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Bacterial communities in soils as indicators of the potential of syenite as an agromineral

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Abstract – The objective of this work was to identify microbial communities associated with the surfaces of alkali feldspars and to determine whether these microbes might be involved in the weathering of these rocks for agronomic benefit. Samples were taken from weathering profiles and soils developed on a syenite, considered as a raw material for agromineral production, located in the municipality of Triunfo, in the state of Pernambuco, Brazil. Molecular microbiological techniques (qPCR and 16S rRNA gene sequencing) were used, and data were interpreted by the analysis of variance, hierarchical cluster analysis, and principal coordinates analysis. In addition, scanning electron microscopy was used to image mineral surfaces. Similar bacterial communities were observed in all samples, showing that the bacteria found in soil are present at the earliest stages of rock weathering and are available to play a role in nutrient release. In particular, Actinobacteria and, within this phylum, Actinomycetales were proportionally more abundant than other taxa in rock-dominated soil samples, i.e., in thin soils on or between fractured or broken syenite. The analysis of rock dust used as a remineralizer, crushed with no further treatment, shows that Actinobacteria play a role in the early stages of weathering of feldspar-bearing rocks.

Index terms: Actinobacteria, Actinomycetales, agromineral, bacteria, microbial community, syenite.

Comunidades bacterianas associadas aos processos intemperizados como indicadores do potencial do sienito como agromineral

Resumo – O objetivo deste trabalho foi identificar comunidade microbianas associadas às superfícies de feldspato alcalino e determinar se esses micróbios podem estar envolvidos no intemperismo dessas rochas, para benefício agronômico. As amostras foram coletadas de perfis intemperizados e solos desenvolvidos sobre um sienito, considerado como matéria prima para produção de agrominerais, localizado no município de Triunfo, no estado de Pernambuco, Brasil. Foram usadas técnicas de microbiologia molecular (qPCR e sequenciamento de genes 16S rRNA), e os dados foram analisados por análise de variância, análise de grupos hierárquicos e análises de coordenadas principais. Além disso, utilizou-se a microscopia eletrônica de varredura para gerar imagens das superfícies minerais. Foram observadas comunidades similares em todas as amostras, o que mostra que as bactérias encontradas nos solos estão presentes nos estágios iniciais do intemperismos da rocha e estão disponíveis para desempenhar um papel na liberação de nutrientes. Em particular, Actinobacteria e, dentro desse filo, Actinomycetales, foram proporcionalmente mais abundantes do que os outros táxons nas amostras de solo dominadas por rochas, isto é, em solos finos sobre ou entre sienito fraturado ou quebrado. A análise do pó de rocha usado como remineralizador, moído sem outros tratamentos, mostra que Actinobacteria desempenham um papel nos estágios iniciais do intemperismo de rochas compostas por feldspatos.

Termos para indexação: Actinobactéria, Actinomycetales, agromineral, bactéria, comunidade microbiana, sienito.

Introduction

Given the growing global population, food security is an issue of increasing relevance worldwide. The major crop producing regions are experiencing decreases in productivity due to climate change and soil degradation (Keesstra et al., 2016). In Brazil, for example, the Cerrado, a major area of agricultural production, has deeply weathered soils that are often deficient in nutrients, especially phosphorus but also potassium (Haridasan, 2008; Lannes et al., 2020), which need to be replaced by the addition of fertilizers. Conventional chemical fertilizers are usually applied, but another approach is to use locally-derived agrominerals, such as silicate minerals, which can contain a wide range of nutrients (Manning & Theodoro, 2020; Marchi et al., 2020).

In deeply leached tropical soils, primary silicate minerals are destroyed by weathering, releasing nutrients for plant growth (Leonardos et al., 2000). The effectiveness of silicate rocks used as remineralizers has been assessed in Brazil (Tavares et al., 2018; Marchi et al., 2020), and their use for global crop production is proposed as part of the process of mitigating climate change worldwide (Beerling et al., 2020). However, the selection of rocks suitable for use as remineralizers is not straightforward since, although the content of their nutrients can be determined by chemical analysis, it is also important to consider their rate of release, which depends on mineral dissolution rates (Manning, 2010). To date, the published mineral dissolution rates are based on laboratory experiments undertaken in the absence of associated microbial communities (Palandri & Kharaka, 2004). However, the role of soil microbial community in mineral weathering (Balland et al., 2010; Huang et al., 2014) is fundamental to explain the mechanisms that account for the increased plant growth observed in trials with agrominerals.

Among the nutrients vital for plant growth and development, potassium stands out, influencing yield and drought resistance (Manning, 2010). This element is most commonly supplied to agricultural soils as potash fertilizers, which contain K in a soluble form (KCl). However, Brazil produces less than 10% of its potash demand, and around 4 million tons have to be imported annually, creating a dependency on global markets with their associated fluctuations and instability (Berge, 2012).

In this context, there are a number of initiatives to search for locally-available alternatives, including K-rich silicate rocks such as phonolite and syenite (Manning, 2010). Phonolite (fine grained) and syenite (coarse grained) have similar chemical and mineralogical compositions; containing 12–13% K_2O, they are largely composed of potassium feldspar ($KAlSi_3O_8$) (Manning et al., 2017). Feldspar is inherently insoluble in water, but it decomposes through biotic and abiotic weathering, both resulting in a residual clay mineral product and supplying other elements (K and Si) to the soil solution, which become available to the plants. In the Cerrado region, to address K deficiencies, occurrences of syenite that are close to important agricultural areas have been investigated (Ciceri et al., 2017b).

However, as previously mentioned, the ability of silicate rocks to act as sources of nutrients depends on the rate at which weathering takes place. There are several approaches to rock weathering, including: mechanical processing, to reduce grain size, which enhances reaction rates by increasing surface area; chemical treatment, which should be done with degradable products; and mining, with added costs due to the additional processing of the agromineral, increasing prices to consumers (Ciceri et al., 2017a).

In mineral weathering, microorganisms may play a major role by producing organic and inorganic acids and metal-complexing ligands (Uroz et al., 2009; Balland et al., 2010). These biological products can increase feldspar dissolution rates either by decreasing pH, by forming surface complexes that destabilize the crystal structure, by complexing metals in solution, or by changing the mineral saturation state (Balland et al., 2010). Moreover, specific microbial taxa, fungal and bacterial, have been observed in association with particular minerals (Olsson-Francis et al., 2016). In the case of bacteria, those associated with weathering have been found within the phyla Actinobacteria, Alphaproteobacteria, Betaproteobacteria, Gammaproteobacteria, and Firmicutes (Uroz et al., 2009; Huang et al., 2014; Wang et al., 2014). Although fungi are also involved in biological weathering (Uroz et al., 2009) and produce greater concentrations of more effective chelating agents, bacteria are ubiquitous and inhabit extreme environments where fungi may not survive (Sterflinger, 2000).

Based on these results, the present study investigates the bacterial communities associated with the weathering of a syenite considered as a raw material for agromineral production (Ciceri et al., 2017b). The hypothesis is that specific bacterial communities are associated with feldspars, and, consequently, are also likely to be associated with mineral weathering and the release of nutrients, including K. The identification of a specific association would, therefore, indicate potential for an indigenous rock or rock-soil community to release nutrients from feldspar within silicate rocks added to soils as a remineralizer, providing a mechanism that explains the observed agronomic benefits (Tavares et al., 2018).

The objective of this work was to identify microbial communities associated with the surfaces of alkali feldspars and to determine whether these microbes might be involved in the weathering of these rocks for agronomic benefit.

Materials and Methods

Field work was carried out in the municipality of Triunfo, in the state of Pernambuco, Brazil, allowing the sampling of minerals associated with soils developed on syenite and other rocks, as well as from weathering profiles within the syenite (Souza et al., 2010). In the study area, which is part of the Caatinga biome (Santos et al., 2012; Silva & Cavalcanti, 2012), agricultural production is low, with bananas and other crops cultivated on a small scale. The chemical composition of the syenite from this location is described in Manning et al. (2017).

The focus of the sampling strategy adopted in the present study was originally to investigate mineralogical changes due to weathering, not soil microbial communities. However, the observation of microbes on the mineral surfaces led to an investigation of community structure, on an exploratory basis, similarly to that carried out by Nagler et al. (2016). Samples were collected from areas mapped by Santos et al. (2013), with soils classified as: Cambissolos Háplicos Tb eutróficos (eutrophic Tb Haplic Cambisol; Inceptisol); and Luvissolos Crômicos Órticos (Orthic Chromic Luvisol; Altisol/Aridisol). Sample origin, associated land use, and location are presented in Table 1 and Figure 1.

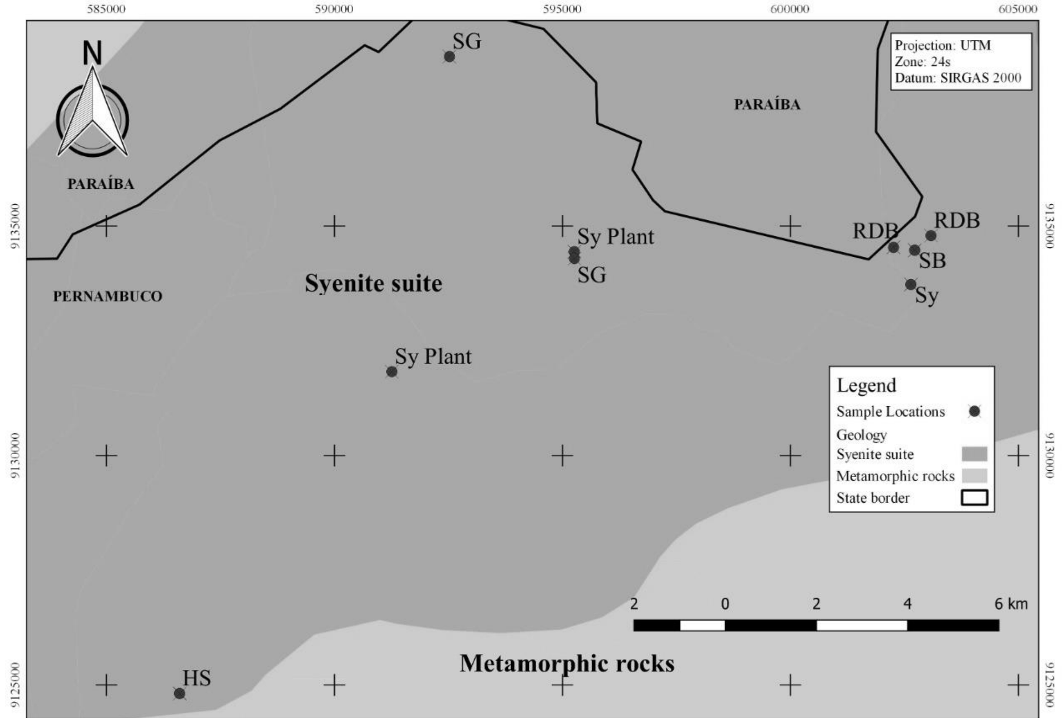
The samples were collected with the aim to identify bacterial community structure for different weathering environments, represented by heterogeneous field locations, including saprolite and rocky soils. For this, only single samples (22 in total) were taken, since composite ones could potentially introduce confounding factors, by, for example, mixing differing proportions of minerals, rock, and soil. Nine samples of saprolite minerals were collected, using a hand trowel or knife, from vertical surfaces in the weathering profiles of a syenite below the soil, i.e., saprolite (Figure 2 A), up to a depth of 20 cm, where possible. Four soil samples were collected from rock-dominated soils, developed immediately on syenite (rdb1–rdb3 and rds1) (Figure 2 B), where banana grew in the cracks between syenite boulders. Three soil samples were taken from hillsides with scrub growing on soil mixed with syenite boulders (scrub soils and hs1–hs3) (Figure 2 C). Another three samples were collected from soils in alluvial valley floors cultivated with banana (*Musa* sp.) (sb1–sb3) (Figure 2 D), whereas two were taken from land producing forage of Guinea grass (*Panicum* spp.) (sg1–sg2) (Figure 2 E) and one from land producing maize (*Zea mays* L.) (sm1) (Figure 2 F).

Based on their field characteristics, three sample types were distinguished: weathered syenite (saprolite); rock-dominated soil developed on syenite; and cultivated soil. However, the second and third sample types were also collectively considered as “soil-derived” for a simpler statistical comparison of “soil” and “syenite” categorized data. Saprolite profiles in weathered syenite were exposed in existing excavations and roadside exposures, typically showing a network of kaolin-dominated joints (carrying tree roots) within iron-stained weathered syenite (Figure 2 A). Rock-dominated soils occurred on hills (slopes and summits), where bananas or scrubby vegetation grew either within a patchy and shallow soil dominated by rock fragments > 1 cm in size (Figure 2 B and C) or in fissures. Cultivated soils were sampled in valley floors or shallow slopes, and represented deeper soils used for crop production (Figure 2 D, E, and F).

Table 1. Mineral samples, with their origin and associated land use[(1)].

Sample origin	Sample	UTM coordinates (SAD69, zone 24S)		
		X	Y	Z
Weathered syenite (saprolite)	sy1	595301	9134484	969
	sy2	595301	9134484	969
	sy3	592562	9138737	875
	sy4	591299	9131871	981
	sy5	591299	9131871	981
	sy6	602682	913377	1047
	sy7	602682	913377	1047
	sy8	602682	913377	1047
	sy9	602682	913377	1047
Rock-dominated soil with bananas, developed on syenite	rdb1	602302	9134579	1081
	rdb2	602302	9134579	1081
	rdb3	603123	9134834	1111
Rock-dominated soil with scrub, developed on syenite	rds1	602536	9134079	1079
Uncultivated hill-side soil with scrub	hs1	586643	9124857	751
	hs2	586643	9124857	751
	hs3	586643	9124857	751
Cultivated soil (bananas)	sb1	602767	9134517	1047
	sb2	602767	9134517	1047
	sb3	602767	9134517	1047
Cultivated soil (grass)	sg1	592562	9138737	875
	sg2	592562	9138737	875
Cultivated soil (maize)	sm1	595303	9134336	946

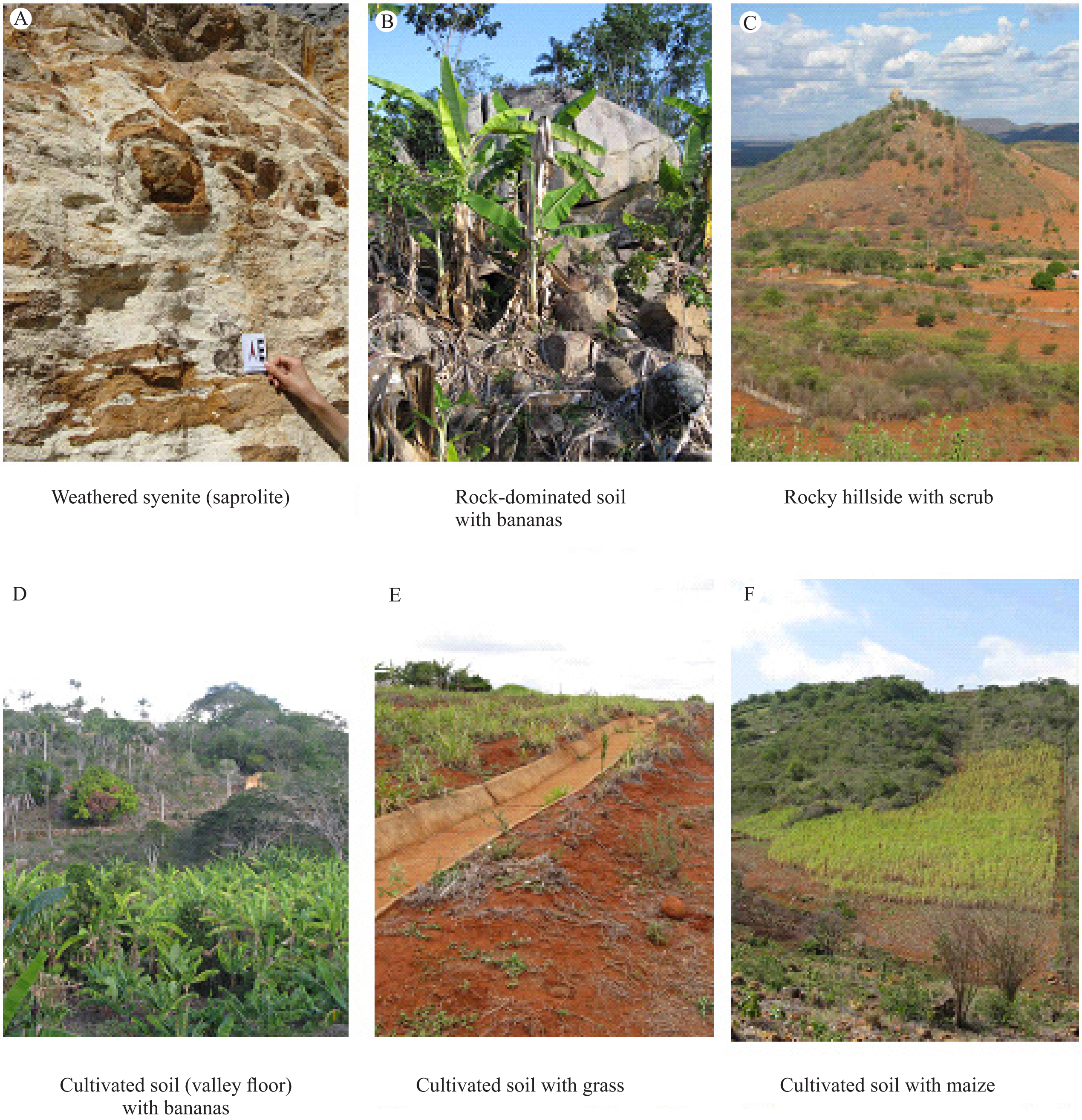
(1)Samples hs1, hs2, and hs3 are associated with soils mapped as Orthic Chromic Luvisols, and the rest, with soils mapped as eutrophic Tb Haplic Cambisols (Santos et al., 2013).



AFigure 1. Sample locations in the vicinity of the municipality of Triunfo, in the state of Pernambuco, Brazil. Without crops: Sy, syenite without plant activity; Sy Plant, syenite with plant activity; and HS, uncultivated hill-side soil with scrub. With crops: RDB, rock-dominated soil with banana; SB, soil cultivated with banana; and SG, soil cultivated with grass. Crosses denote UTM grid coordinates. Map drafted by Bruno Timóteo Rodrigues.

At the time of collection, the samples were immersed immediately in 100% ethanol, to preserve the indigenous community. These ethanol-sterilized mineral samples were taken to Newcastle University, placed in a freezer, and kept at -20°C until analysis.

For scanning electron microscopy, syenite grains, 1–3 mm in size, were selected from the mineral samples and washed in 70% ethanol. Samples were air-dried before being mounted on an aluminum stub with a carbon disc and an Acheson Silver Dag (Agar Scientific Ltd, Essex, UK) and then dried overnight. Specimens were gold-coated (15 nm), using the E5000 sputter coater (Quorum Technologies Ltd, East Sussex, UK), and examined with the TESCAN VEGA LMU scanning electron microscope (Tescan Orsay Holding, a.s., Kohoutovice, Czech Republic), housed within



Weathered syenite (saprolite)

Rock-dominated soil with bananas

Rocky hillside with scrub

Cultivated soil (valley floor) with bananas

Cultivated soil with grass

Cultivated soil with maize

Figure 2. Representative views of the locations where samples were collected. Photographs taken by David Manning.

Electron Microscopy Research Services at Newcastle University. Digital images were collected with the software supplied by Tescan Orsay Holding.

For high-throughput sequencing, genomic DNA was extracted from a ~0.5 g sample after ethanol evaporation using the FastDNA Spin Kit for Soil and the FastPrep ribolyzer (MP Biomedicals, LLC, Irvine, CA, USA) according to the manufacturer's protocol. To confirm that the kits were clear of contaminants, a procedural blank was carried out using 250 µL Just Water, (Microzone, Haywards Heath, UK), a sterile RNAase and DNase free water. The presence of extracted DNA was checked by agarose gel electrophoresis in 0.7% (w/v) agarose gels, made in 1 x tris-acetate-EDTA buffer (40 mmol L^{-1} tris, 20 mmol L^{-1} acetic acid, 1 mmol L^{-1} EDTA, and pH 8.3), and stained with 1.6 µL ethidium bromide. DNA extracts were stored at -20°C until further use.

A subset of DNA extracts from the samples was amplified following the protocol of Lee-Cruz et al. (2013), using the same bacterial primers targeting the V3 region of the 16S rRNA gene. PCR products were sequenced using the MiSeq benchtop sequencer (Illumina, Inc., San Diego, CA, USA) at Nu-Omics (Northumbria University, Newcastle, UK), in order to produce paired end reads. Sequences were analyzed using the Quantitative Insights into Microbial Ecology (QIIME) pipeline (Caporaso et al., 2010b). Briefly, the Uclust algorithm (Edgar, 2010) was employed for operational taxonomic units picking at a 97% similarity level (species-equivalent), PyNAST (Caporaso et al., 2010a) was used for sequence alignment, chimeric sequences were identified with ChimeraSlayer (Haas et al., 2011), and the Greengenes reference database, version 12_10, was used for taxonomy assignment (McDonald et al., 2012).

Statistical analyses were performed in the Vegan package, version v.1.15-1, in the R, version 2.9.1, software (R Core Team, 2009). The output file generated by QIIME contained the taxa detected in the samples grouped into operational taxonomic units with a minimum of 97% sequence similarity (species-equivalent). No major differences between soil and syenite samples were detected at this similarity level, and, therefore, taxa were reorganized into phyla for the bacteria, which yielded a similar number of taxonomic groups for both. The relative abundances of the different taxonomic groups in the soil and syenite samples were compared using the analysis of variance (ANOVA) or, if the data was not normal and could not be transformed, the Kruskal-Wallis test. The hierarchical cluster analysis and principal coordinates analysis, both using the Jaccard index, were carried out to compare the structure of the microbial communities in the samples from the different sampling environments. To assist with the interpretation and presentation of the data, the samples were divided into three groups: syenite-dominated, rock dominated soils, and soils supporting well-established vegetation or crops (banana, grass, and maize).

Results and Discussion

Scanning electron microscope investigations showed mineral weathering in all syenite samples, with corrosion of the feldspar grain surfaces. In some of the samples (Figure 3), it was possible to observe microbial cells (some dividing) attached to the weathered mineral surface, supporting the hypothesis that microbes were at least partly responsible for the degradation of the mineral, potentially influencing the release of nutrients into a soluble form that, in a planted soil, could be used by plants.

A comparison of the taxonomic identity of the bacterial sequences found in the samples associated with weathered syenite or soil revealed some differences between these environments, with certain families only present in one or the other based on determined absences (Table 2). However, there were no differences at the taxonomic level of phylum for samples from both environments.

Some bacterial families were only present in samples from weathered syenite and absent from those from soil. However, because these families were only observed in three of the nine syenite samples, they may not be associated specifically with weathering.

There were a few more bacterial taxa absent from samples derived from syenite than from soil, but this could be due to there being more soil-derived than syenite-derived samples in the present study. The number of bacterial taxa per sample was statistically similar for both sample types (ANOVA, p = 0.92).

The statistical analysis of the microbial data as a whole, divided at a 97% similarity cutoff (species-equivalent), did not reveal any significant differences between weathered syenite and soil. However, some differences were apparent once the data were grouped into phyla.

The following bacterial phyla were detected in all samples: Acidobacteria, Actinobacteria, Armatimonas, Bacteroidetes, Chloroflexi, Cyanobacteria, Deinococci, Firmicutes, Gemmatimonadetes, Nitrospirae, Planctomyces, Proteobacteria (Alpha, Beta, Delta, and Gamma), and Verrucomicrobia. The order Actinomycetales, from the phylum Actinobacteria, was also included in the analysis due to the reported importance of actinomycetes – a general term for members of Actinomycetales – in feldspar weathering (Abdulla, 2009).

The statistical comparison of the relative abundance values of the bacterial communities in soil and syenite revealed significant statistical differences in Actinobacteria, Chloroflexi, and Deltaproteobacteria, as well as in the order Actinomycetales (Table 3). To better illustrate these differences, soil-derived samples were subdivided into those from rock-dominated soils and from cultivated soils (Figure 4 A–E).

When samples were grouped according to type (Figure 5), the relative abundance data showed the statistically significant preponderance of Actinobacteria and Actinomycetales within rock-dominated soils. Actinobacteria are widely found in soil samples worldwide (Fierer & Jackson, 2006) and typically constitute a major proportion of the soil

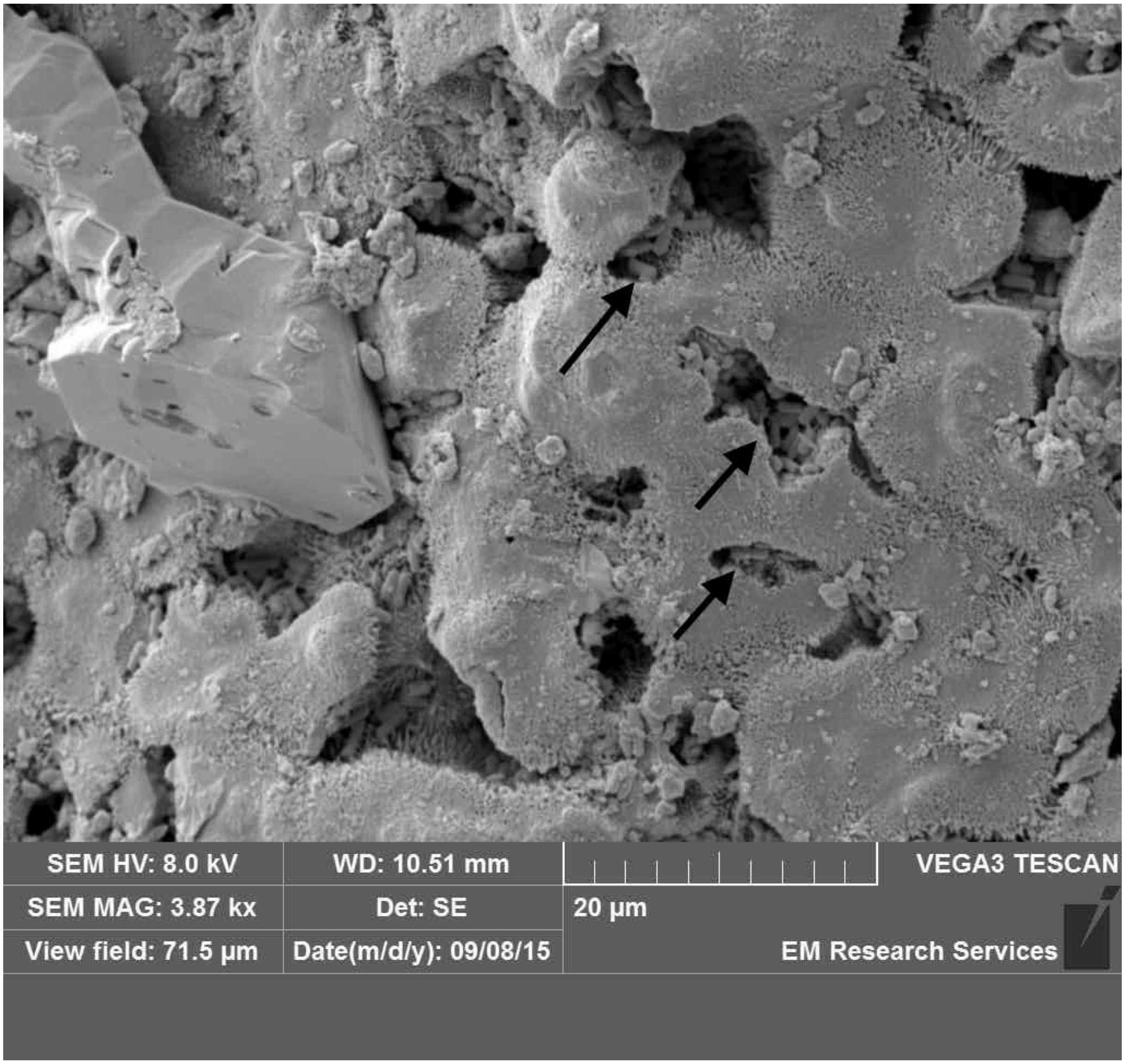


Figure 3. Examples of corroded feldspar in the different syenite sites with bacteria in cavities (indicated by arrows), observed through scanning electron microscopy.

microbial community regardless of soil type or climate (McCann et al., 2016). These organisms play a major role in the cycling of organic compounds, namely, organic matter decomposition and humus formation, which would explain why they were more abundant in soil than in syenite. However, some Actinobacteria, particularly Actinomycetales, form branching filaments, enabling them to reach nutrients in the soil. Moreover, bioactive metabolites are produced by many actinobacterial taxa, which can have antibacterial, antifungal, and antiviral properties, increasing disease resistance in plants and animals inhabiting the soil (De Silva et al., 2013). It is important to note that these taxa are disproportionately more abundant in soils that are partially formed from weathering of syenite, which suggests that they play a role in pedogenic processes.

Table 2. Absences of bacterial families in the evaluated soil and weathered syenite.

Bacteria absent from soil	Bacteria absent from weathered syenite	
Acidobacteria; GAL08	Acidobacteria; AT-s54	Firmicutes; Bacilli; Lactobacillales; Streptococcaceae
Acidobacteria; Holophagae; Holophagales; Holophagaceae, *1	Acidobacteria; BPC102; B110	Firmicutes; Clostridia; Clostridiales; [Tissierellaceae]
Acidobacteria; PAUC37f, *3	Acidobacteria; OS-K	Planctomycetes; Phycisphaerae; mle1-8
Acidobacteria; Solibacteres; Solibacterales; AKIW659, *3	Actinobacteria; Acidimicrobiia; Acidimicrobiales; Iamiaceae	Planctomycetes; Phycisphaerae; MSBL9
Actinobacteria; Acidimicrobiia; Acidimicrobiales; Microthrixaceae, *1	Actinobacteria; Actinobacteria; Actinomycetales; Actinopolysporaceae	Planctomycetes; Phycisphaerae; S-70
Actinobacteria; Actinobacteria; Actinomycetales; Dietziaceae, *1	Actinobacteria; Actinobacteria; Actinomycetales; Glycomycetaceae	Planctomycetes; Planctomycetia; B97
Bacteroidetes; [Rhodothermi]; [Rhodothermales]; Rhodothermaceae, *2	Actinobacteria; Actinobacteria; Bifidobacteriales	Proteobacteria; Alphaproteobacteria; Rickettsiales; Rickettsiaceae
Chlorobi; c_BSV26; o_A89, *2	Actinobacteria; Nitriliruptoria; Euzebyales; Euzebyaceae	Proteobacteria; Alphaproteobacteria; Sphingomonadales
Chlorobi; Ignavibacteria; Ignavibacteriales, *1	Chloroflexi; Chloroflexi; Chloroflexales; FFCH7168	Proteobacteria; Betaproteobacteria; Gallionellales; Gallionellaceae
Chloroflexi; Anaerolineae; pLW-97, *1	Chloroflexi; Chloroflexi; Chloroflexales; Oscillochloridaceae	Proteobacteria; Deltaproteobacteria; MBNT15
Chloroflexi; P2-11E, *1	Chloroflexi; Dehalococcoidetes; Dehalococcoidales	Proteobacteria; Deltaproteobacteria; NB1-j; MND4
Elusimicrobia; Elusimicrobia; MVP-88, *1	Chloroflexi; Ktedonobacteria; TK10	Proteobacteria; Gammaproteobacteria; Chromatiales
Firmicutes; Clostridia; Clostridiales; Dehalobacteriaceae, *1	Chloroflexi; SAR202	Proteobacteria; TA18; PHOS-HD29
Gemmatimonadetes; Gemmatimonadetes; Gemmatimonadales; Gemmatimonadaceae, *1	Chloroflexi; Thermomicrobia; Sphaerobacterales	Spirochaetes; [Leptospirae]; [Leptospirales]; Sediment-4; SJA-88
Proteobacteria; Betaproteobacteria; Thiobacterales, *1	Cyanobacteria; 4C0d-2; SM1D11	Spirochaetes; Spirochaetes; Spirochaetales; Spirochaetaceae
Proteobacteria; Deltaproteobacteria; DTB120, *1	Elusimicrobia; Elusimicrobia; Iib	Synergistetes; Synergistia; Synergistales; Dethiosulfovibrionaceae
Proteobacteria; Gammaproteobacteria; Alteromonadales; 211ds20, *1	Elusimicrobia; OP2	Tenericutes; Mollicutes; RF39
Proteobacteria; Gammaproteobacteria; Methylococcales; Crenotrichaceae, *1	Firmicutes; Bacilli; Bacillales; Sporolactobacillaceae	
Proteobacteria; Gammaproteobacteria; Methylococcales; Methylococcaceae, *1	Firmicutes; Bacilli; Lactobacillales; Lactobacillaceae	
Proteobacteria; TA18, *1		

*Number of syenite samples, where present.

Most of the Deltaproteobacteria present in the samples belonged to the order Myxococcales, several of whose members prefer warmer environments and have the ability to form spores, often being found in hot climates, such as the Cerrado (Garcia & Müller, 2014). Many bacteria in this order produce powerful hydrolytic enzymes that have the ability to degrade insoluble compounds and could potentially contribute to mineral weathering, justifying their high abundance in samples from weathered syenite (Garcia & Müller, 2014). Chloroflexi are also often associated with warm environments and have been abundantly found in hot springs containing sediments with high mineral concentrations, also being related to K-feldspars (Vick et al., 2010; Hanada, 2014); their association with extreme environments could explain their strong presence in the syenite samples.

The cluster analysis and principal coordinates analysis by the Jaccard index confirmed the observations made using the relative abundance data. Actinobacteria show clear associations (Figure 6 A and B). Samples from rock-dominated soils form a discrete cluster (NB1-j found in sample rdb1 is from a site that differs, having been treated with a chemical fertilizer). All cultivated soils except one with grass (sg2) and one with bananas (sb2) form a single domain within the dendrogram; sample sg2 differs in that it was derived from a saprolite, 2 m below the crop root zone from which the first grass sample (sg1) was collected. Sample sb2 was taken from a location with very thin soils developed on syenite, containing blocks of the unweathered rock. In both of these cases, samples were spatially close to the parent rock on which the soil was developed. The weathered syenite samples are distributed across the dendrogram. As would be expected, similar relationships are shown by the principle component plot (Figure 6 B). In contrast to that for Actinobacteria, the cluster diagrams for Chloroflexi and Deltaproteobacteria show no similar systematic differences between samples of similar origin (Figure 6 C and D). This may reflect the sensitivity of Actinobacteria to the early stages of weathering, besides a lack of sensitivity of Chloroflexi and Deltaproteobacteria to the same process.

As proposed, the bacteria that could be active in weathering were identified in the evaluated samples. The dominant phyla in samples from weathered syenite, with no soil development (but with plant roots in some cases), and from established soils were: Actinobacteria, Chloroflexi, and Deltaproteobacteria; the order that stood out was Actinomycetales. In samples from rock-dominated soils, Actinobacteria, and Actinomycetales were most abundant, compared with the other bacterial taxa; in this case, since soil development had started, plant growth (bananas, trees, and shrubs) was supported, occurring on boulders and within fractures in a rock mass.

The obtained results suggest focusing future studies on Actinobacteria and, within this phylum, on Actinomycetales, aiming to understand the role of mineral surfaces and associated bacterial communities in the release of K from agrominerals based on syenite or other feldspar-bearing rocks. This is in alignment with the findings of Abdulla (2009), who associated feldspar weathering in Egyptian soils with the presence of Actinomycetales.

It should be noted that the chemical treatment of syenite has been carried out to accelerate the availability of nutrients (Ciceri et al., 2017a) and is appropriate where rapid release is required. However, the results of the present study show that natural microbial activity, especially involving Actinobacteria, appears to play a role in rock weathering, although it is still necessary to determine how this affects the rate of release of nutrients from syenite.

Table 3. Bacterial taxa with significant p-values(1), obtained from the comparison between the relative fractional abundances of bacterial taxa in all combined soil samples and syenite sample sequence libraries using the one-way analysis of variance.

Group	Relative abundance		p-value(1)
	Soil	Syenite	
Actinobacteria	0.37	0.15	0.0022
Actinomycetales	0.22	0.065	0.0020
Chloroflexi	0.094	0.15	0.038
Deltaproteobacteria	0.012	0.029	0.016

(1)At a 95% confidence level

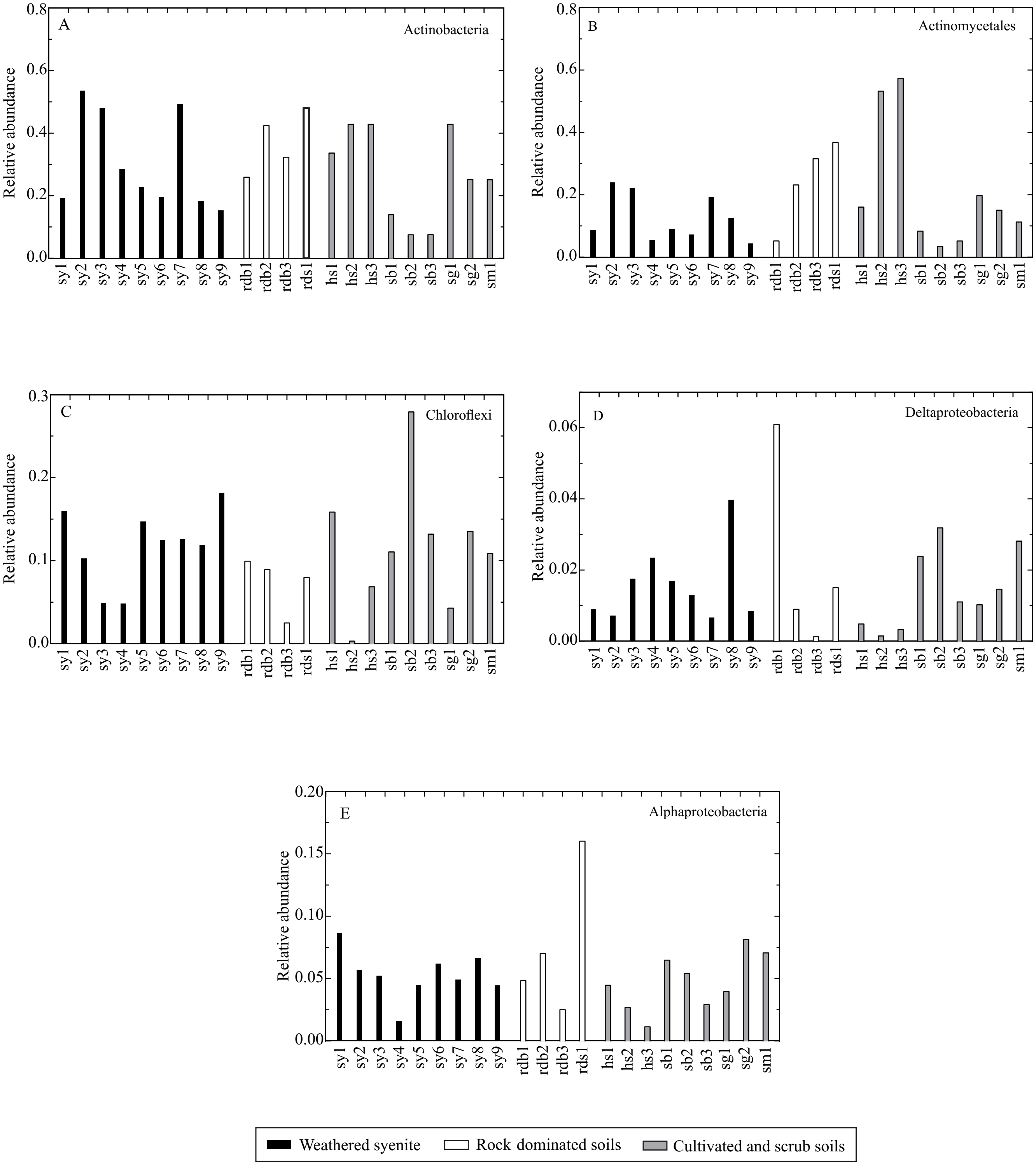


Figure 4. Relative abundances of: Actinobacteria (A), Actinomycetales (B), Chloroflexi (C), Deltaproteobacteria (D), and Alphaproteobacteria (E) in mineral samples from weathered syenite, rock-dominated soils on syenite, and cultivated and scrub soils. sy1–sy9, syenite without plant activity; rdb1–rdb3, rock-dominated soil with banana; sb1–sb3, soil cultivated with banana; sg1–sg2, soil cultivated with grass; hs1–hs3, uncultivated hill-side with scrub; and rds, rock-dominated soil with scrub, developed on syenite.

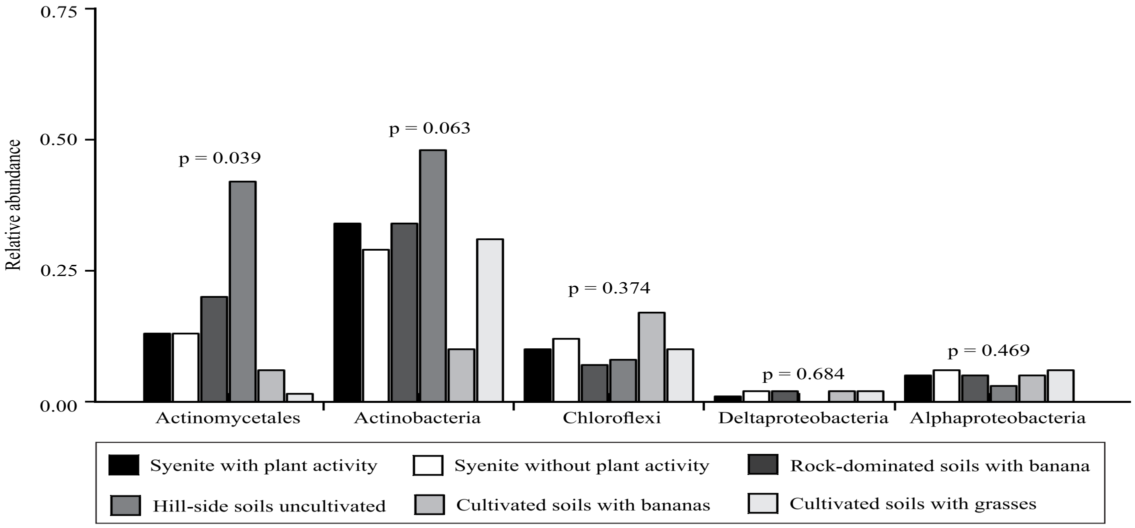


Figure 5. Summary of the relative abundance data of samples from different origins.

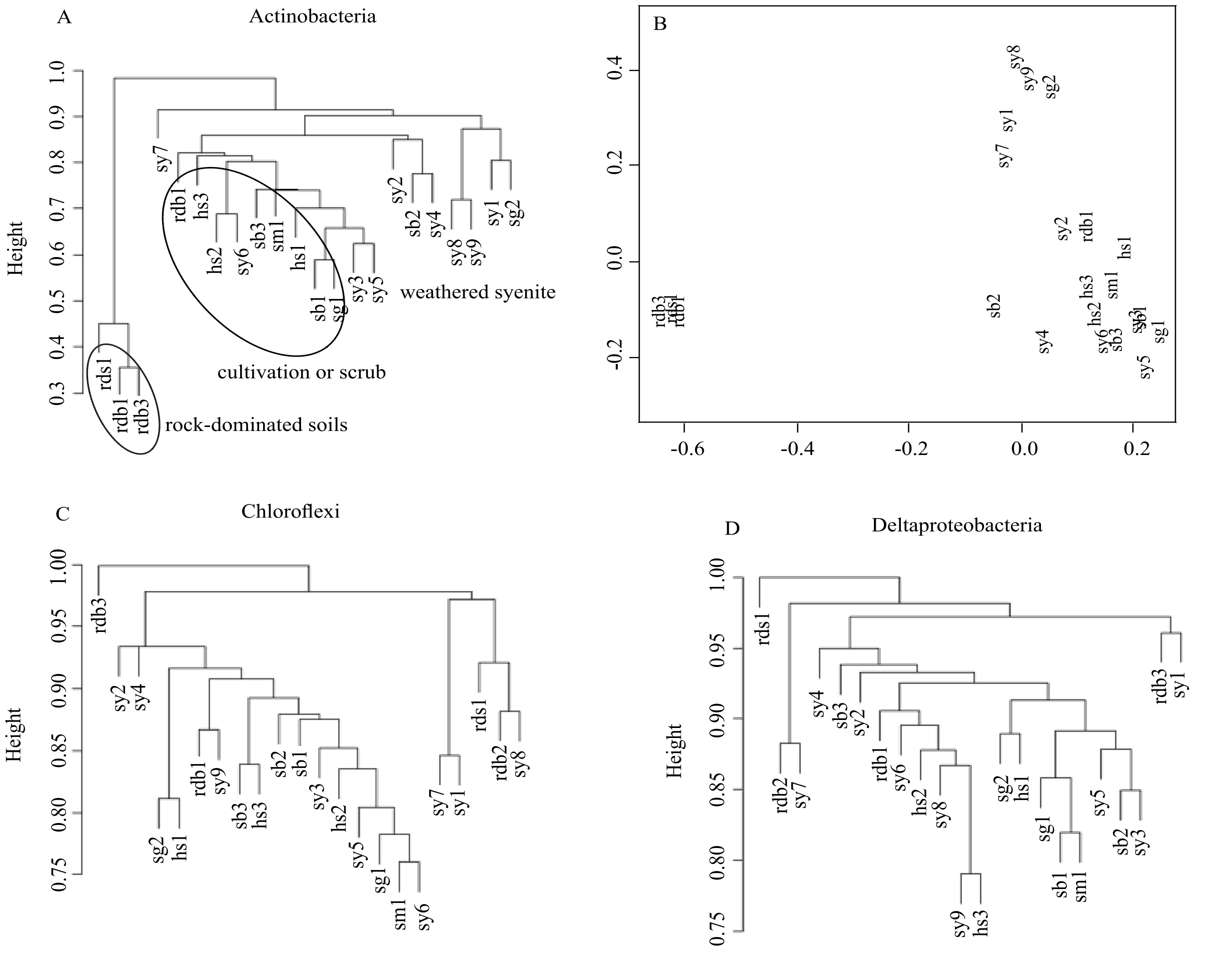


Figure 6. Cluster diagram and principle coordinate plot for Actinobacteria (A and B) and cluster diagrams for Chloroflexi (C) and Deltaproteobacteria (D). sy1–sy9, syenite without plant activity; rdb1–rdb3, rock-dominated soil with banana; sb1–sb3, soil cultivated with banana; sg1–sg2, soil cultivated with grass; hs1–hs3, uncultivated hill-side with scrub; and rds, rock-dominated soil with scrub, developed on syenite.

Conclusions

1. The bacterial community associated with weathered syenite and with rock-dominated and established soils shows similarities in diversity, covering the same broad taxonomic groups.
2. When relative abundances are compared, Actinobacteria and, within this phylum, Actinomycetales are proportionately dominant, either in rock fragments or mass, in soils from locations where syenite is predominant.
3. The availability of potassium derived from feldspar in syenite may be enhanced by the presence of specific bacterial communities.

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