# HOST FUNCTIONALITY AS A DRIVER IN THE MODULARIZATION OF FUNGI-ROOTS ASSOCIATION

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## INTRODUCTION

- Several drivers modulate the **rhizosphere microbial** community, which in turn interacts with the **host species**.
- This interaction plays important **ecological roles**, from the regulation of nutrient uptake to host-host interactions.
- **Species-specific** interactions are still being unraveled, and often these **associations** are considered either random or linked to selection due to the **functional traits of the host**.

## MOTIVATION

- Our main interest lies in the analysis of non-random **associations** between **roots** and **fungi**.
- We hypothesize that **network compartmentalization** of rhizosphere fungal community and host community will be explained by **host functionality** and **phylogenetic relatedness**.


Photo: Nando Gafar.

Fig 1 Sampling below-ground biodiversity. Soil bulk and apparent roots.
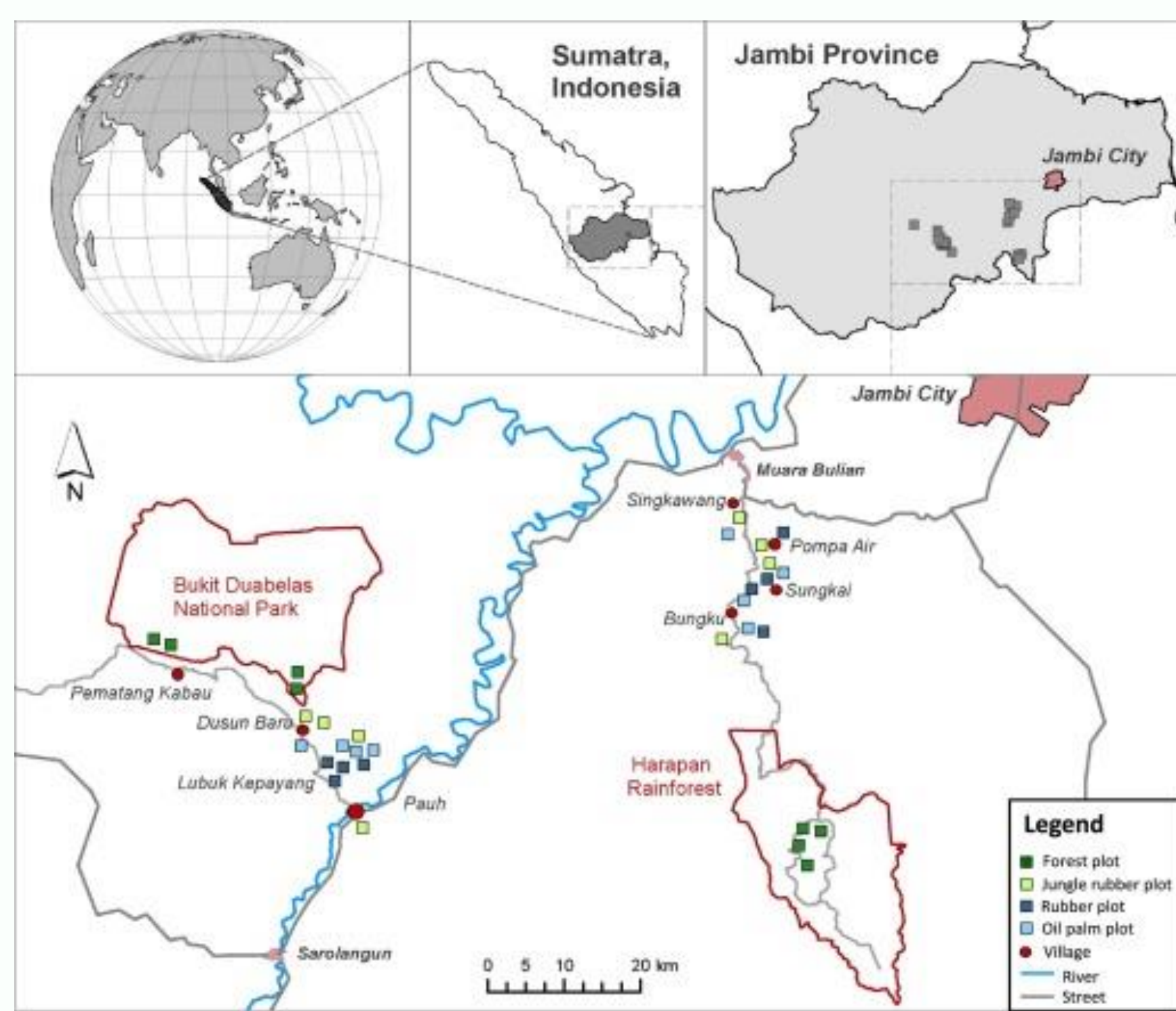
## STUDY DESIGN

### Study Area



Fig 2 Map of the study area in Sumatra, Indonesia.

### Experimental Approach

**Conversion of tropical forests into agricultural systems**



Forest   Jungle rubber   Rubber   Oil Palm

Fig 3 Land-use systems sampled in this study.

- We sampled five soil cores to obtain **fine roots** in 32 plots sited in **four land-use types** with different levels of forest conversion.
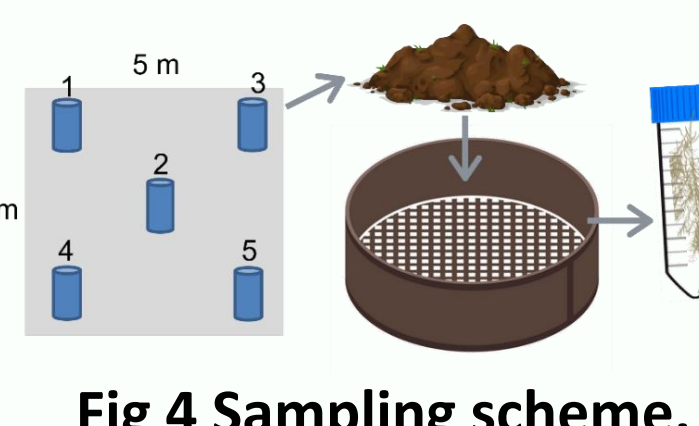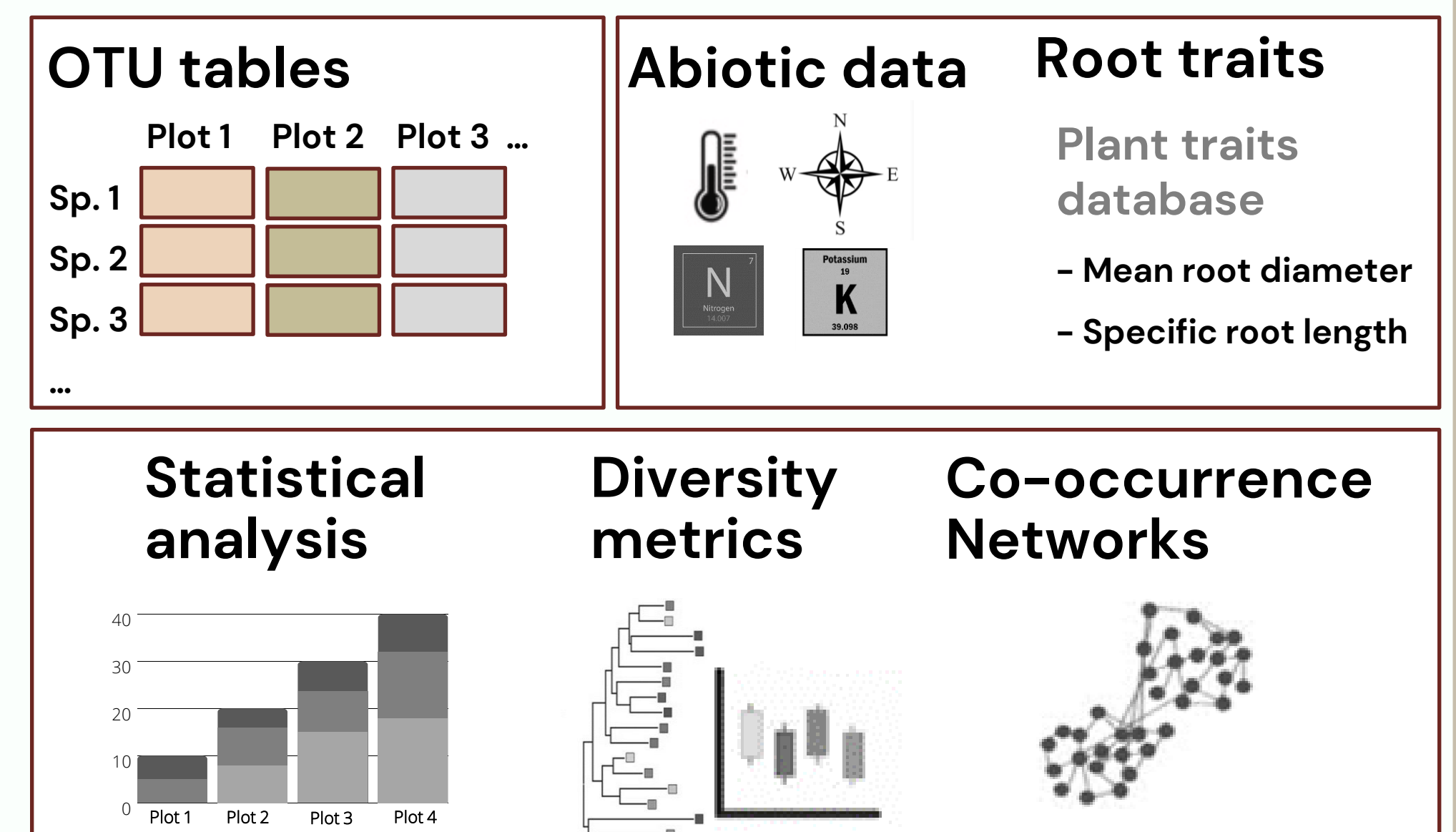

Fig 4 Sampling scheme.

### Data Analysis Pipeline

- Metabarcoding approach was used for identification of **roots** (*rbcL*) and **fungi** (ITS)



OTU tables | Abiotic data | Root traits
Plant traits database
– Mean root diameter
– Specific root length

Statistical analysis | Diversity metrics | Co-occurrence Networks

## RESULTS & DISCUSSION

### Compositional similarity and diversity

- A clear **structure** in the **community composition** was linked to the **land-use** type.
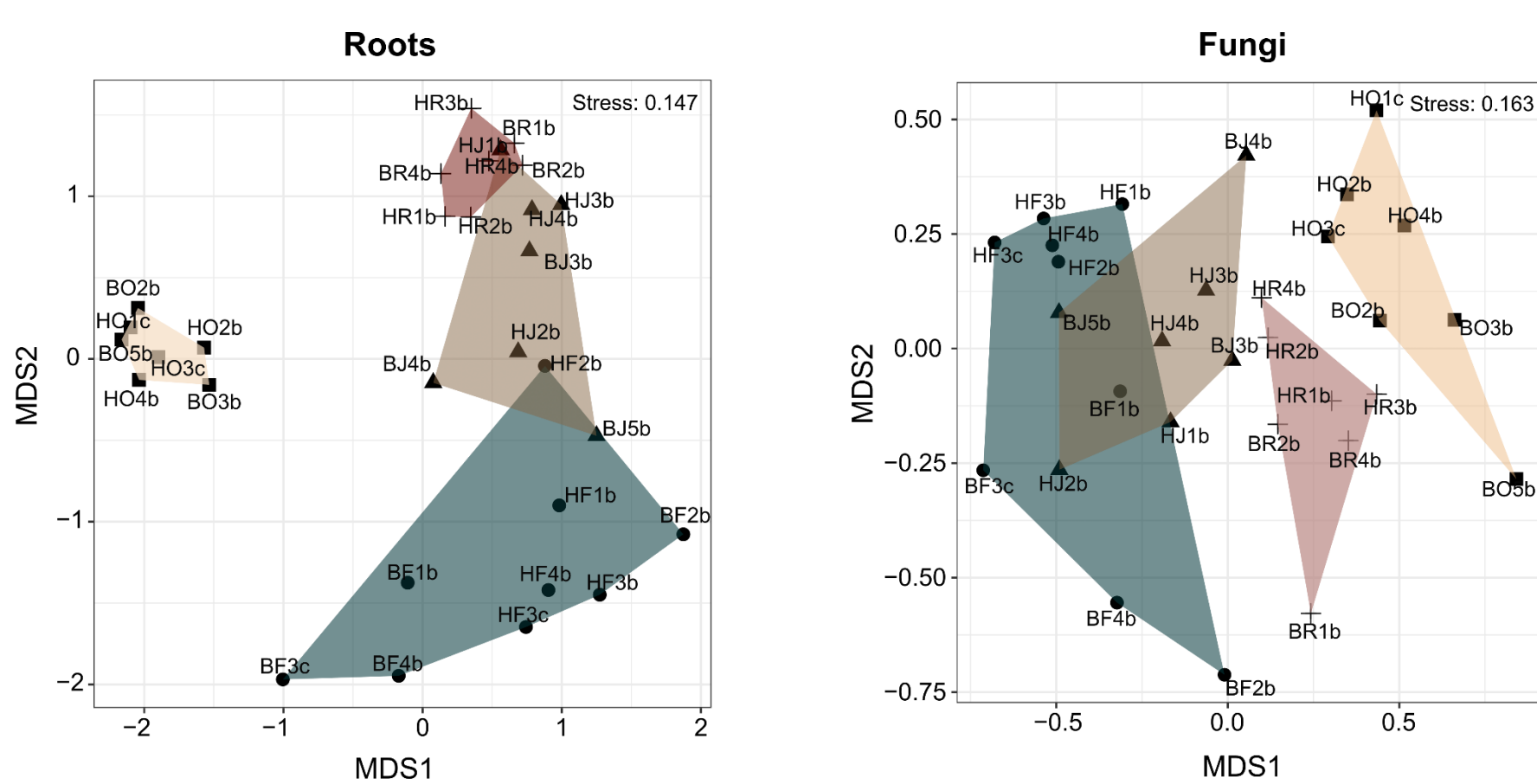


Fig 5 Compositional similarity of roots and fungi communities.

- **Diversity of pathotroph** fungi **reduced** in land-use systems with **higher roots diversity**, while the diversity of **saprotroph** and **ectomycorrhiza** fungi was **higher in forest**.
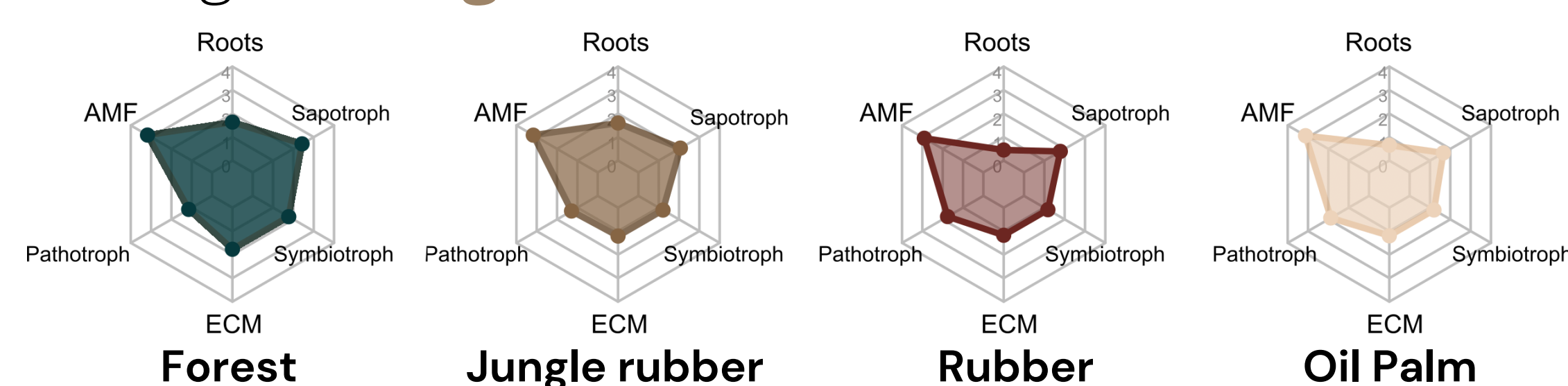

Forest   Jungle rubber   Rubber   Oil Palm

Fig 6 Shannon diversity of roots and fungi guilds in the four land-use types.
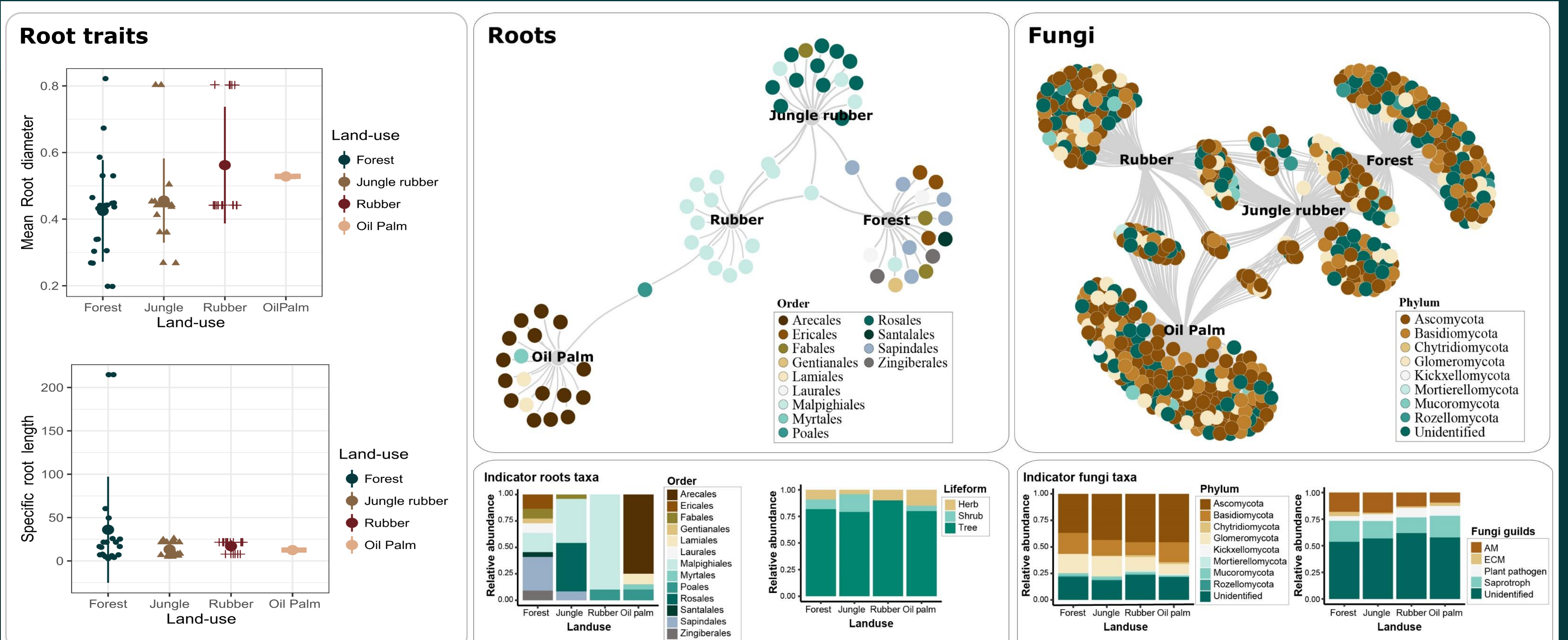
### Indicator Species Networks



Fig 7 Mean root diameter and specific root length per land-use.

Fig 8 Networks demonstrate association of specific indicator species and land-use systems at different conversion degrees.

- **Higher diversity** of indicator OTUs was observed in the **forest** in comparison with the other systems.
- In the monocultures, *Elaeis guineensis* (palm tree) and the **herbs** *Centotheca lappacea*, *Asystasia gangetica*, *Clidemia hirta* were identified as indicators species in **oil palm plots**, and **only** *Hevea brasiliensis* (rubber tree) **in rubber plots**.

## REMARKS

- Network partition recovered four main groups, corresponding to each land-use system.
- Pairwise genetic distances between modules were greater than within modules for the roots data.

## NEXT

- Determine modularity metrics and composition for multi-kingdom co-occurrence network.
- Verify the relationship of species modules composition with phylogenetic distance and traits trend of plant-hosts.