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**Drought constrains the rhizosphere's bacterial diversity in the semiarid over a broad landscape**

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Microbial communities are shaped by many factors such as pH, moisture, temperature and redox potential. In the past decade, researchers have started to pay attention to how these environmental factors influence community structure on a broad landscape. Therefore, this study was designed to test the effect of moist over the bacterial community in a broad landscape. To achieve this we sampled rhizosphere soils of the Caatinga, a semiarid biome located in the northeast of Brazil. As with many other semiarid environments this biome is subjected to two different seasons one in which it rains and another of drought. So, to identify how moist affect a community that is used to go through these drought/rain periods, we have sampled five different sites, about 100 km apart during this two seasons. These samples were subjected to physical and chemical analysis and to 16S rRNA sequencing of the V6 region on an ion torrent. The community of the drought season presented a high abundance of Actinobacteria while the rain season had a higher abundance of Proteobacteria. Canonical correspondence analysis followed by forward selection indicates that relative air humidity is the only factor with significant effect over these communities (6%). Similarly, partial Mantel test shows that there is a significant correlation of the community and environmental similarities when considering both seasons and during rain season; however, during drought the correlation was not significant. This result indicates that although environmental factors do drive the diversification of these communities the effect of drought diminishes this effect. According to the variation partitioning more than half of the variation cannot be explained by neither the environmental parameters nor the spatial distance. ANOSIM and PERMANOVA tests indicate that there are significant differences between drought and rain as well as between sites (within each season). The majority of the OTUs that presented abundances, which are significantly different by the Metastats test, increased during drought and many of them belonged to the phylum Actinobacteria. Also, distance decay analysis indicated that during drought the samples presented a lesser effect of distance over community similarity. Similarly the taxa area relationship ( $z$ ) was lower during drought. Altogether, these findings indicate that drought is not only the most intense driver of diversity in this sort of environment but significantly limits diversity on a broad landscape. Hence, we tested our data to identify whether it fits any taxa abundance model with Akaike Information Criterion. The AIC indicated that these communities best fit a zero-sum multinomial (ZSM) distribution and is, therefore, limited by geographical distance. Overall, these data indicates that during periods of drought the diversity is limited which decreases the diversity observed on the broad area sampled.