

# Diversidad e interactómica de microbiota bacteriana en una cronosecuencia de recuperación de bosques tropicales.

Yuri Peña  
17 de noviembre 2022



# Deforestación



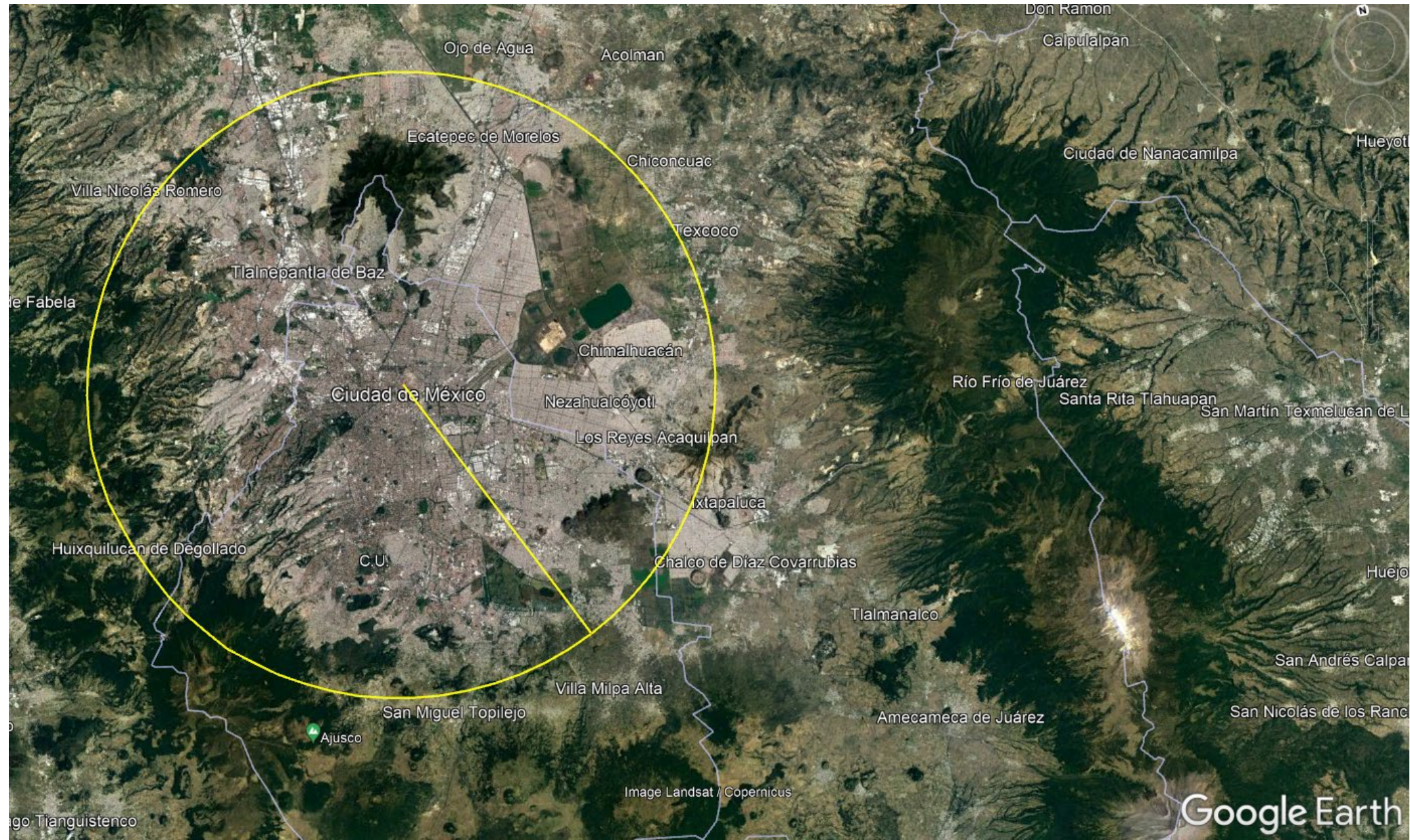
# ¿De qué tamaño es el problema?



2010: 11.2 MHa  
2020: 9.2 Mha

Pérdida: 2 MHa

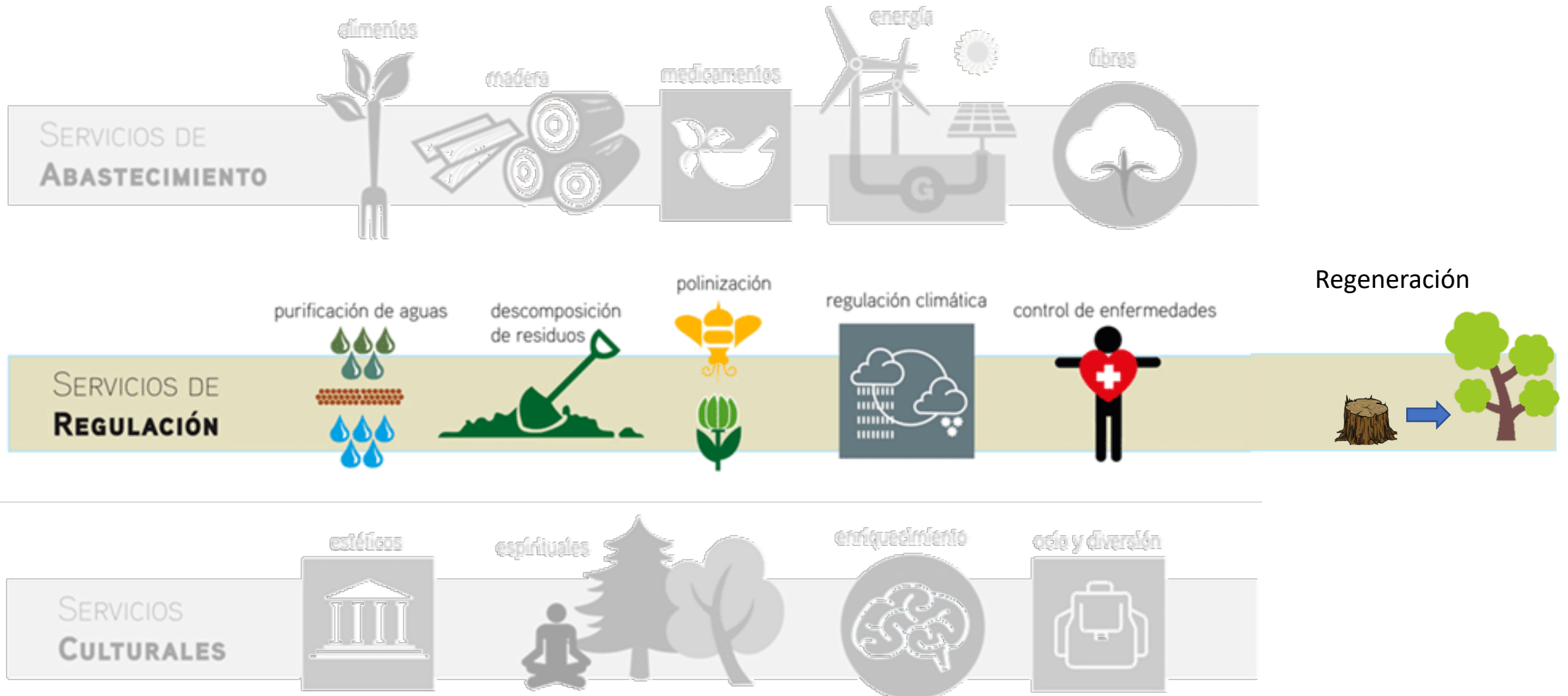
# ¿Cuánto son 2 millones de hectáreas?



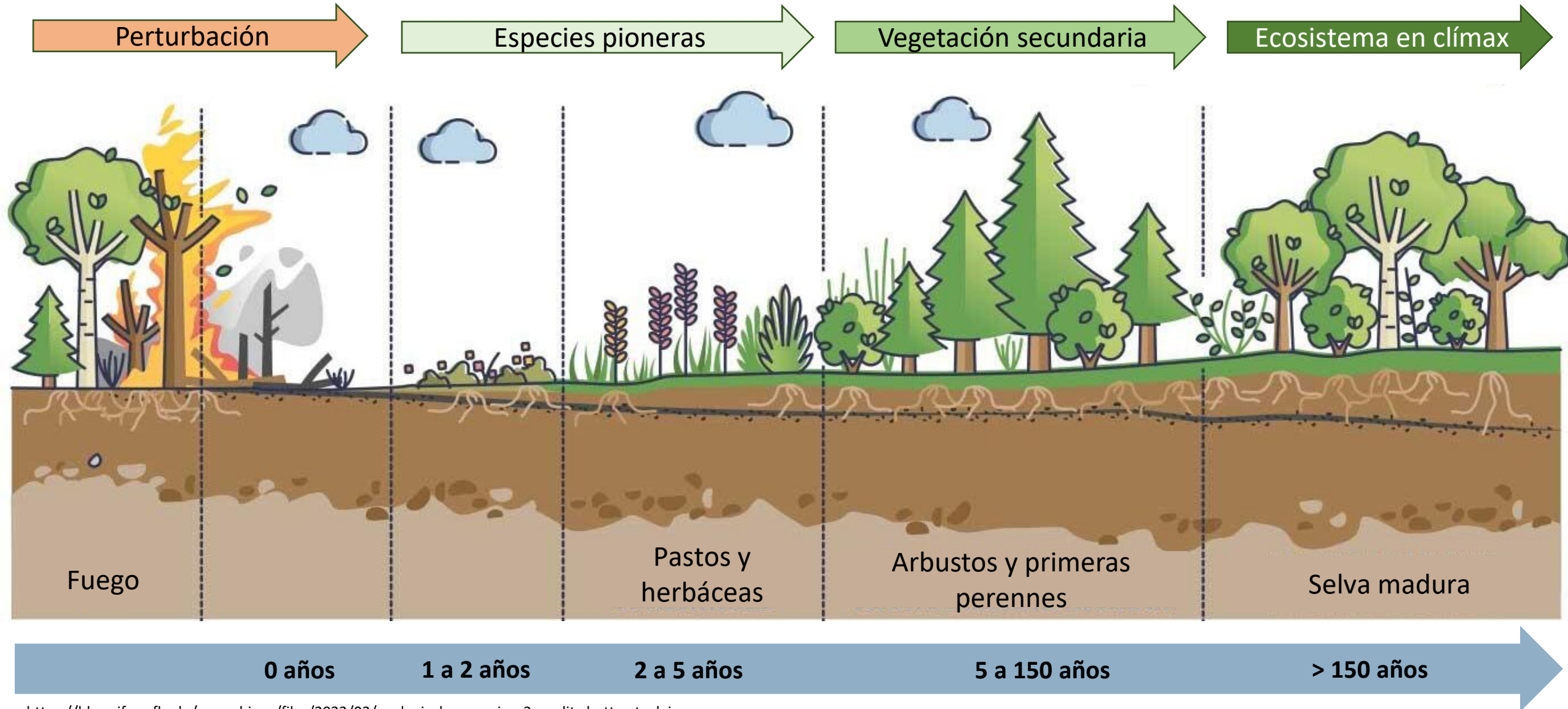
# ¿Qué se pierde? Servicios ambientales



# ¿Qué se pierde? Servicios ambientales



# Regeneración en cronosecuencia

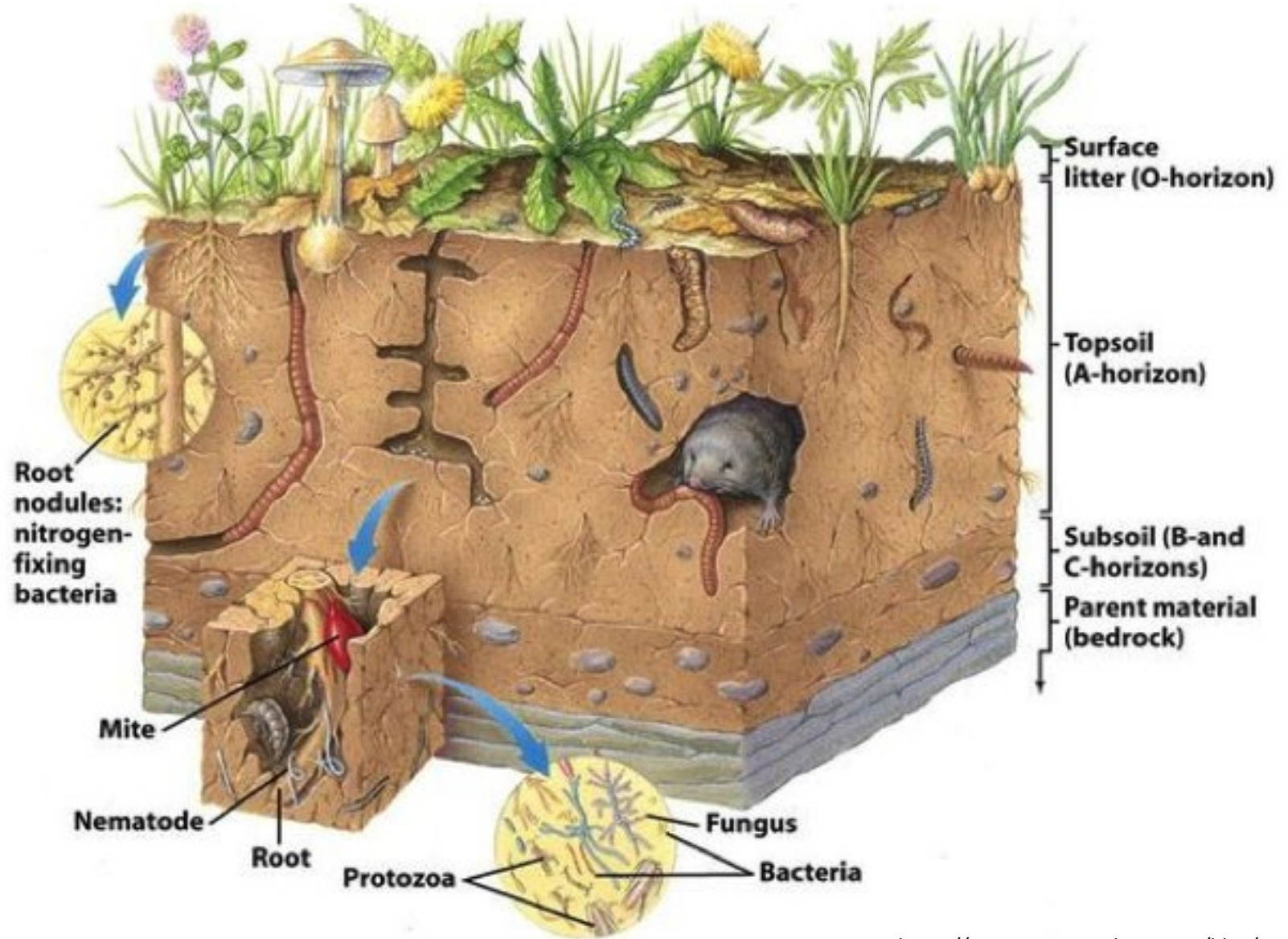


# Dificultad para regeneración

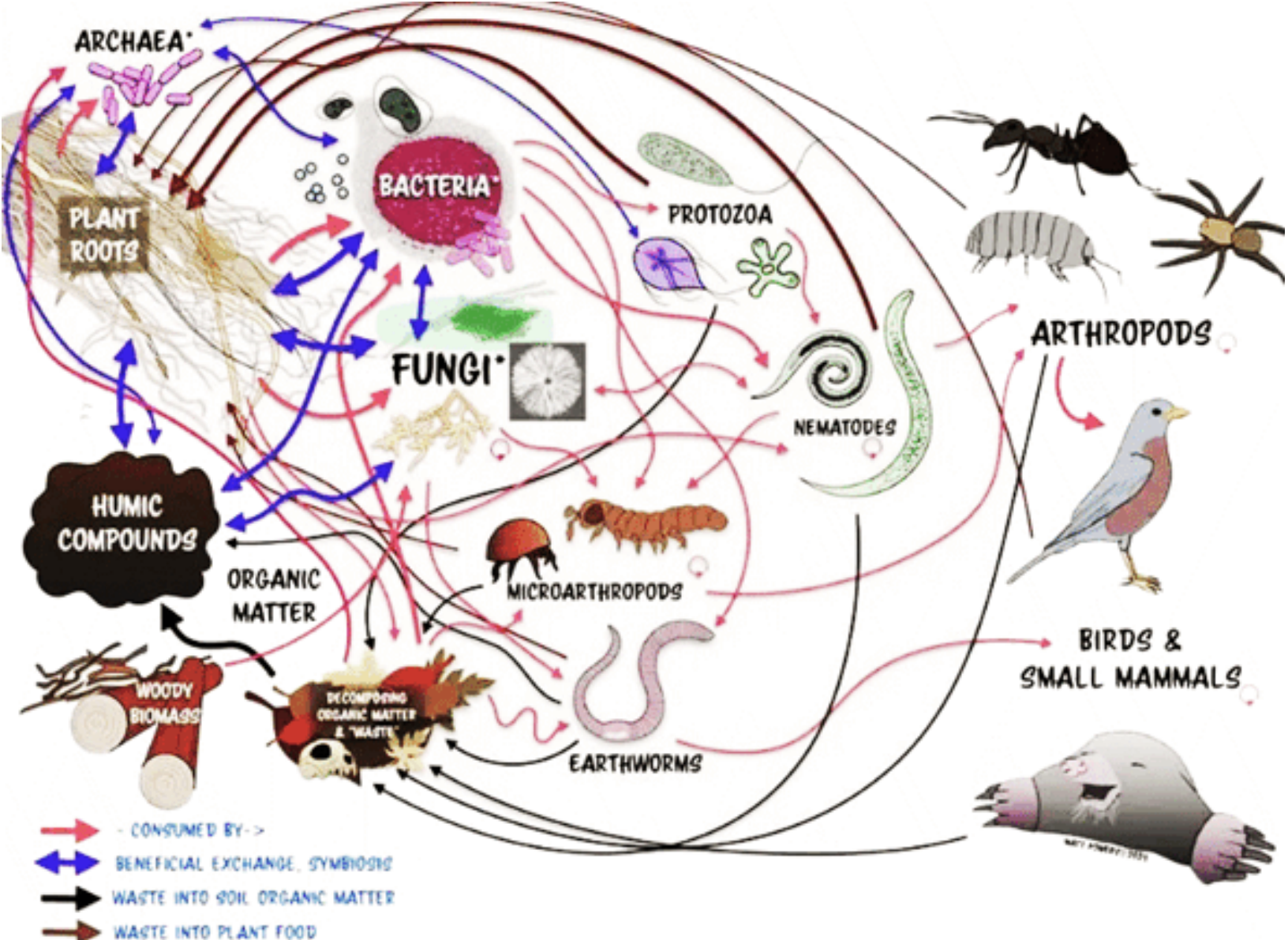




# ¿Y lo que no vemos? El suelo sustenta la vida



# Las redes tróficas dependen del suelo



# HEALTHY Soils are Full of Life!



## HEALTHY

USING DIVERSE SPECIES TO INCREASE DIVERSITY IN THE SOIL LEADS TO MORE ORGANIC MATTER AND HEALTHY SOIL!

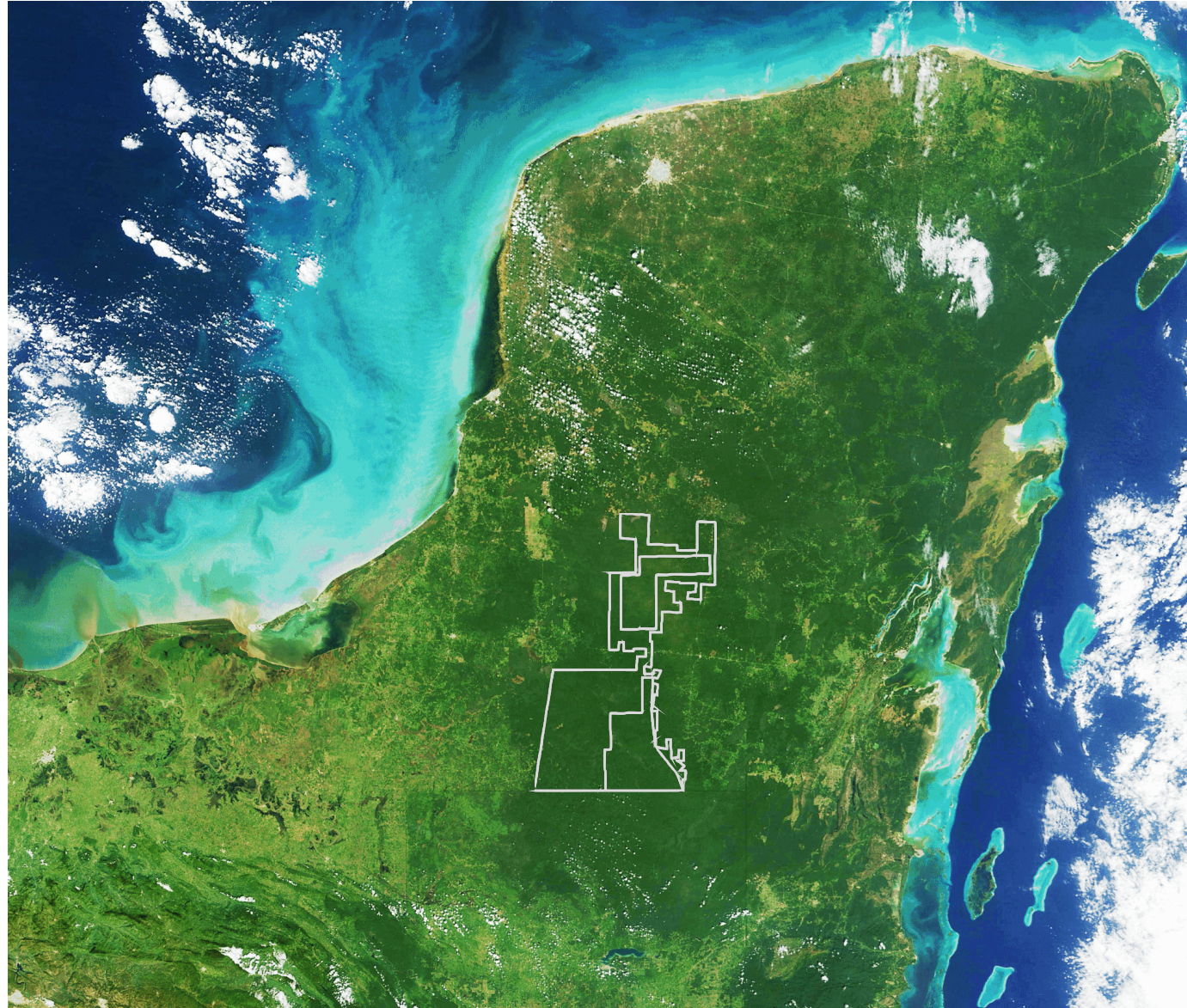


## UNHEALTHY

WITHOUT DIVERSE PLANT SPECIES IN THE SOIL, THE SOIL BECOMES BARREN AND LIFELESS

!

# Diversidad bacteriana en Calakmul, Campeche



Current Microbiology  
https://doi.org/10.1007/s00284-021-02603-9



## Diversity and Interactomics of Bacterial Communities Associated with Dominant Trees During Tropical Forest Recovery

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### Abstract

Bacterial communities have been identified as functional key members in soil ecology. A deep relation with these communities maintains forest cover. Trees harbor particular bacteriomes in the rhizosphere, endosphere, or phyllosphere, different from bulk-soil representatives. Moreover, the plant microbiome appears to be specific for the plant-hosting species, varies through season, and responsive to several environmental factors. This work reports the changes in bacterial communities associated with dominant pioneer trees [*Tabebuia rosea* and *Handroanthus chrysanthus* (Bignoniaceae)] during tropical forest recovery chronosequence in the Mayan forest in Campeche, Mexico. Massive 16S sequencing approach leads to identifying phylotypes associated with rhizosphere, bulk-soil, or recovery stage. Lotka–Volterra intercommune modeling suggests the presence of putative regulatory roles of some phylotypes over the rest of the community. Our results may indicate that bacterial communities associated with pioneer trees may establish more complex regulatory networks than those found in bulk-soil. Moreover, modeled regulatory networks predicted from rhizosphere samples resulted in a higher number of nodes and interactions than those found in the analysis of bulk-soil samples.

### Introduction

The Mayan forest, including the Calakmul Biosphere Reserve (CBR), which is one of the largest protected area of tropical forests in Mexico and Central America, has recently been affected by different anthropogenic activities such as urbanization, agriculture, and pasture land expansion [1]. The loss of vegetal cover caused by anthropogenic or natural disturbances affects not only macroorganisms but also soil microbes. A recent meta-analysis shows how deforestation and land use changes in tropical forests are consistently followed by shifts in bacterial communities [2], which

alter the abundance of some bacterial groups with crucial functional roles in biogeochemical processes such as carbon allocation, nitrogen fixation, and mineral solubilization [3–5]. Previous studies in the CBR demonstrated how loss of the vegetal cover alters carbon and nutrient flows, driving important shifts during tropical forest recovery [6, 7]. As tree-associated microbes appear to participate in a large number of processes that affect plant development [8, 9], such as seedling survival [10], individual performance, and ecosystem functionality [11], the recovery of impacted landscapes is expected to be accompanied by regeneration of functional microbial communities [12]. Microbiome recovery in perturbed ecosystems may be a result of mutual and complex interactions between plants and microbial communities in different successional phases. Emerging evidence has suggested that soil microbiome richness and diversity may be strongly regulated by the host tree [13, 14], including the associated seed-borne microbiome [15]. Moreover, some evidence underlines the particular influence of the microbiome associated with dominant tree species [16].

In the Mayan forest, two closely related dominant tree species belonging to the Bignoniaceae family, *Handroanthus chrysanthus* Jacq. (previously *Tabebuia chrysantha*, Jack) and *Tabebuia rosea* (Bertol) Bertero ex A. DC., are

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# Selección de sitios de muestreo en cronosecuencia



# HEALTHY Soils are Full of Life!



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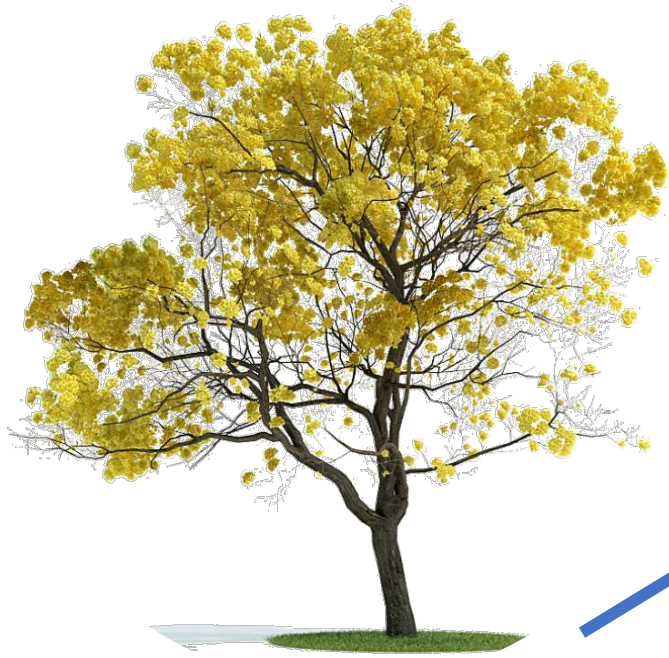
# Distintas herramientas de análisis

Dependientes de cultivo

Independientes de cultivo



# Especie forestal modelo



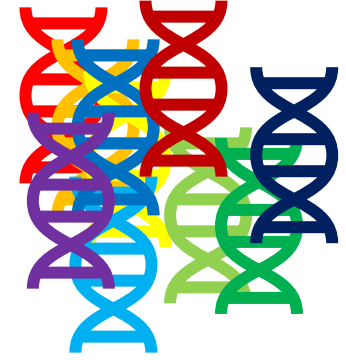
**Guayacán**  
*Handroanthus chrysanthus*



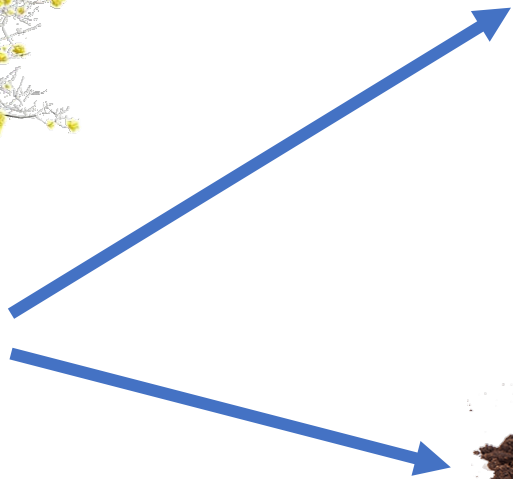
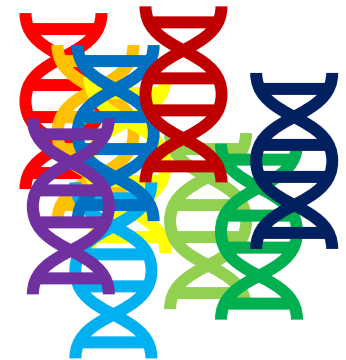
Raíces



Suelo

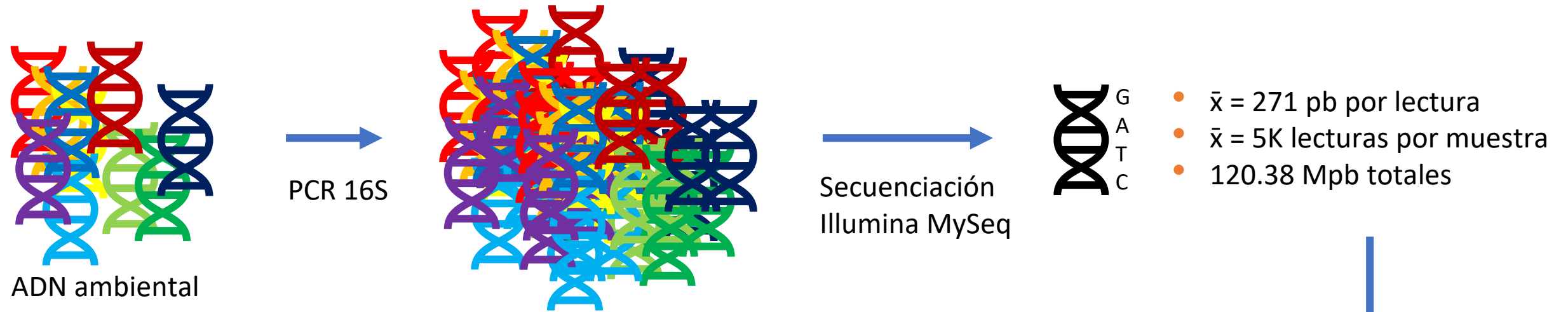


ADN ambiental



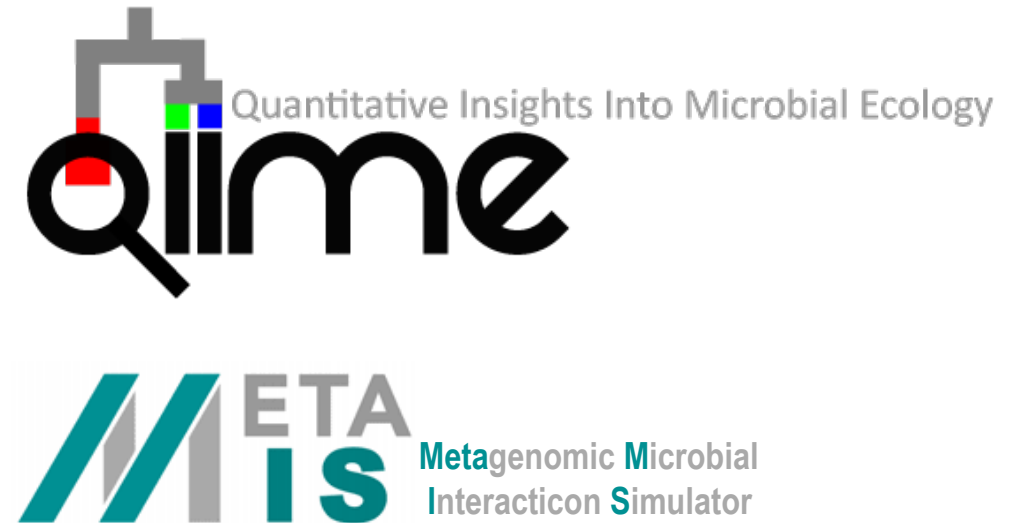
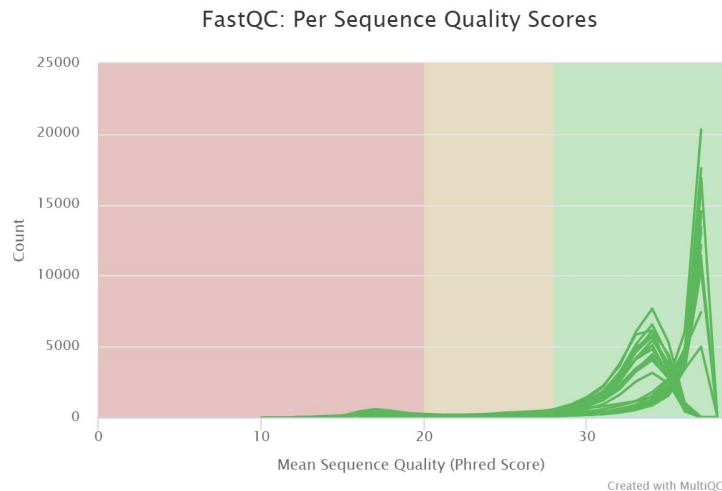


# Secuenciación masiva de amplicones

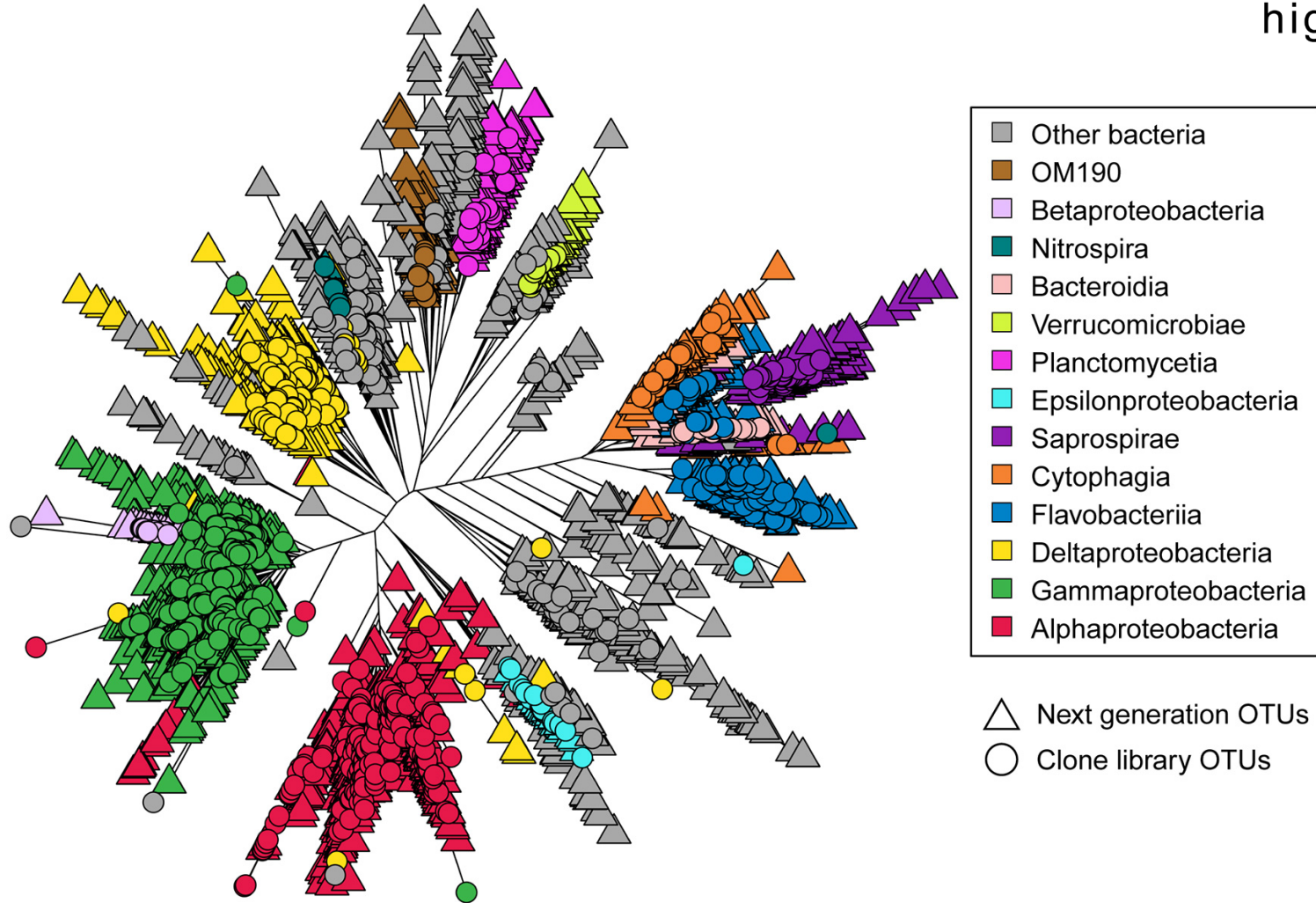


Archivos \*.fastq

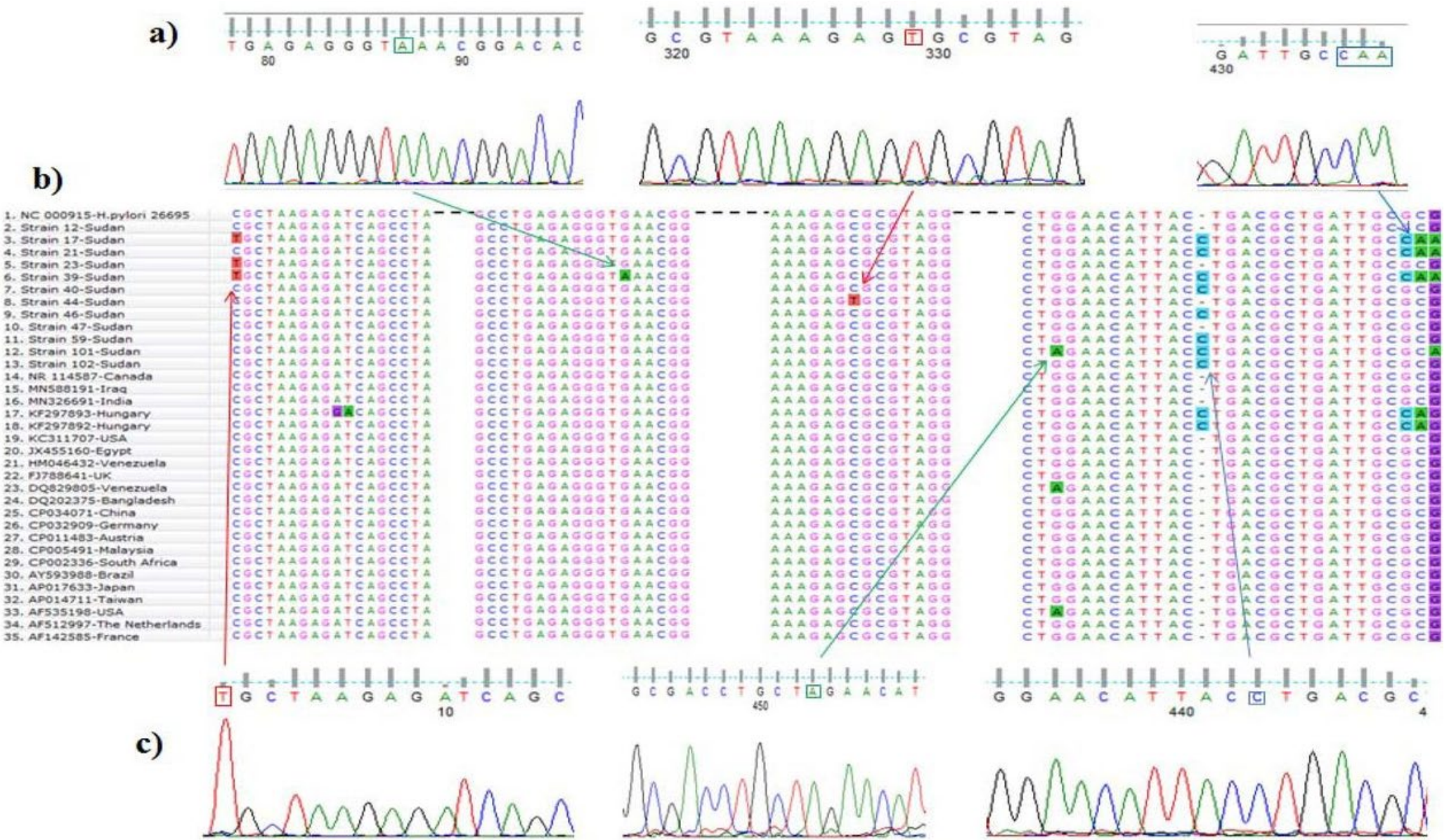
Calidad



# Asignación taxonómica



# Alineación múltiple de secuencias

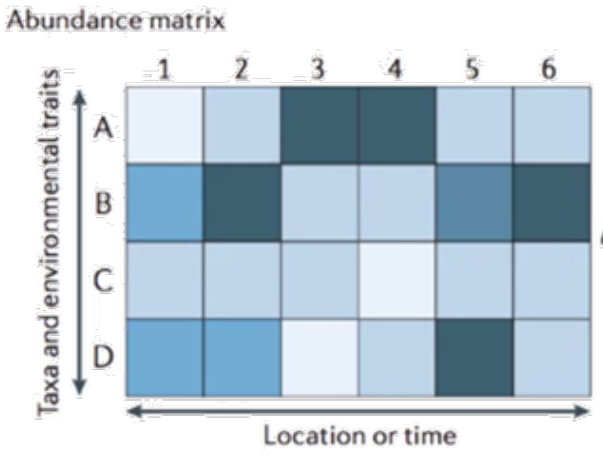
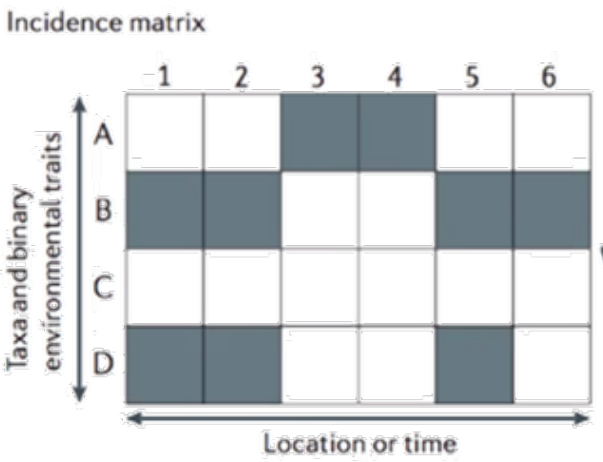




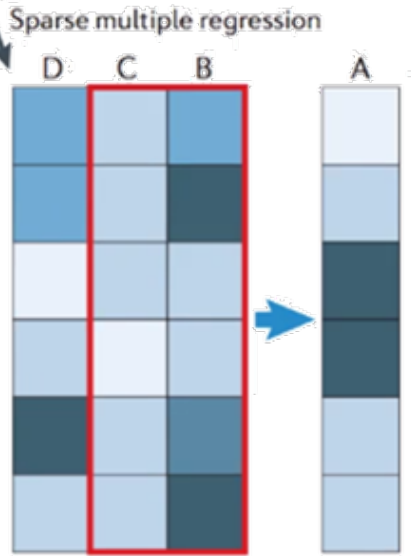
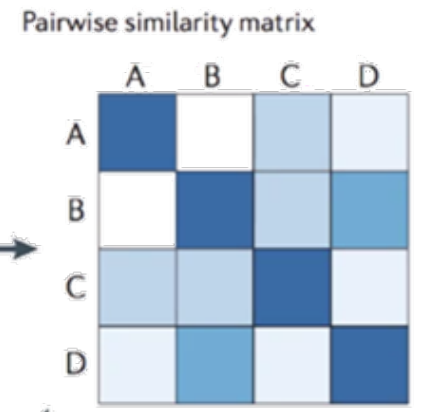


# Elucidación de redes ecológicas

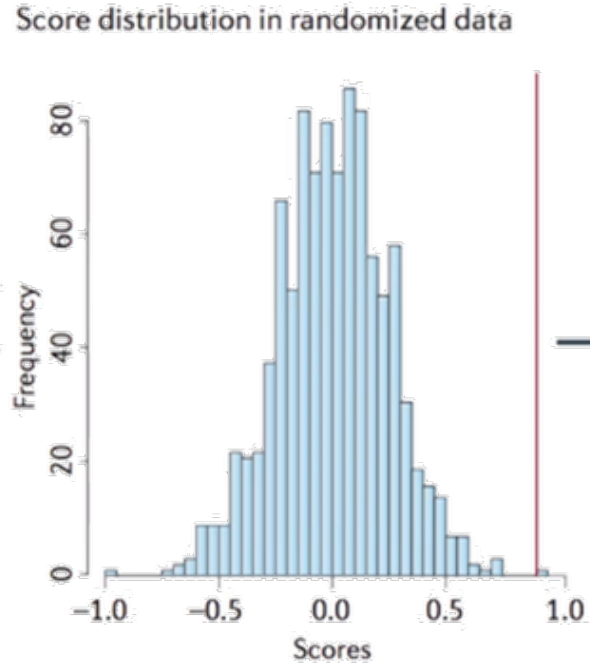
**a Input**



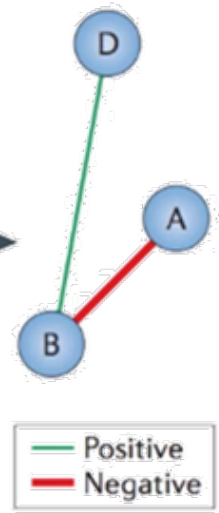
**b Scoring**



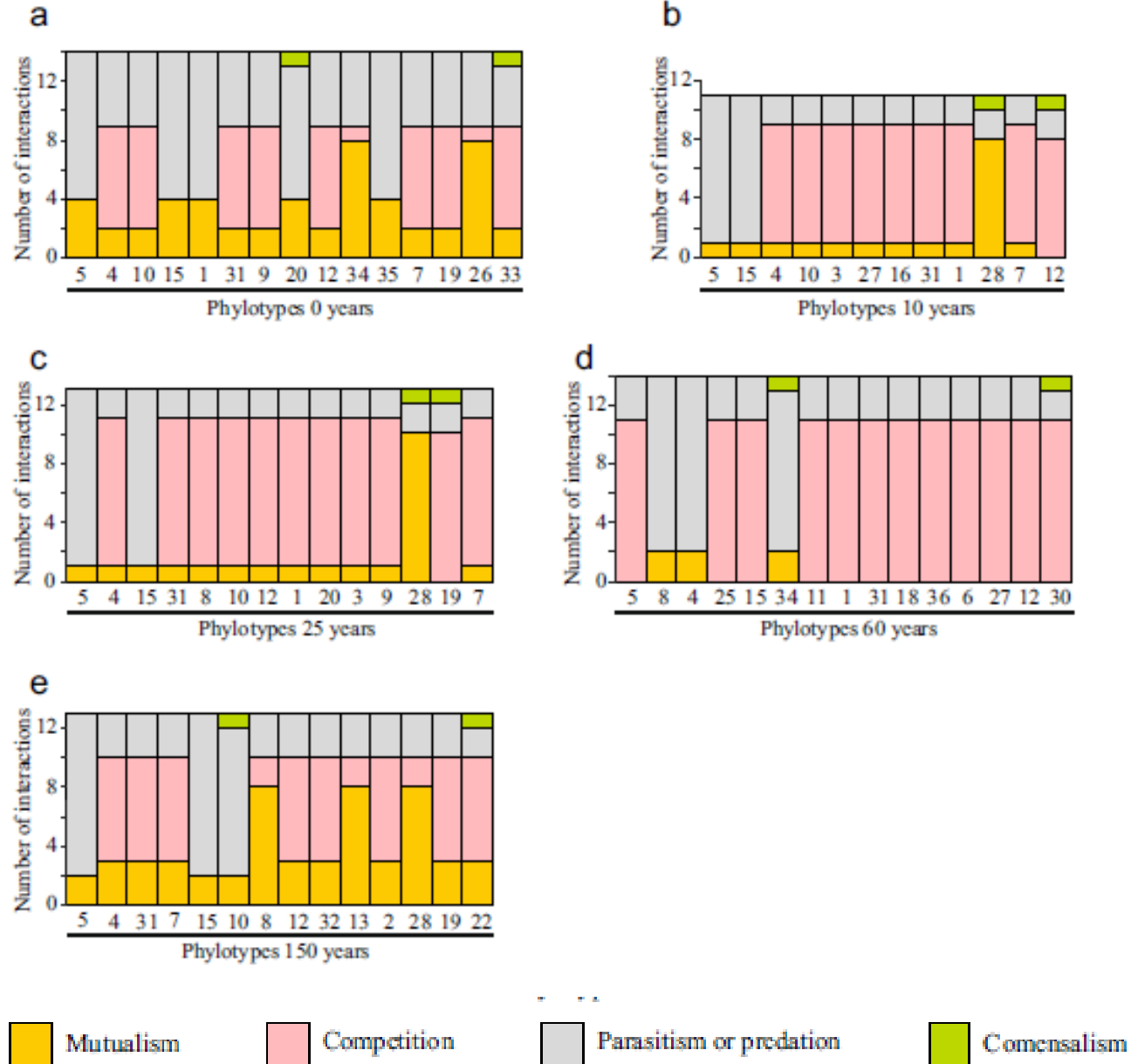
**c P value assignment and filtering**



**d Network output**

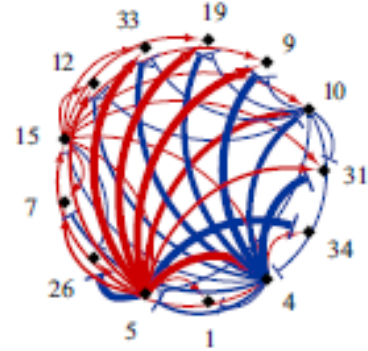


# Cambios en los roles ecológicos

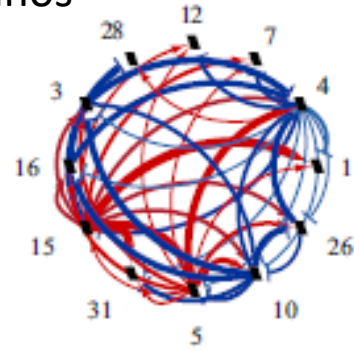


# Redes de interacción

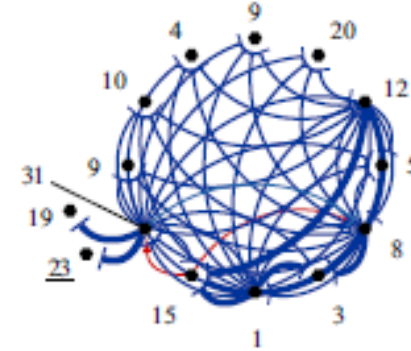
0 años



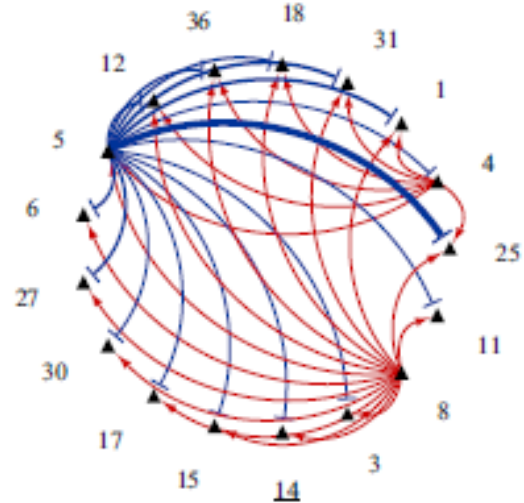
10 años



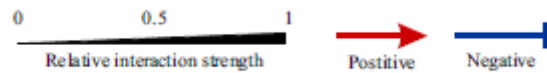
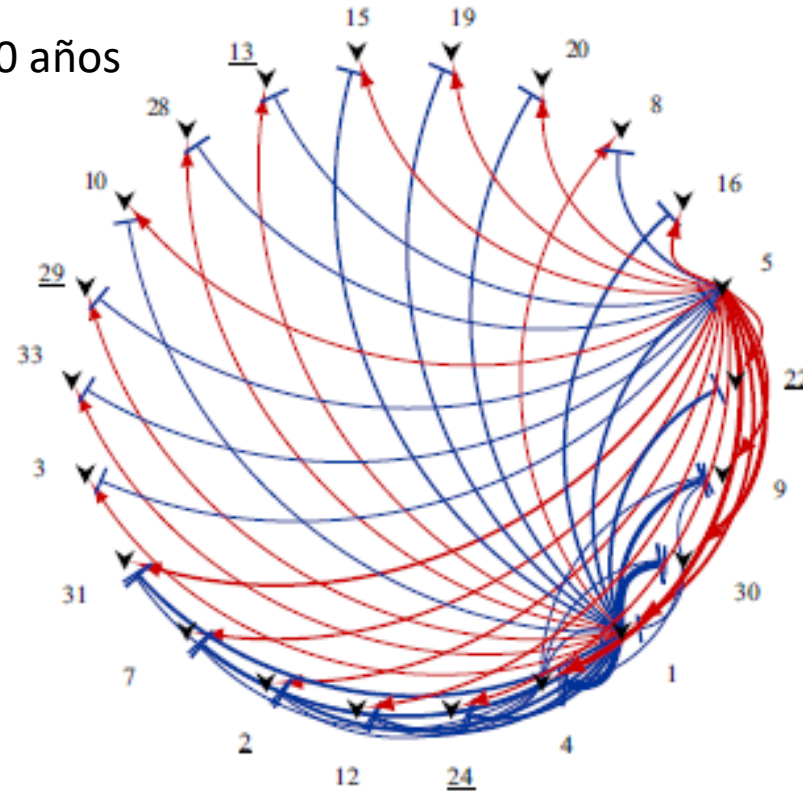
25 años



60 años



150 años





# Conclusiones

- Existen diferencias significativas en la diversidad de bacterias a lo largo de la cronosecuencia y entre suelo y rizósfera.
- Se identificaron filotipos minoritarios exclusivos de momentos en la cronosecuencia y microambiente (suelo o rizósfera).
- Las interacciones ecológicas modeladas sugieren papeles distintos para los filotipos encontrados, jugando algunos de estos papeles regulatorios más importantes.

# Créditos y agradecimientos



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Alejandra Becerra  
Flor Trujillo



**COESICYDET**  
CONSEJO ESTATAL DE INVESTIGACIÓN CIENTÍFICA Y  
DESARROLLO TECNOLÓGICO DE CAMPECHE

Agradezco su atención

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