

Urochloa hybrid can inherit P-cycling genes related to microbial communities and their P-cycling abilities

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BACKGROUND

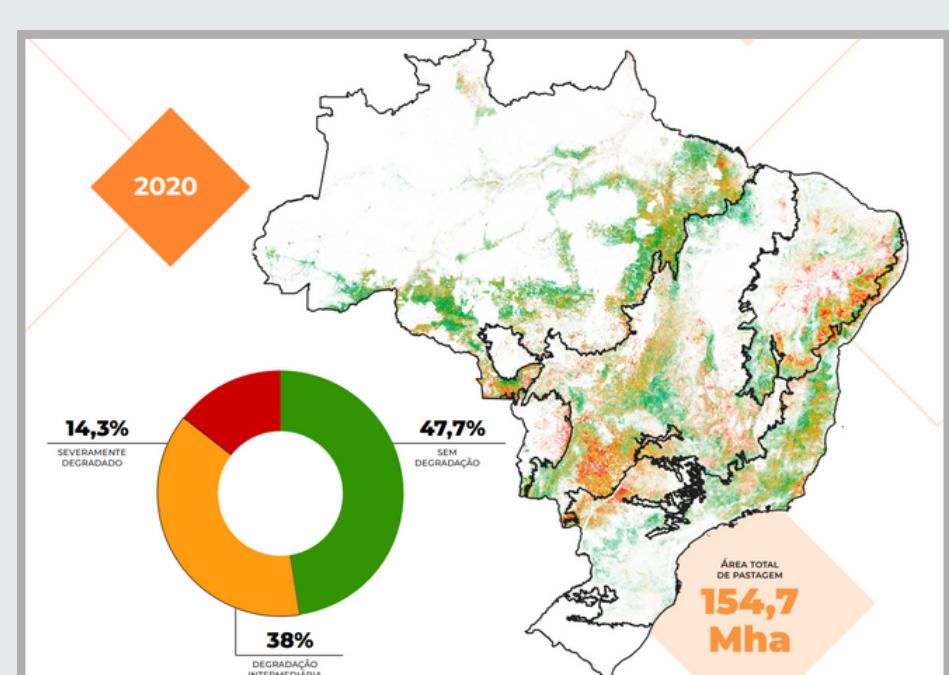
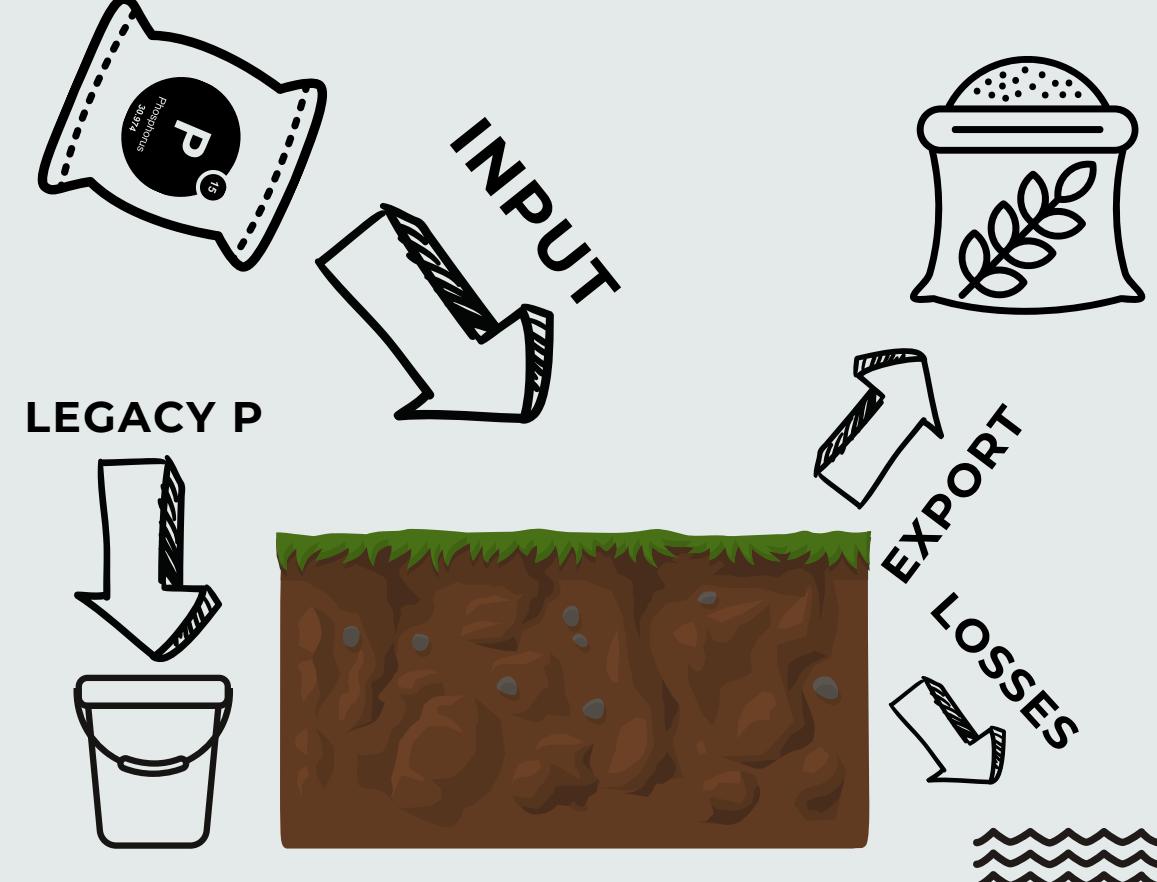
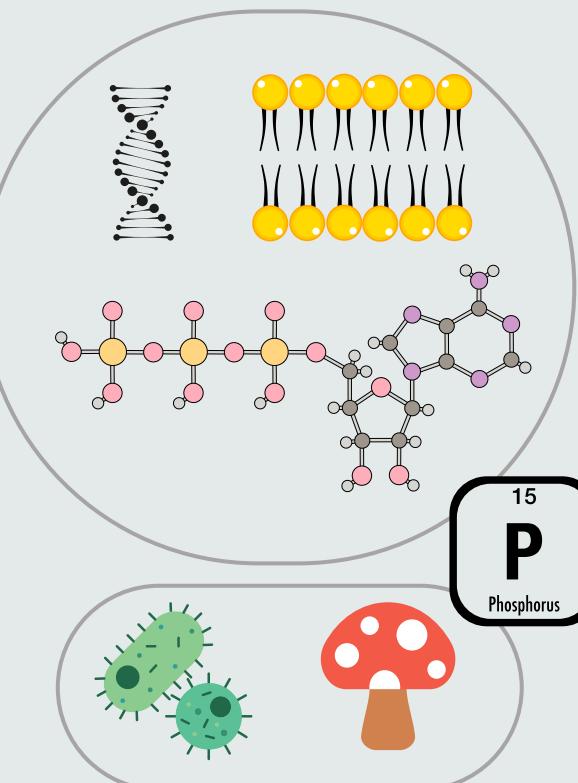
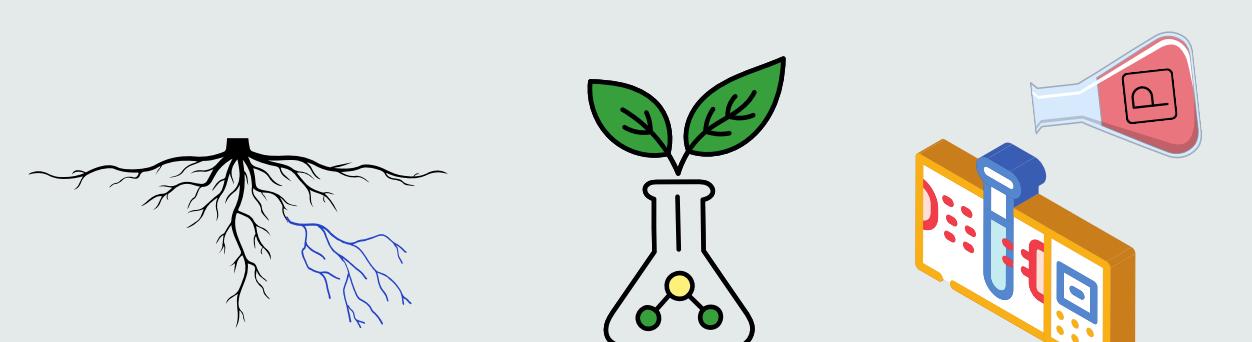


Fig 01. Map of pasture quality in Brazil in 2020. Source: MapBiomass.



Legacy P is the buildup of phosphorus in agricultural soils from historical fertilizer applications and manure deposition. It is essential to comprehend the dynamics of Legacy P in Brazilian soils for sustainable agriculture and environmental management.

METHODS



- AMF colonization
- Enzymatic activity
 - Phosphatases
- P fractionation



- DNA extraction
- PCR and qPCR
 - 16S, ITS, *pqqC* and *phoD*



Packages: vegan, devtools, lsmmeans, multcomp, factoextra, corplot.

Statistical analysis at R environment



Scan here to access the githhub with all the scripts used

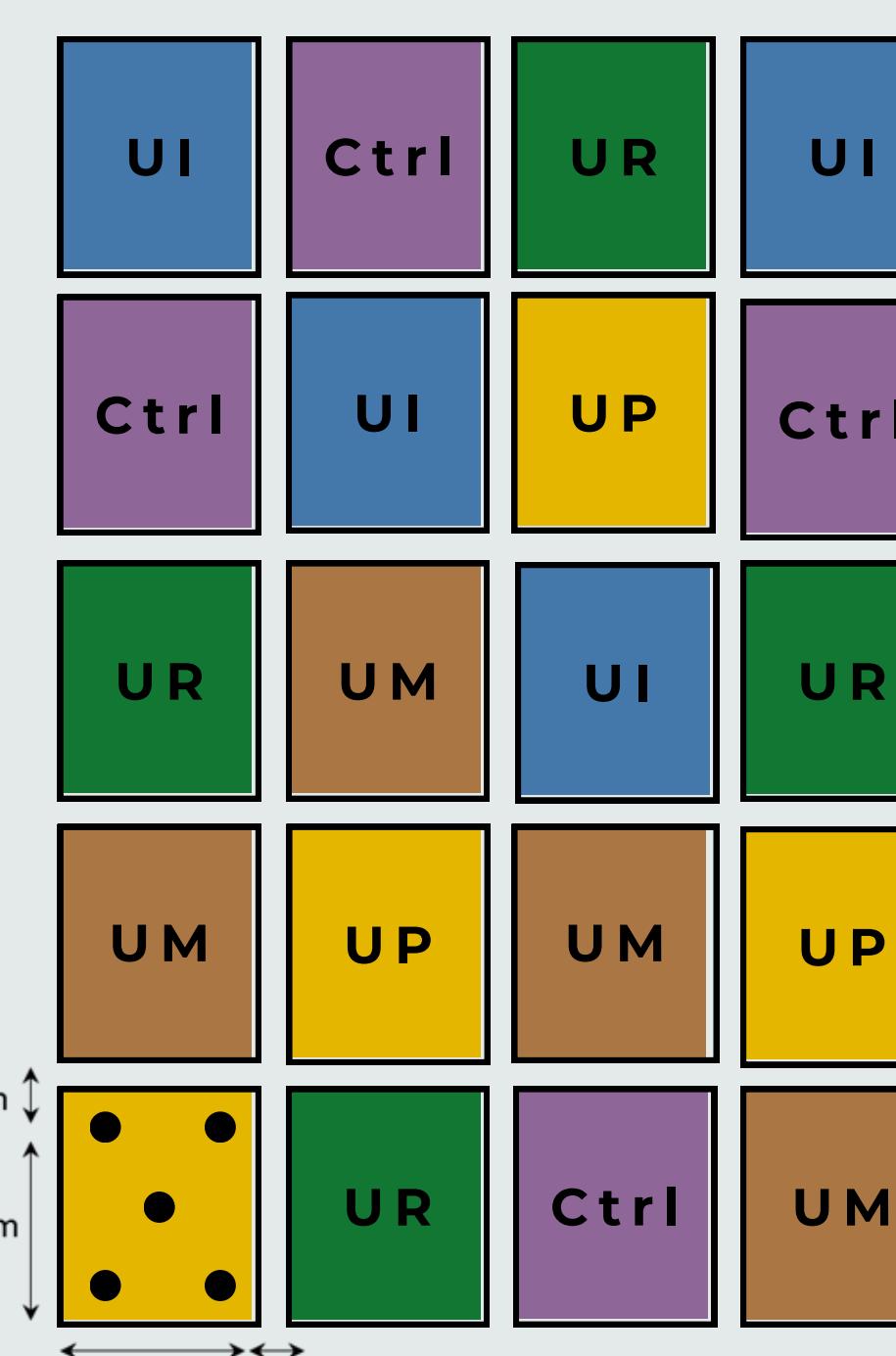


RESEARCH QUESTION

WHAT IS THE INFLUENCE OF UROCHLOA PLANT BREEDING ON THE P-CYCLING MICROBIAL COMMUNITIES?

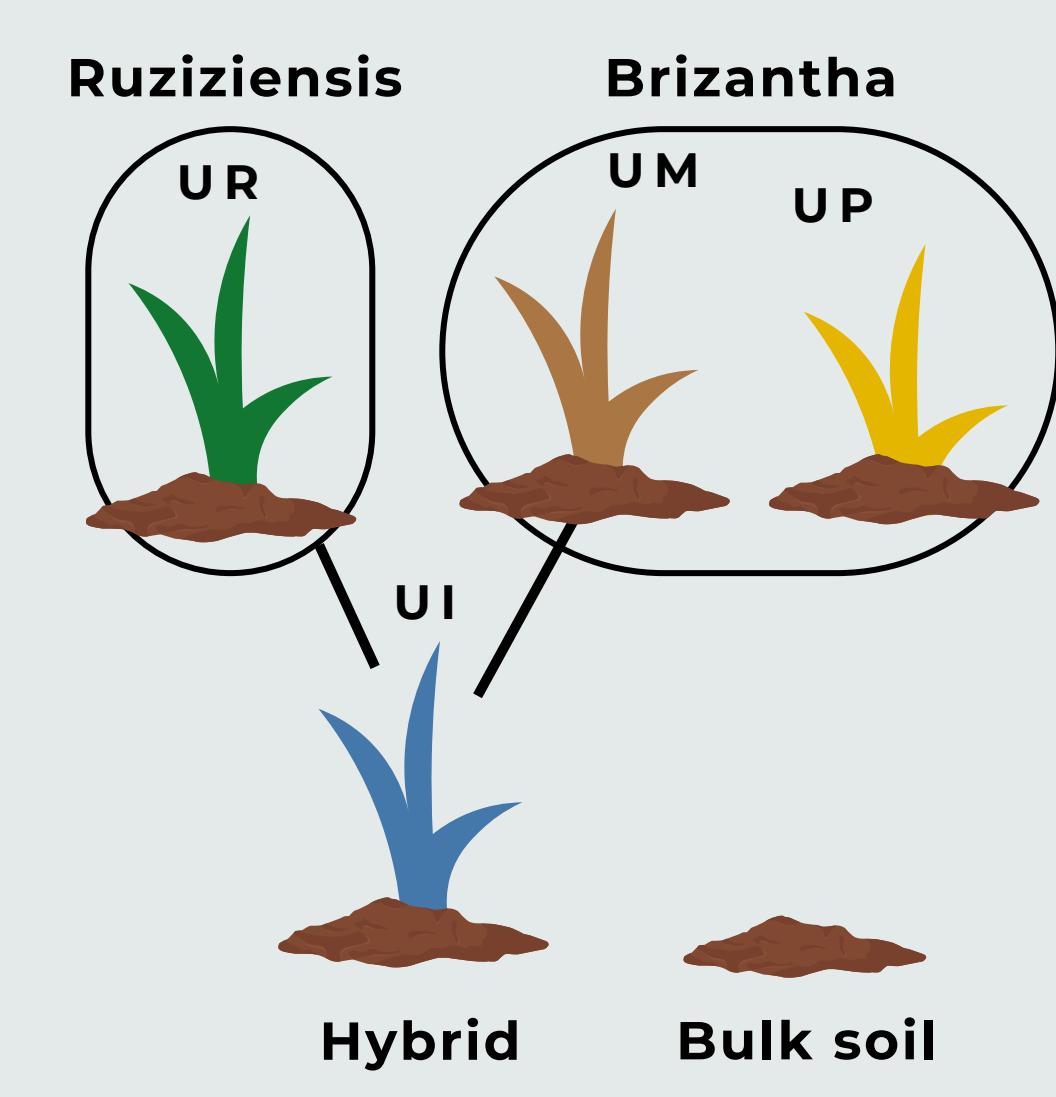


EXPERIMENTAL DESIGN



A field experiment was conducted with five treatments: Control (bulk soil), *U. ruziziensis* (UR), *U. brizantha* cv Marandu (UM), *U. brizantha* BRS Paiaguás (UP), and *Urochloa* spp. Hybrid Ipyporá (UI). The experiment was completely randomized with four replicates, and soil samples were collected from three different depths. Each sample consists on a compost sample with 5 subsamples.

CULTIVARS HISTORY



RESULTS

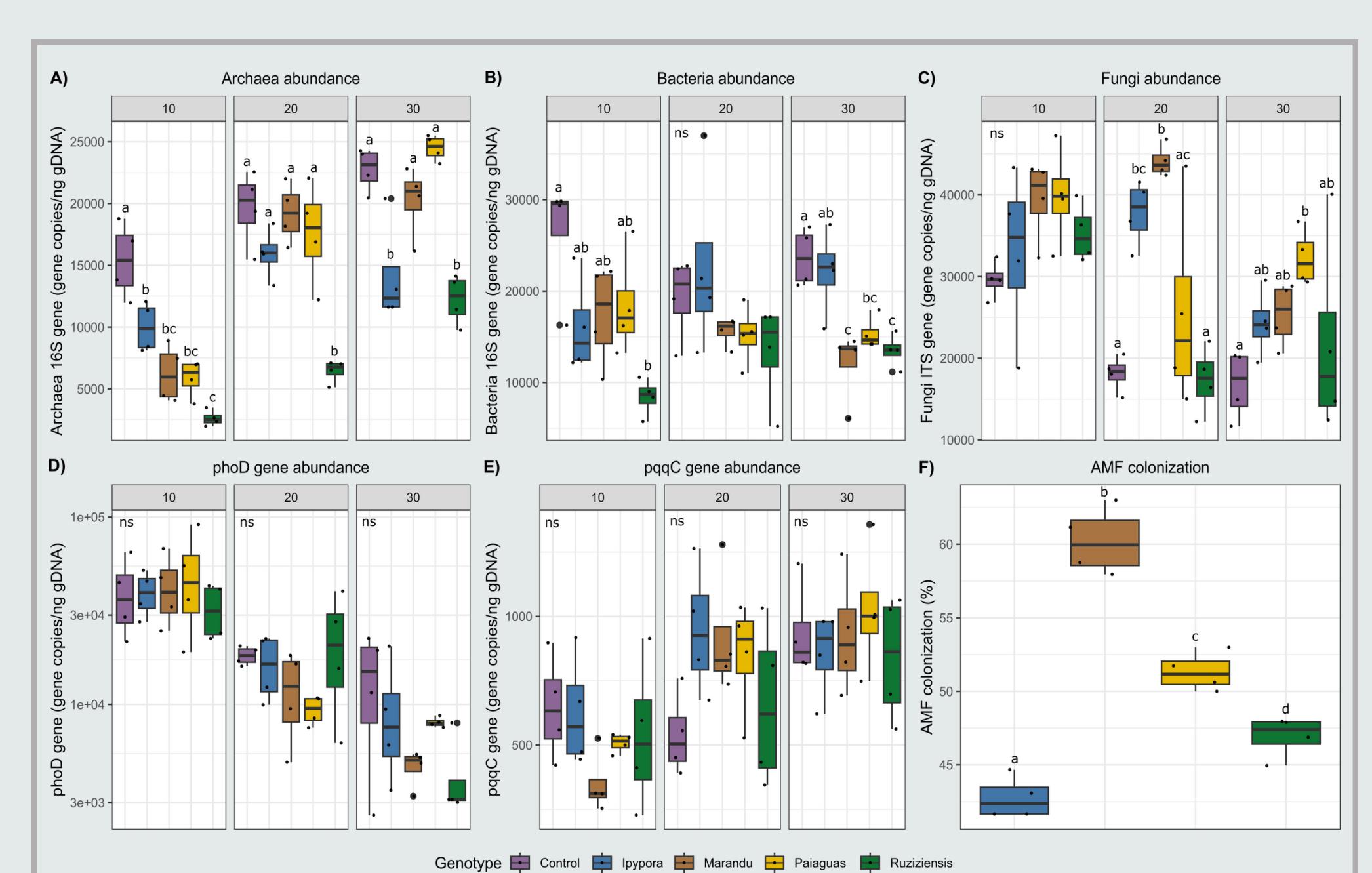


Fig 2. Abundance of A) Archaeal; B) Bacterial and C) Fungal communities; and abundance of functional genes related to D) P solubilization; and E) production of alkaline phosphatase, in the different depths evaluated. F) Root colonization by AMF.

RESULTS

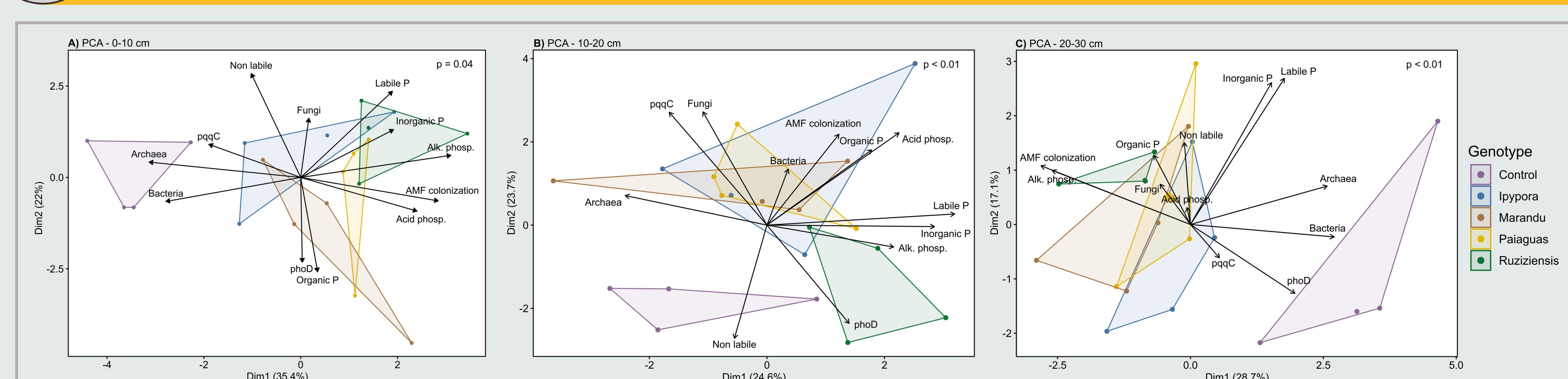


Fig 3. Principal Component Analysis (PCA) using biotic and abiotic variables related to P uptake and cycling to explain the model, where A) represents the depth of 0-10cm; B) the depth of 10-20cm and C) the depth of 20-30c.

Contribution of variables:
A) PC1: Archaea, Alk. phosphatase, AMF and Bacteria; PC2: Non-labile P, Organic P, Labile P and *phoD*.
B) PC1: Labile P, Inorganic P, Archaea and Acid phosphatase; PC2: Fungi, Non-labile P, *pqqC*.
C) PC1: AMF, Bacteria and Alk. phosph. and Archaea; PC2: Labile P, Inorganic P and Non-labile P.

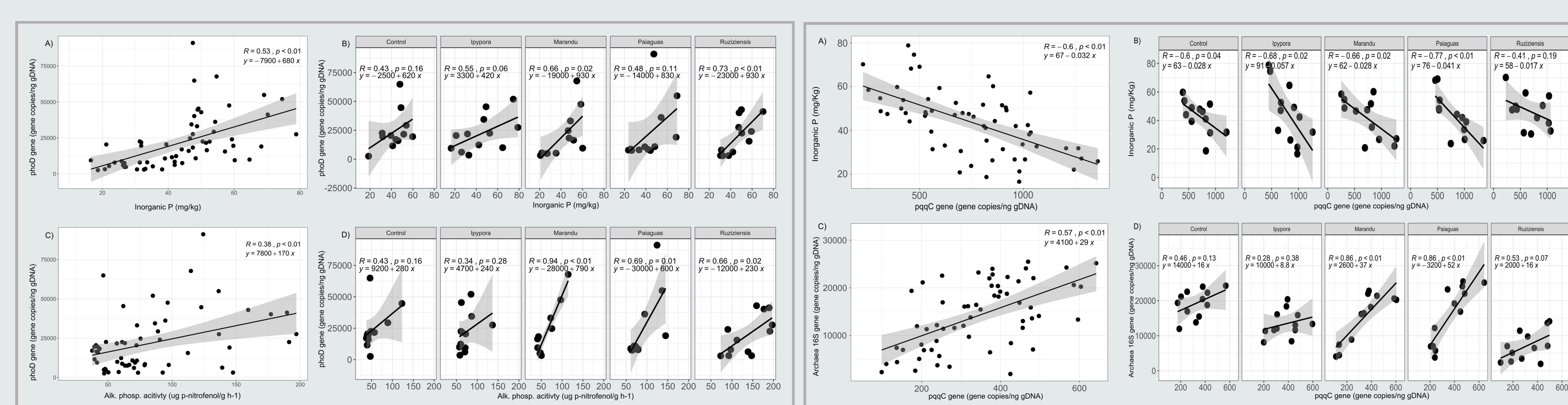


Fig 4. Correlation plots between variables A) *phoD* gene and general soil inorganic P and B) by genotypes; C) *phoD* gene and general soil inorganic P and D) by genotype

Fig 5. Correlation plots between variables A) *pqqC* gene and general soil inorganic P and B) by genotypes; C) *pqqC* gene and 16S gene of archaea general and D) by genotype

TAKE HOME

Each variety can shape the abundance of certain microbial groups to fulfill their strategies on P absorption for *Urochloa* genetic breeding.

Our results also indicated a possible contribution of Archaea for P mineralization based on the *pqqC* gene.