Landsliding and rhizobiota link the short- and long-term carbon cycles.

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The exposure of fresh rock surfaces and primary minerals in response to landsliding sets in motion biogeochemical and biological processes that have not been conceptually linked. On the one hand, landslide activity may enhance chemical weathering and the release of mineral-bound nutrients. On the other hand, microbial communities associated with plant roots may play an important, albeit mostly undocumented role in rock weathering. Of particular interest, is the occurrence of landslides in terrain underlain by (Ca, Mg)-bearing silicate rocks given that their weathering plays a critical role in the long-term carbon cycle. The main goal of this study is to characterize the rhizobiomes of plants developing in contrasting weathering environments, namely landslides and forest, underlain by carbon and magnesium (Ca, Mg)-bearing silicate rocks in a tropical environment. We collected bulk soil and soil from roots of eleven plant species belonging to three life forms (terrestrial fern, arboreal fern, and shrubs) growing at landslide and forest sites underlain by granodiorite of the Utuado batholith in central Puerto Rico. We extracted DNA from these soil samples using the MoBio Powersoil kit and sequenced the 16S V4 region in the MiSeq platform. After quality filtering, de-replication, and rarefaction to an even depth our 180 samples yielded 1,230,080 sequences that were assigned to a total of 22,083 operational taxonomic units (OTUs) in 49 phyla. Most OTUs in the Bacterial domain belonged to four phyla [Proteobacteria (36%), Acidobacteria (24%), Verrucomicrobia (11%) and Planctomyces (7%)], whereas in Archaea most OTUs belonged to one phyla [Crenarchaeota (97%)]. The first two axes of a Principal Coordinates Analysis (PCoA) explained 52% of the variation among our samples. The landslide and forest samples were clearly separated along axis 1 (32%) whereas the rhizosphere and bulk soil samples along axis 2 (20%) of the PCoA. Using the Lineal Discriminant Analysis-Effect Size (LEfSe) algorithm, we detected indicator taxonomic groups that differentiated landslide and forest. Indicator phyla in landslides were Verrucomicrobia and TM7, whereas in forests, Crenarchaeota, Euryarchaeota, Acidobacteria, Gemmatimonadetes, GN02, Nitrospirae, NKB19, OP11, Spirochaetes and Planctomycetes. From these phyla, Verrucomicrobia, TM7, GN02 and Spirochaetes were more abundant in the rhizosphere, whereas Crenarchaeota, Euryarchaeota, and Nitrospirae were more abundant in soil samples, regardless of the weathering environment. Recent work suggests that Verrucomicrobia contributes to the weathering of rocks which may explain their presence in rhizobiomes from landslide habitats. To our knowledge, this is the first microbiome study using Next-Generation Sequencing (NGS) technologies to link rhizobiota to the short and long-term carbon cycles in areas underlain by silicate rocks subjected to landslide activity.