

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

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AIM

This work aims to understand how the genetic breeding of *Urochloa* (through hybridization between *U. brizantha* and *U. ruzizienensis*) modifies the soil microbial groups in soil depths and their related P-cycling abilities.

METHOD

Four *Urochloa* varieties, *U. brizantha* cv. Marandu (UM), *U. brizantha* BRS Paiaguás (UP), *U. ruzizienensis* (UR) and the hybrid Ipyrora (UI) were evaluated in a 3-year field experiment with soil samples collected at three soil depths. The *pqqC* and *phoD* genes were amplified by qPCR as well as the barcodes for Bacteria, Archaea and Fungi communities. The phosphorus fractionation was conducted; the enzymatic activity was measured for both, acid and alkaline phosphatases. Data were analyzed in R.

RESULTS

There are differences in the Archaea, Bacteria and Fungi abundances, but with different patterns depending on the depth. AMF colonization varied according to the varieties, being higher in UM (60%) and lower in UI (42.8%). The *pqqC* gene specific for gluconic acid production, a marker gene of P-solubilizing Bacteria, was positively correlated with Archaea abundance ($R=0.49$, $p<0.01$) but has no correlation with Bacteria, only indicated previously by *in silico* analysis. Based on a Principal Component Analysis, it was possible to observe that microbiological components are important when genetic components are used to distinguish *Urochloa* varieties.

CONCLUSIONS

We concluded that 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.