How much soil diversity is restored after a cattle ranching pasture is abandoned for its natural regeneration in the Amazon region?

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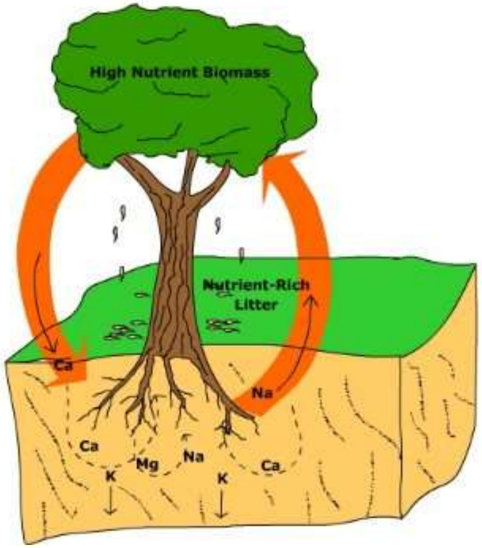
INTRODUCTION

Soil macrofauna contribute to organic matter cycling and the efficient return of nutrients to plants (Ackerman *et al.*, 2009; Six *et al.*, 2004)

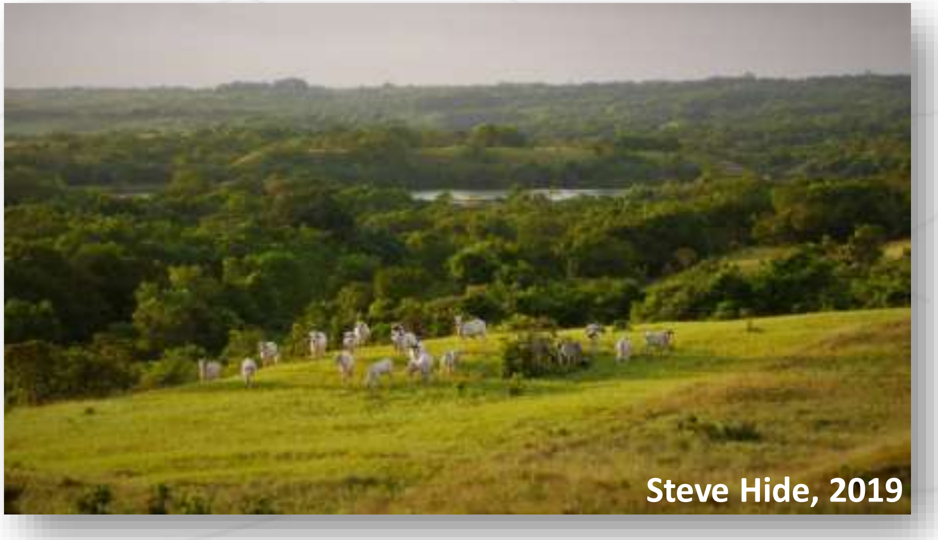
Soil macrofauna communities are highly sensitive to land use (Lavelle, 1997; Pauli *et al.*, 2011).



Arbuscular mycorrhizal (AM) fungi contribute significantly in the efficient phosphorous (P) acquisition of plants through mycorrhizal associations (Smith *et al.*, 2011).

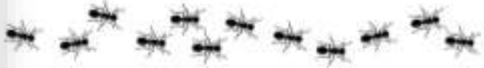
INTRODUCTION

Deforestation of natural forest to transform it in pastures for extensive cattle ranching is common in Amazonia



Steve Hide, 2019

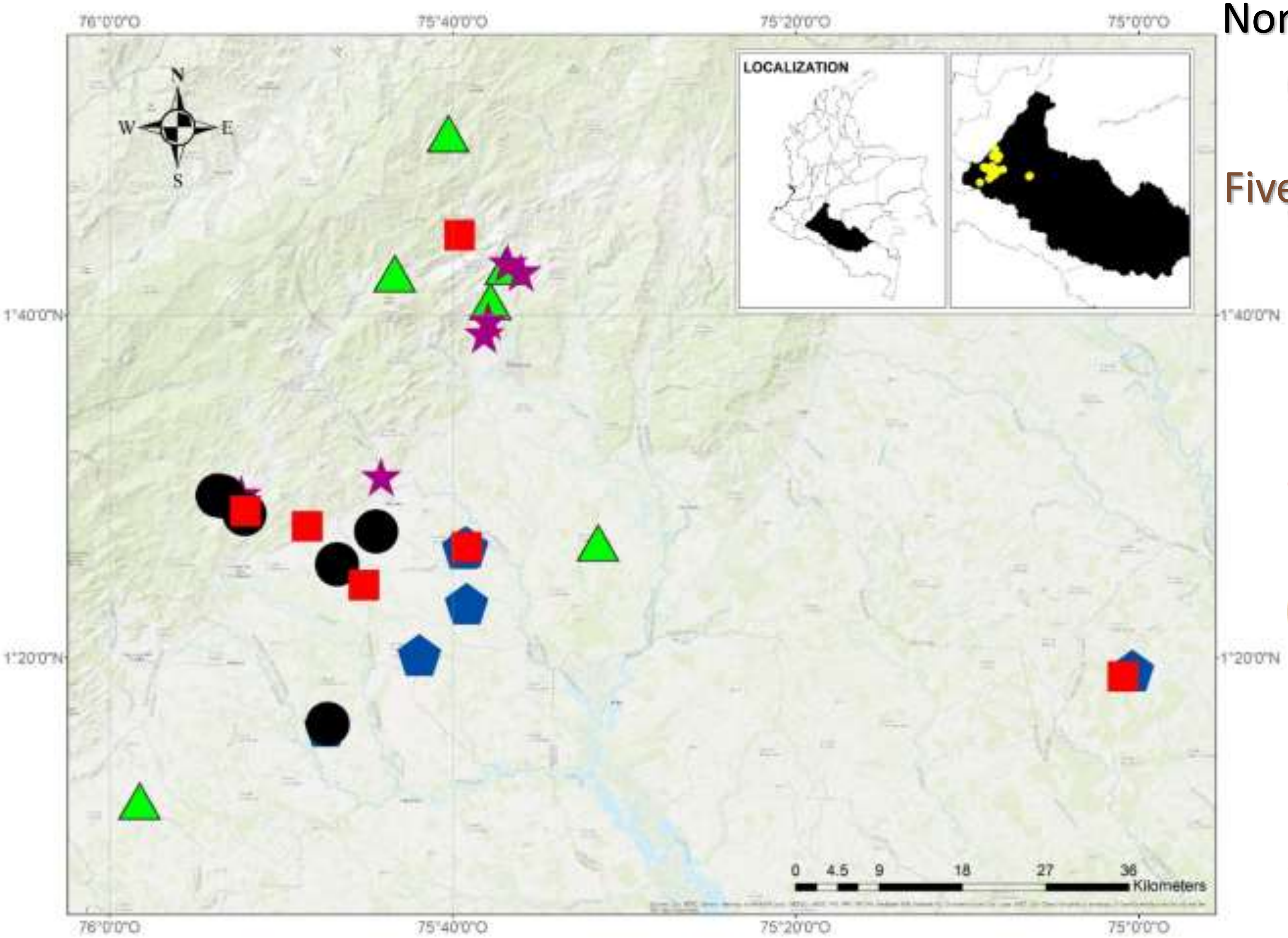
We evaluate how soil macrofauna and AM fungi diversity is affected by deforestation and how much of it is restored through a natural regeneration process.



Soil macrofauna and AM fungal communities are highly sensitive to land use (Lavelle, 1997; Pauli et al., 2011; Sepp et al., 2018)

METHODOLOGY

Study area



Caquetá state
Northwestern of the Colombian Amazon

Five natural regeneration states
Six repetitions

★ 0 - 10 years.
Young secondary vegetation

⬟ 10 - 20 years.
Secondary vegetation

● 20 - 40 years.
Old secondary forest

■ > 40 years.
Mature forest

▲ Pastures

METHODOLOGY

Sampling method – TSBF monoliths (Anderson & Ingram, 1993)

AMF sampling

Litter

0-10cm

10-20cm

20-30cm

Soil macrofauna sampling

Earthworm collection was not included

METHODOLOGY

Data analysis

SOIL MACROFAUNA

Morphological identification into morphotypes and taxonomic groups (families, genera or species)

ARBUSCULAR MYCORRHIZAL FUNGI

Communitarian soil DNA was isolated, extracted and latter amplified with WANDA and AML2 PCR primers.

Illumina sequencing method to identify specific OTU's of AM fungi as virtual taxa (VT).

(Davidson et al. 2012; Drumbrell et al., 2011; Lee et al., 2008)

- ✓ Soil macrofauna density (number of individuals per square meter) data.
- ✓ Species richness data per taxonomic group.

ANOVA
Tukey test

- ✓ AM fungi abundance and diversity

Kruskal-Wallis test

Diversity analysis was done through rarefaction and extrapolation curves

iNETX package
(Hsieh *et al.*, 2016)

R Project

RESULTS

Soil macrofauna community

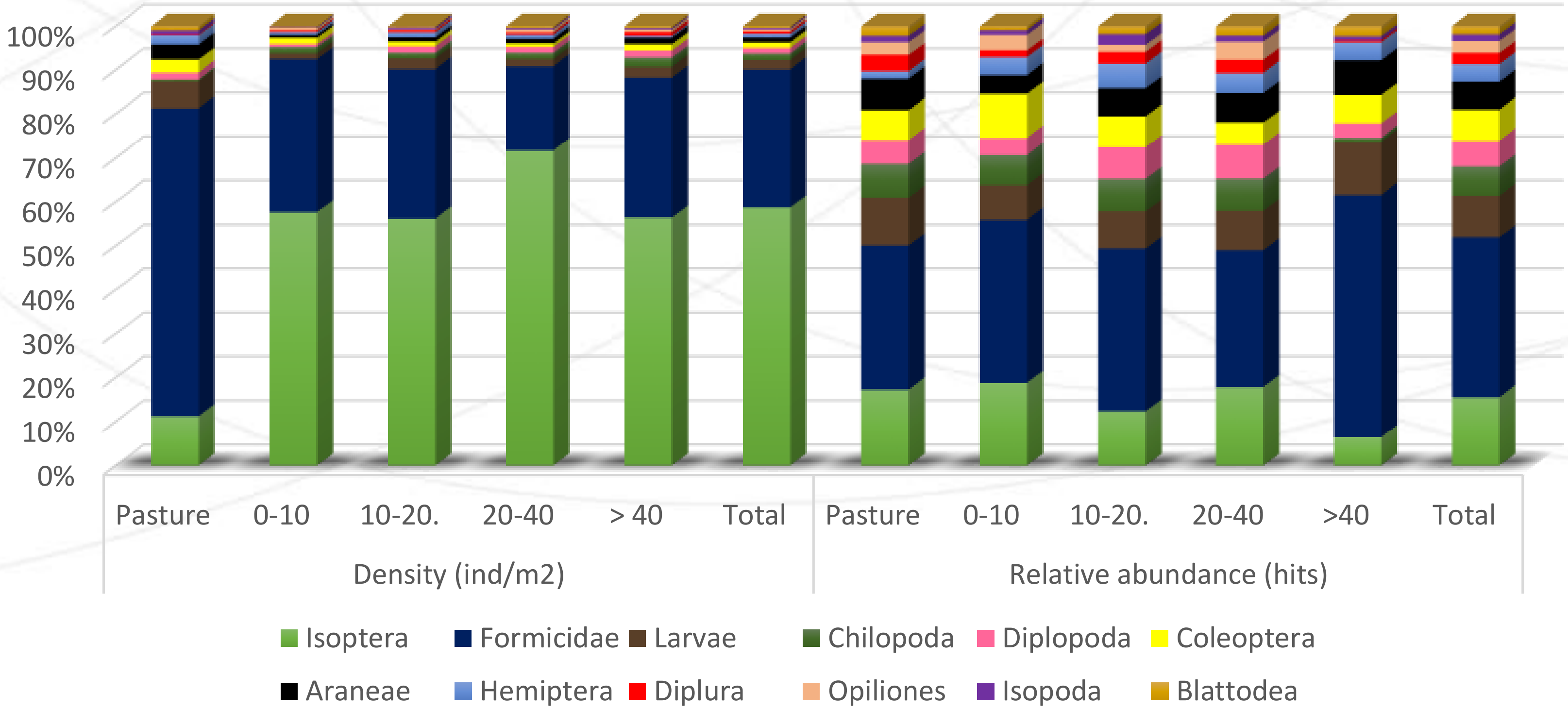
We obtained **13.685 individuals** from **28 taxonomic groups**

Ants (Formicidae) **34,6%**
Termites (Isoptera) **14,8%**
Immature forms (larvae) **8.9%**

PHYLUM (2)	**CLASS** **(9)**	**Orders** **37**	**Families** **124**	**Genera** **106**
Arthropoda Onychophora	Arachnida, Chilopoda, Collembola, Diplopoda, Diplura, **Insecta**, Malacostraca, Onychophora and Symphyla			**Morphotypes** **791** (133 to species level)

RESULTS

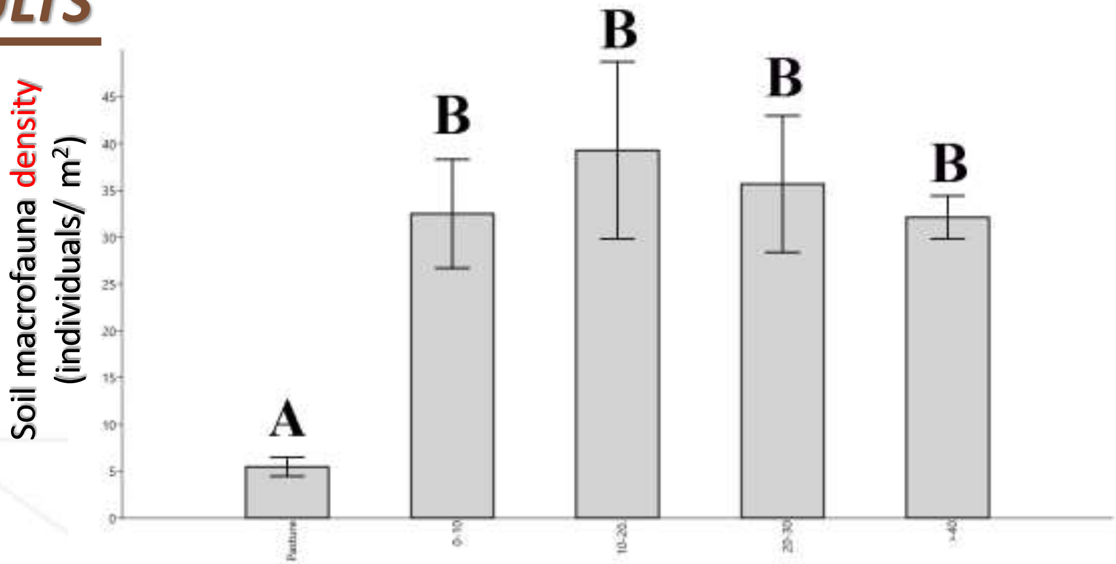
Density and relative abundance of most dominant soil macrofauna groups in a natural regeneration chronosequence



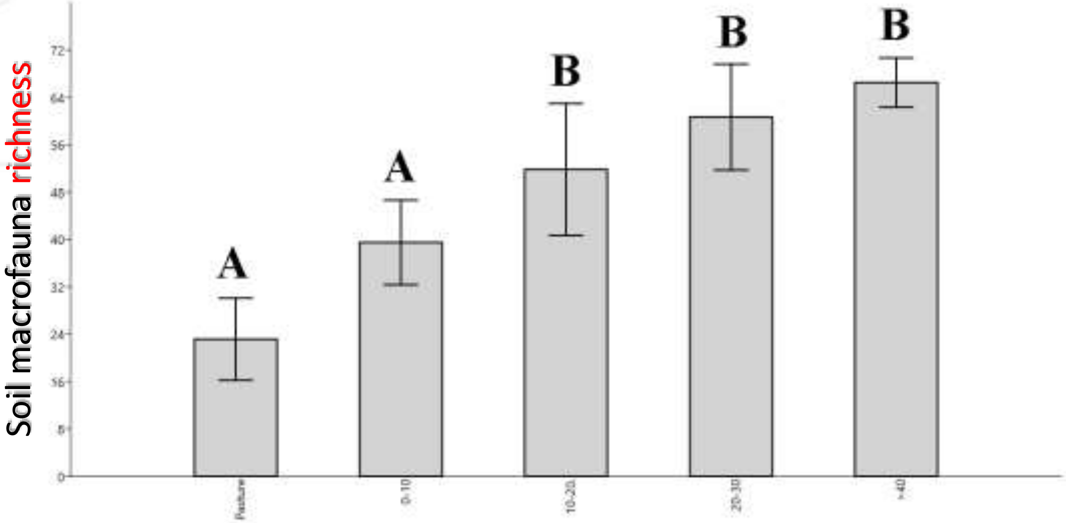
Ants and termites were the most abundant and diverse groups. Termites were very sensitive to soil changes (Amazonas *et al.*, 2018).

RESULTS

Soil macrofauna community



Macrofauna abundance and species richness were not correlated in the natural regeneration chronosequence through the time. (Souza *et al.*, 2016)



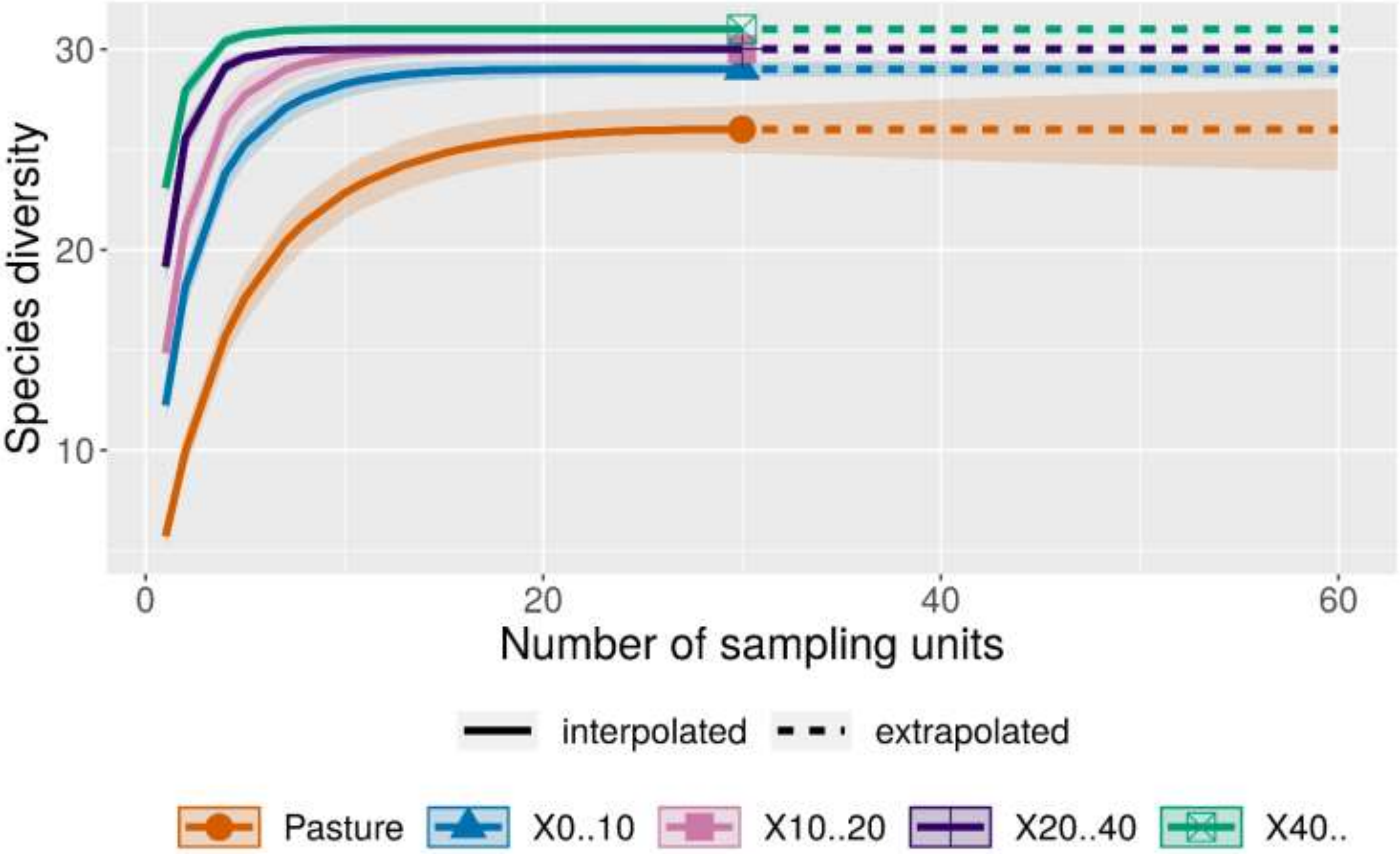
RESULTS

Soil macrofauna community

The lowest species diversity occurred in pastures as expected.

After 40 years of natural regeneration, soil macrofaunal diversity is not restored completely.

But the use of agrosystems instead of the natural regeneration can speed soil macrofaunal restoration (Barros *et al.*, 2002, 2003)

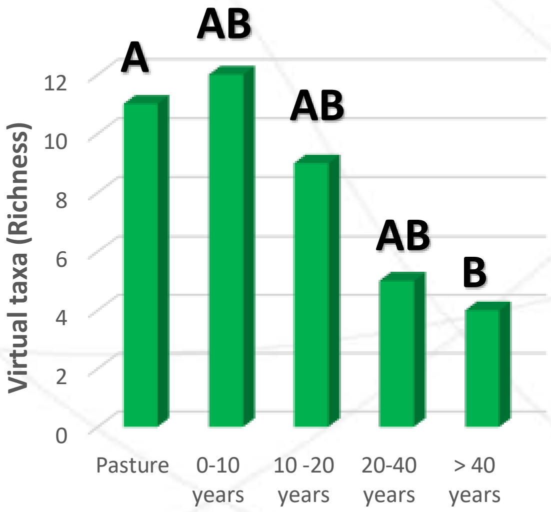


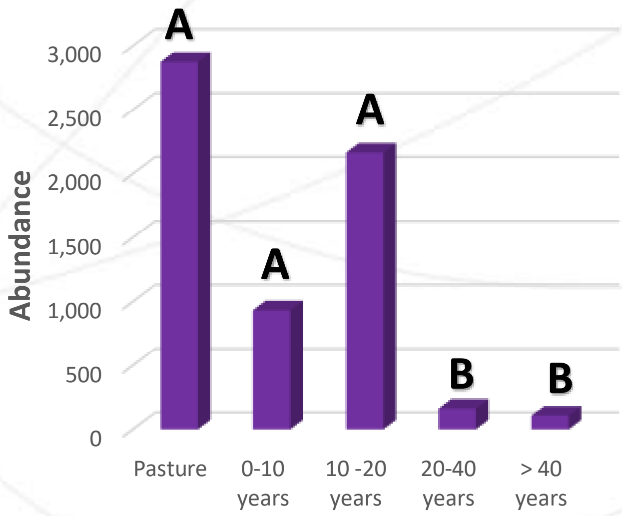
RESULTS

Arbuscular mycorrhizal fungi community

We obtained **44**
Virtual taxa

Genus *Glomus* (71 % of total VT sp richness) was the most abundant, followed by the genus *Acaulospora* (14%).





Most representative VT

🟨 *Glomus* VT126	*G. decipiens* VT39	*Glomus* VT223	🟩 *Paraglomus* VT444	🟩 *Glomus* VT359
Glomus VT60	🟨 *Glomus* VT89	🟩 *Paraglomus* sp. VT444	🟨 *Glomus* VT70	🟨 *Glomus* VT126
🟨 *Glomus* VT89	*Claroideoglomus* sp. LH-Cl01	🟨 *Glomus* VT89	🟨 *Glomus* VT126	*Glomus* VT292
🟨 *Glomus* VT70	*Glomus* VT79	*Glomus* VT253	🟩 *Glomus* VT359	🟩 *Paraglomus* VT444
Glomus VT398	*Glomus* VT292	*Acaulospora* sp. VT15	*Claroideoglomus* sp. LH-Cl01	*Glomus* VT79

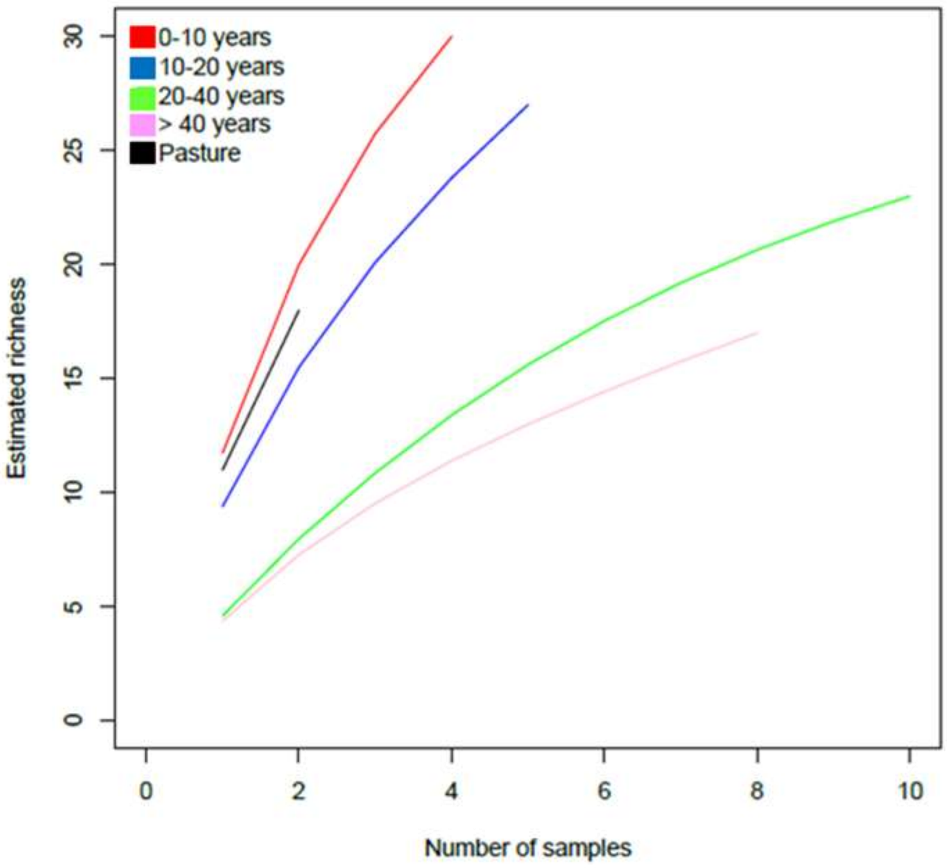
Abundance $p = 0.002$
Richness $p = 0.034$

🟨 VT that were in pastures and persist through the years are in yellow.

🟩 VT that are present in mature forest and appeared in old secondary forest are in green.

RESULTS

Arbuscular mycorrhizal fungi community



Rarefaction curves indicated that sampling was not enough to estimate the richness for this microbiological community.

AM fungal communities were different at the five forest stages of the chronosequence.

The soil contains less AM fungal biomass due to the obligate root endophyte condition of mycorrhizal fungi (Helgason & Fitter 2009), and consequently, a lower concentration of AM fungal DNA. It is reflected as a more abundant and diverse AM fungal community in plant roots than in the soil (Saks et al., 2014; Varela-Cervero et al., 2015).

Conclusions

- ✓ Degraded pastures that are abandoned for their natural regeneration restore naturally their soil macrofauna and AMF communities through the time. However, some diversity is lost.

- ✓ Abundant and diverse AM fungal communities into the soil reflects a high degree of ecosystem disturbance.

- ✓ A degraded pasture will need more than 20 years of natural regeneration to rich similar species richness than a non-disturbed Amazonian forest, but after 20 years its species composition is different from a mature Amazonian forest.

- ✓ Changes in soil macrofauna composition and soil macrofauna biomass could have consequences in Amazonian forest nutrition that have not been evaluated yet.

Acknowledgements

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Thanks for you attention

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