

B02

Impact of rainforest transformation on phylogenetic and functional diversity of soil prokaryotic communities in Sumatra

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In this project, the impact of lowland rainforest transformation on diversity and ecosystem function of soil prokaryotic communities will be investigated. To identify changes soil prokaryotic community and key metabolic functions of rainforest transformation events, comparative phylogenetic and functional profiling of soil samples from lowland rainforest, jungle rubber, rubber plantations, and oil palm plantations will be performed. For this purpose, culture-independent metagenomic and metatranscriptomic approaches are employed. Changes in the soil prokaryotic diversity associated with rainforest transformation to plantations should be investigated, also regarding the overall functional diversity. In addition, the effect of the rainforest transformation on biogeochemical functions of soil microorganisms regarding the Nitrogen cycle should be studied (fig.1).

Materials & methods:

Soil samples from 32 core sites including two different landscapes with each four different land-use have been taken. The four land use systems comprise rainforest, jungle rubber, rubber plantation and oil palm plantation. From each sub-plot three 5 cm soil cores have been taken (fig.2). The prokaryotic soil community was analyzed by using the 16S rRNA gene. Therefore, DNA was isolated from soil samples and amplicons of the 16S rRNA region V3-V5 were generated using primers specific for Bacteria as well as Archaea. Amplicons were sequenced and the sequence datasets was processed and analyzed by bioinformatic tools and. Furthermore, the active soil prokaryotic community will be analyzed by using reverse transcribed RNA (cDNA), also targeting the 16S rRNA region.

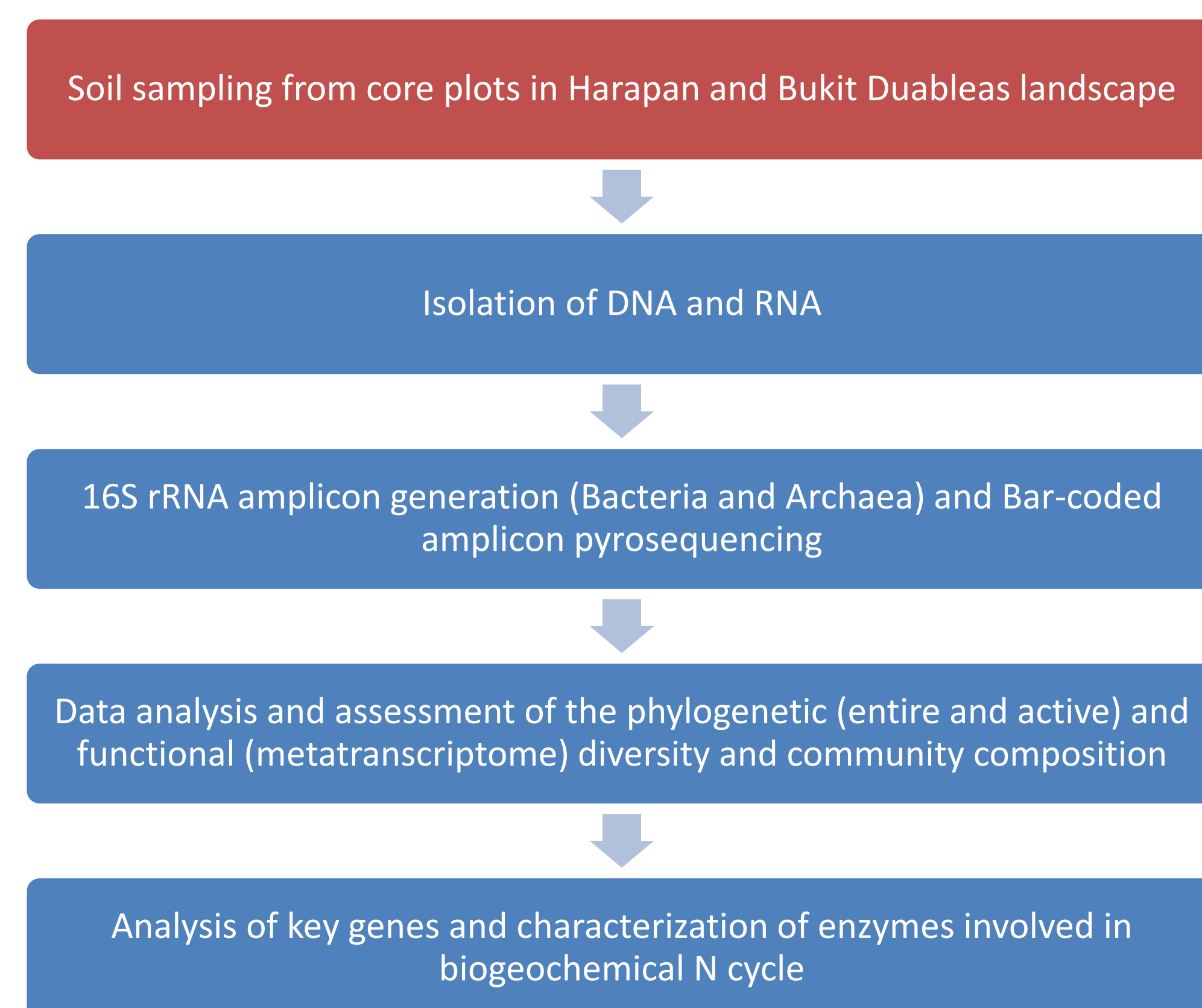


Fig. 1: Flowchart of the proposed research procedure.

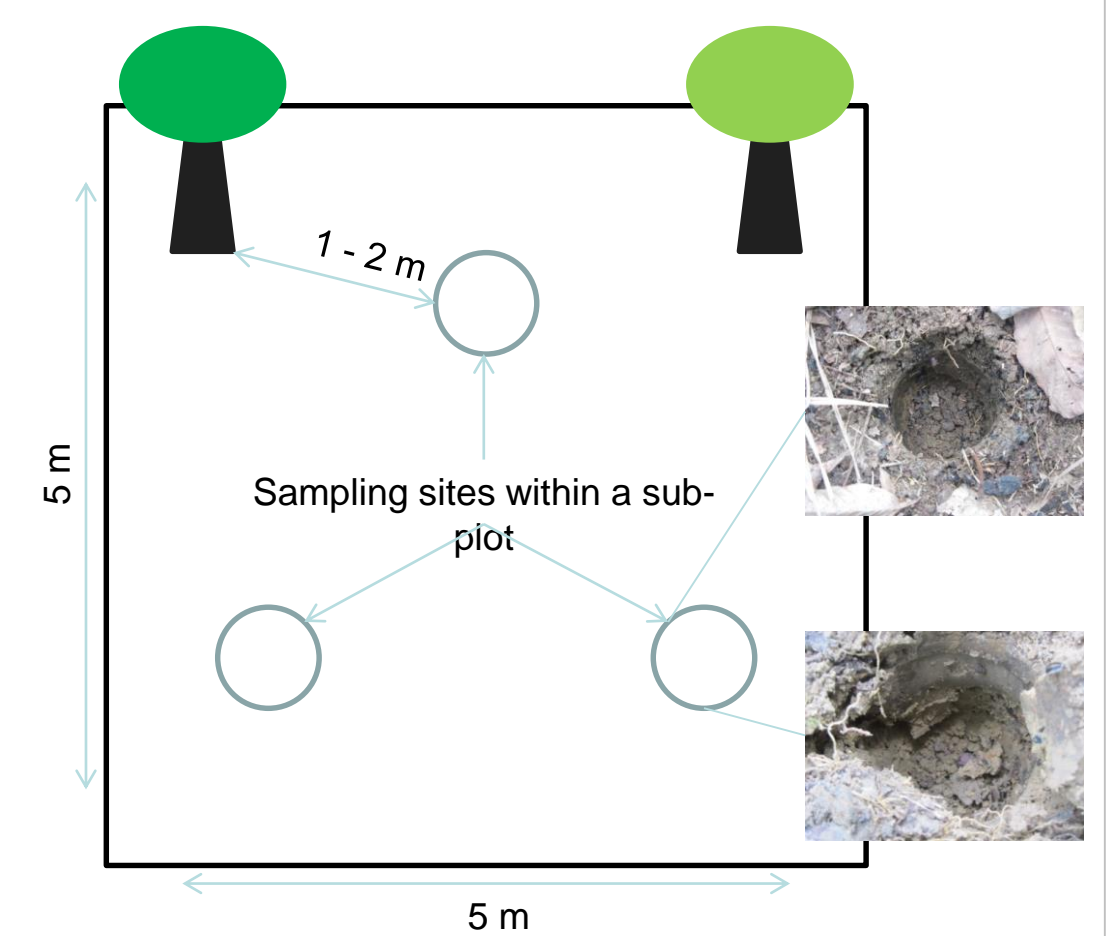


Fig.2: sampling sceme within a sub-plot.

Results:

Using high-throughput next-generation sequencing methods approximately 421,400 and 225,600 high-quality 16 S rRNA gene sequences could be assigned to the domains Bacteria and Archaea, respectively. In general, 8 bacterial phyla and 4 proteobacterial classes abundant in all soil samples (98.4 % of all sequences). The rare bacterial community (< 0.5 %) include 31 phyla and 4 protepbacterial classes. The prokaryotic community was dominated by the Acidobacteria (approx. 40-60 %). Furthermore, all samples show high abundance *Alphaproteobacteria*, *Gammaproteobacteria*, *Actinobacteria*, *Deltaproteobacteria* and *Betaproteobacteria* (fig.3). The archeal community was dominated by the Euryarcheota and the Thaumarchaeota. Preliminary analysis indicated the Euryarcheota seemed to be more abundant in the Bukit Duabelas landscape than in the Harapan landscape. Whereas, the Thaumarchaeota seemed to be more abundant in the Harapan landscape (fig.4).

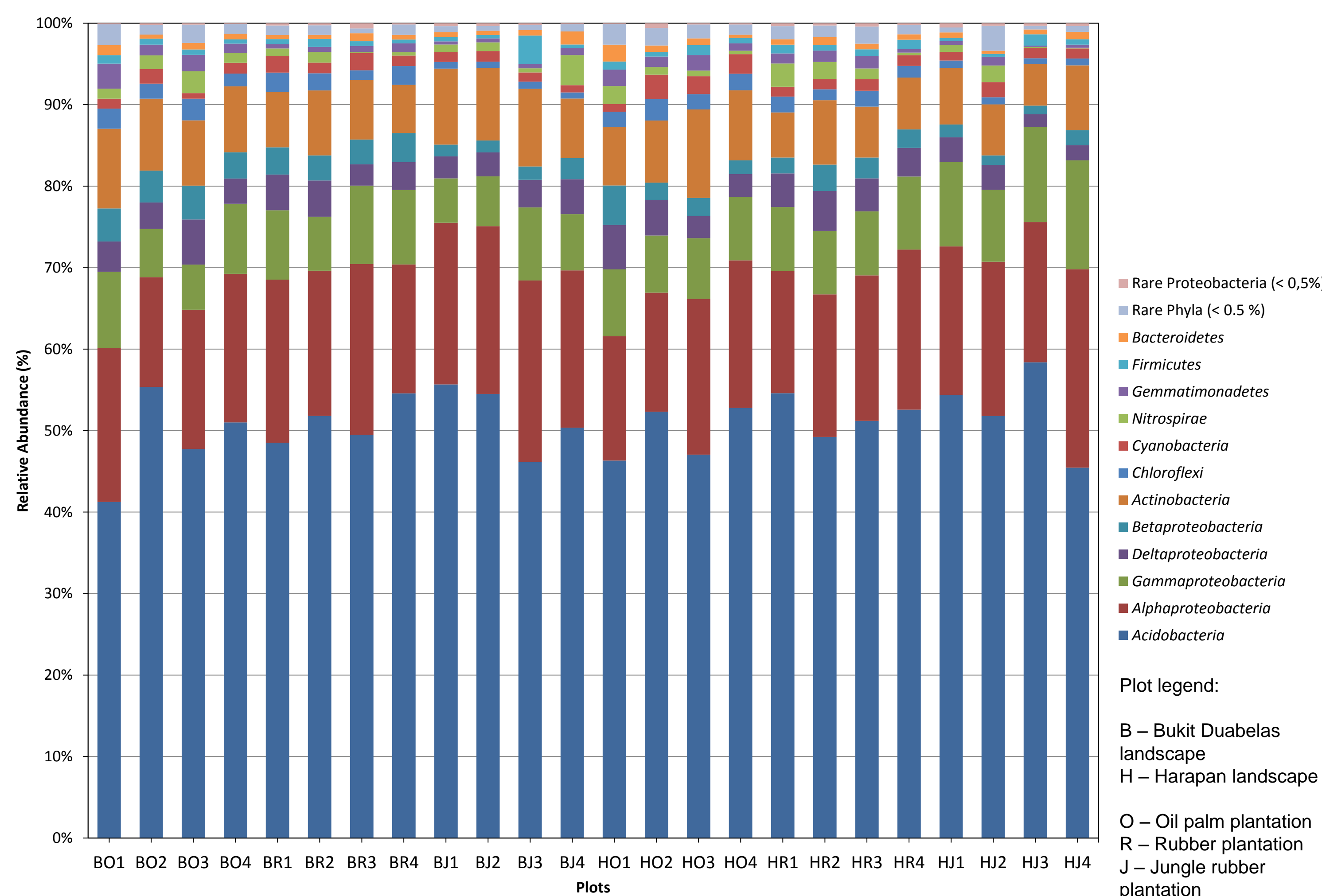


Fig.3: Relative abundance of bacterial phyla and proteobacterial classes from soil of different land-use systems.

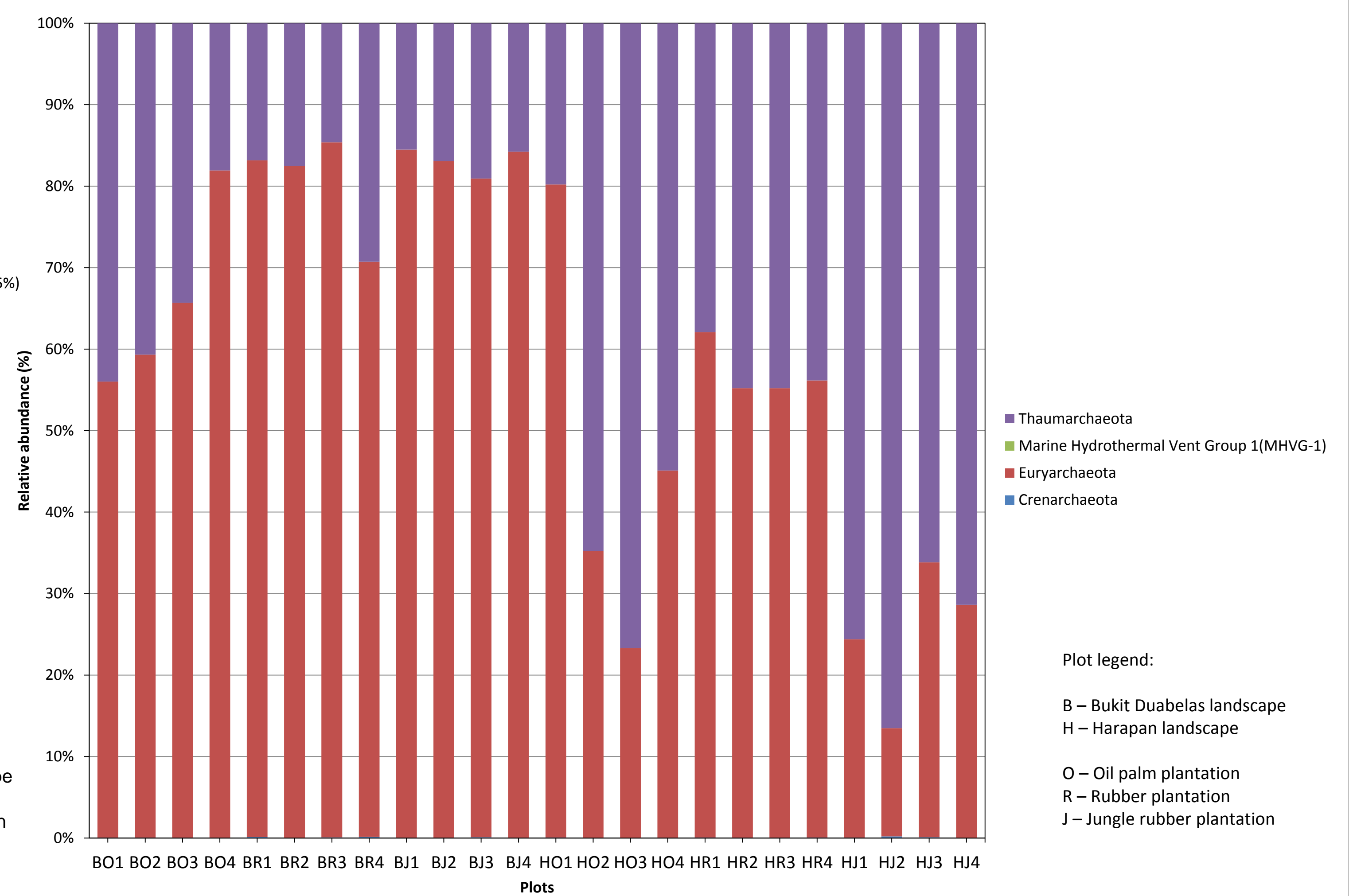


Fig.4: Relative abundance of archeal phyla from soil of different land-use systems.