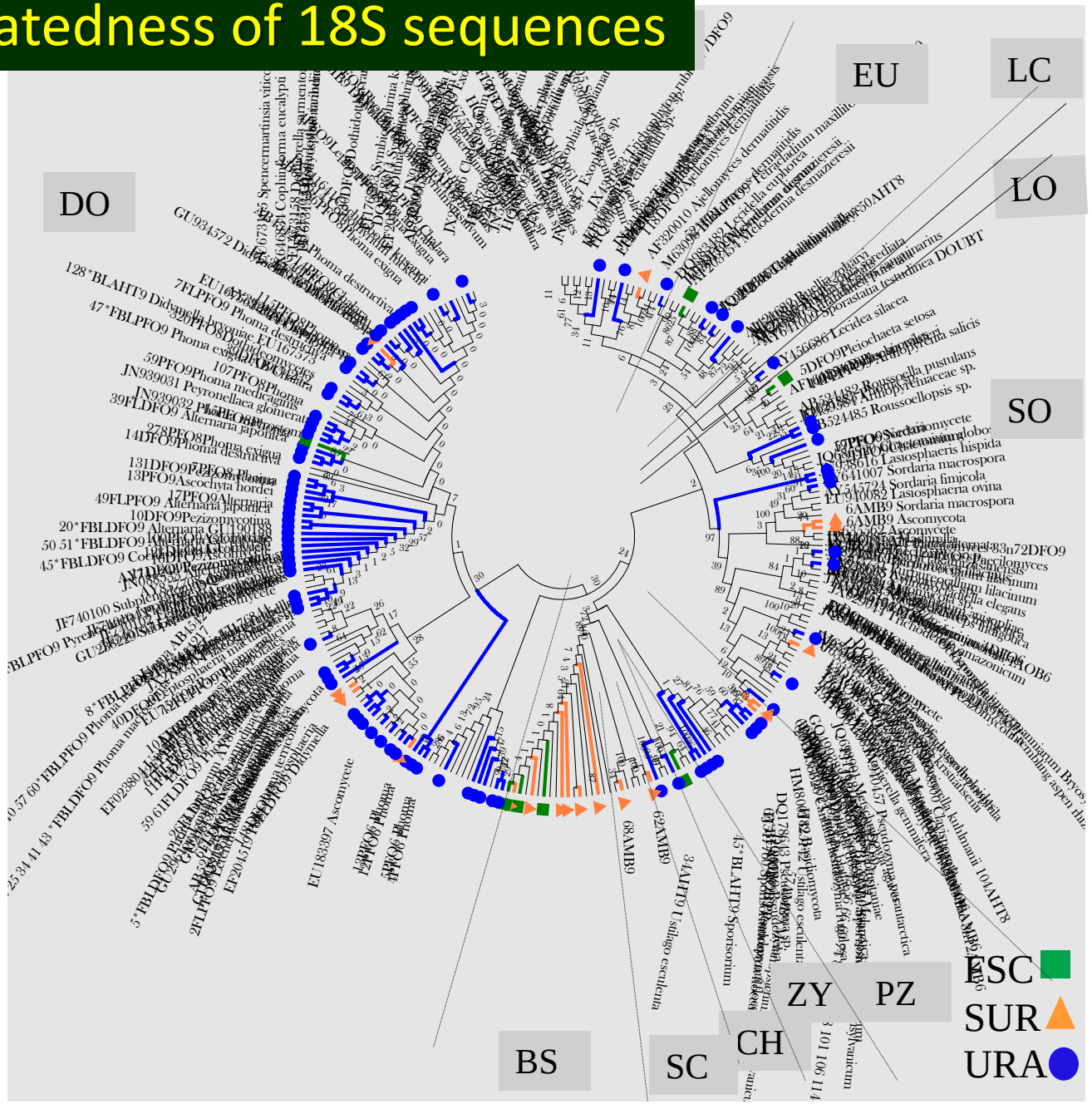
APB: *Alphaproteobacteria*
BPB: *Betaproteobacteria*
GPB:*Gammaproteobacteria*
DPB: *Deltaproteobacteria*
GM: *Gemmatimonadetes*
PM: *Planctomycetes*
CY: *Cyanobacteria*
AC: *Actinobacteria*
VR: *Verrucomicrobia*
AD: *Acidobacteria* Gp4, 6
BT: *Bacteriodetes*
FC: *Firmicutes*



A Tree showing relatedness of 16S sequences

A tree showing relatedness of 18S sequences

DO: Dothideomycetes
SO: Sordariomycetes
LO: Leotiomycetes
LC: Lecanoromyvetes
EU: Eurotiomycetes
SC: Saccharomycetes
CH: Chytridiomycetes
ZY: Zygomycetes
PZ: Pezizomycetes
BS: Basidiomycetes



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Volume 22, Issue 10
1 October 2024

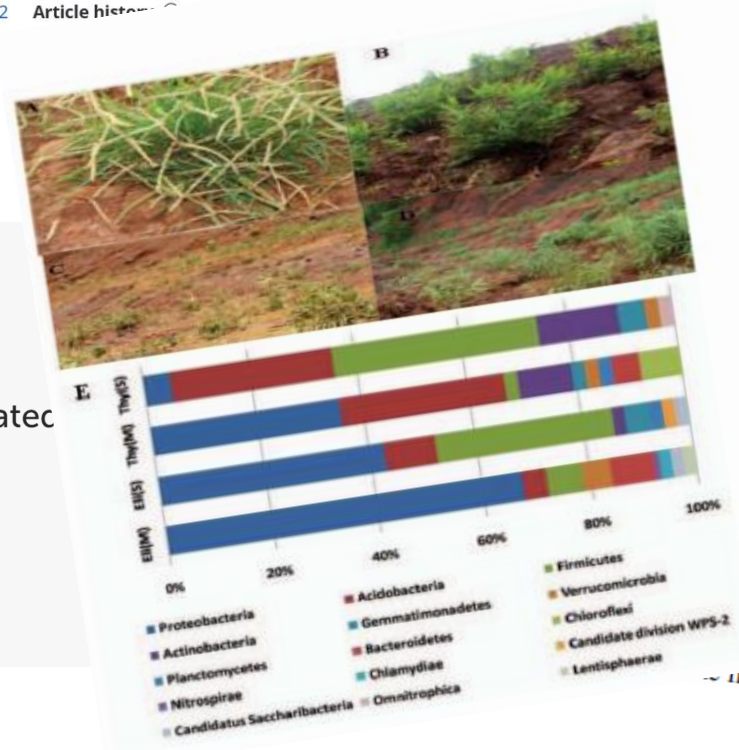
RESEARCH ARTICLE | OCTOBER 01 2024

Characterization of microbial communities in the sewage of a major urban drain

Mansi Bansal; Nidhi Seth; Cheerukeri Raghavendra Babu; Saurav Mazumdar; Sudeshna Mazumdar-Leighton

J Water Health (2024) 22 (10): 1922–1941.
https://doi.org/10.2166/wh.2024.212 **Article histo**

Views



ORIGINAL RESEARCH article

Front. Microbiol. , 18 March 2024
Sec. Aquatic Microbiology
Volume 15 - 2024 | https://doi.org/10.3389/fmicb.2024.1355718

Microbial community diversity of an integratec constructed wetland used for treatment of sewage

Nidhi Seth[1,2] Sharad Vats[3] Suman Lakhanpaul[4] Yasir Arafat[2]
Sudeshna Mazumdar-Leighton[4] Mansi Bansal[4] C. R. Babu[2*]

Metagenomics at Grass Roots

Sudeshna Mazumdar-Leighton and Vivek K Choudhary

Metagenomics is a robust, interdisciplinary approach for studying microbial community composition, function, and dynamics. It typically involves a core of molecular biology, micro- biology, ecology, statistics, and com- al biology. Excit- ng outcomes anticipate- s include unrav- ling of com- ize the ecologi- habitats from e human guts, eposits, polar Knowledge endous po- ecosystem technical ng meth- rovided e grass ds un-

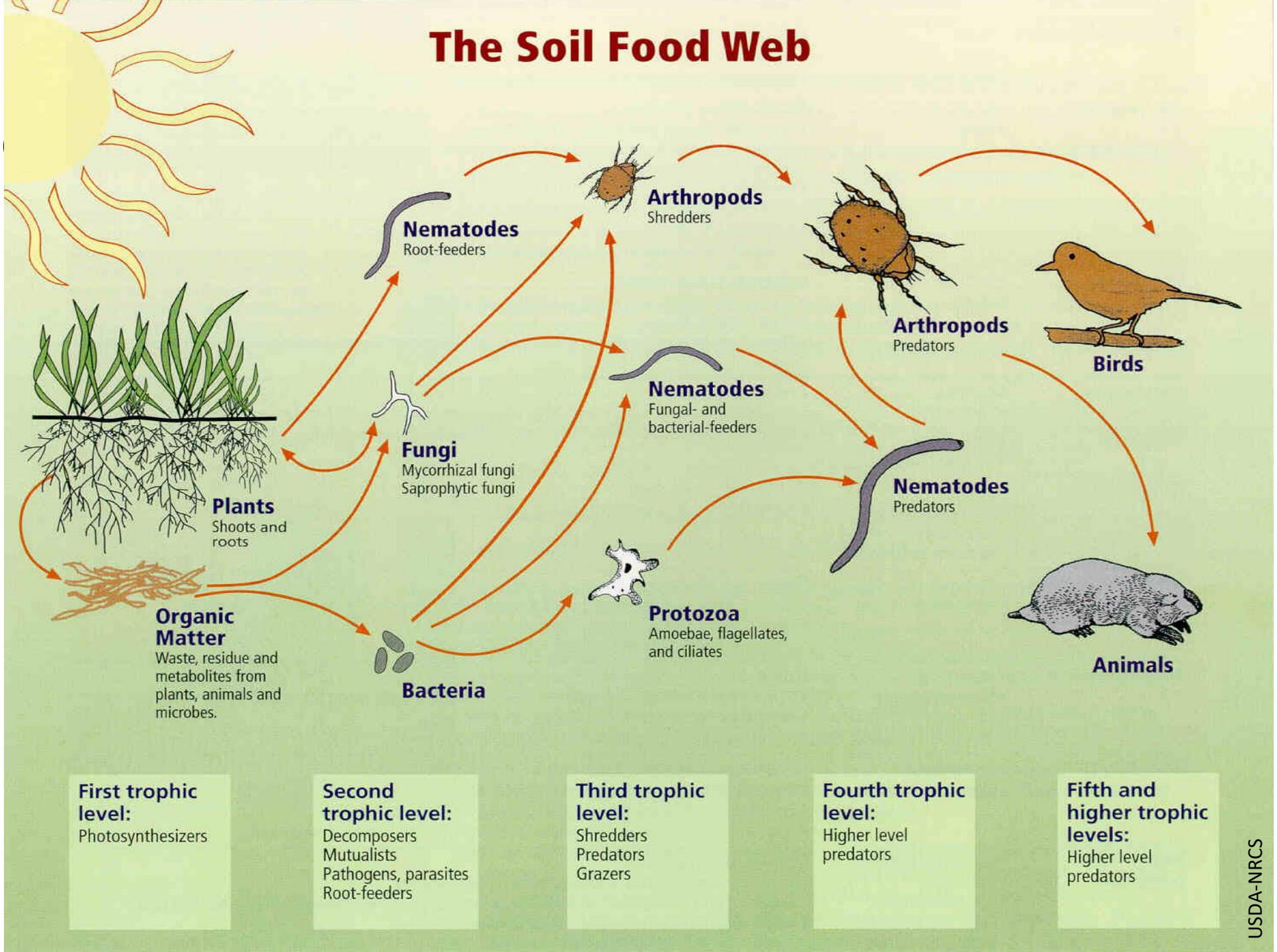
Figure 1. Clumps of grasses of (A) *Eleusine indica* and (B) *Thysanolaena latifolia* growing on slopes of iron-ore mine dump sites undergoing restoration in (C) summer, 2011 and (D) monsoon, 2011. (E) Relative abundance of prominent phyla of rhizospheric bacterial communities of *T. latifolia* (Thy) and *E. indica* (Eli) sampled in the summer (S) and monsoon (M) from degraded mined-out sites from C and D. Rare bacteria (singletons, <2% of total bacteria) are not shown.

man and a- , the gen- medicines and chem- one of the most prominent areas life sciences. Etymology of the word 'metage-

Sudeshna Mazumdar-Leighton is a molecular biologist at Delhi University. Her research interests are plant-biotic environment interactions, relevant to marginalized communities.

Vivek K Choudhary has just completed a PhD dissertation on restoration ecology of iron-ore mine sites in Odisha. He is interested in plant community dynamics, revegetation, and soil metagenomics.

Th


The Soil Food Web
Arthropods
Shredders
Nematodes
Root-feeders
Arthropods
Predators
Birds
Nematodes
Fungal- and
bacterial-feeders
Fungi
Mycorrhizal fungi
Saprophytic fungi
Nematodes
Predators
Plants
Shoots and
roots
Organic
Matter
Waste, residue and
metabolites from
plants, animals and
microbes.
Protozoa
Amoebae, flagellates,
and ciliates
Bacteria
Animals
First trophic
level:
Photosynthesizers
Second
trophic level:
Decomposers
Mutualists
Pathogens, parasites
Root-feeders
Third trophic
level:
Shredders
Predators
Grazers
Fourth trophic
level:
Higher level
predators
Fifth and
higher trophic
levels:
Higher level
predators
USDA-NRCS

Other activities


सेल SAIL
CEMDE PROJECT- PL&DQ PURNAPANI , RMD
SIGNAGE-1
PURNAPANI MINED OUT SITE LAND COVER MAP(2011) SHOWING RESTORED FOREST AREA AND AQUATIC ECOSYSTEM
Restored forest Ecosystem
Restored equatic Ecosystem
1. Bamboo thicket.
2. Dalbergia Sp. dominated Community.
3. Orchard.
4. Sericultural Zone.
5. Grassland.
6. Acacia Spp. dominated Community.
7. Albizia Sp. dominated Community.
8. Anogeissus Sp. dominated Community.
9.&10. Mixed forest Community.
LAND COVER-2011
Agriculture field
Built up
Mine Dump
Path
Tree canopy
Water body

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Development of novel tasar cultivation zones and conservation of vanya silkworms in ecologically-restored sites within degraded mined-out areas of Purnapani, Odisha

V.K.Choudhary[1,2]*, P. Bhardwaj[1], P.K. Kar[3], S. Mazumdar-Leighton[1] and C.R. Babu[2]

[1]Department of Botany, Plant-Biotic Interactions Group, University of Delhi, New Delhi- 110 007, India
[2]Centre for Environmental Management of Degraded Ecosystems, University of Delhi, Delhi- 110 007, India
[3]Basic Seed Multiplication and Training Center, Central Silk Board, Korba-495 449, India

***Corresponding Author Email :** vivekchy007@gmail.com ***ORCiD:** https://orcid.org/0009-0003-1893-5664

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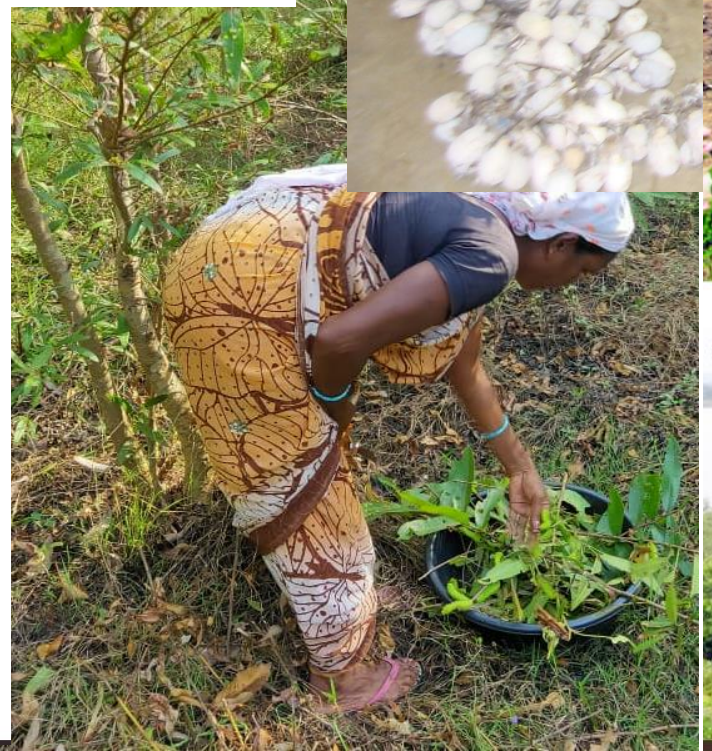
Fig. 3: Cocoon developed on the leaves of different host plants (a) *Terminalia tomentosa*; (b) *Terminalia arjuna*; (c) *Ziziphus mauritiana and* (d) *Shorea*



“Indigenous and local knowledge systems are ecological knowledge practices pertaining to the relationship of living beings, including people, with one another and with their environments. Such knowledge can provide information, methods, theory and practice for sustainable ecosystem management.

This knowledge can enrich applications of modern biology for improved lives and livelihoods for tribal communities.”

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Indigenous Women

Indigenous Peoples Menu

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- Lab#15/18/19, Dept. of Botany, Delhi University