We would like to thank Reviewer #2 for her/his time, effort, and valuable comments. We have prepared a response taking into account all the points raised, as described below. We show the reviewer's comments in bold, while our responses are formatted as standard text. Line numbers refer to the original manuscript.

Krauze at al. investigated the interplay between the microbial community and soil formation after glacier retreat at Maritime Antarctica (here: King George Island). This is a fascinating topic which fits very well to the scope of Biogeosciences. The paper is well written and the quality of English language is high (only spelling error I found is in line 364, ice fee instead of ice free).

Thank you, we corrected the spelling error.

All in all the manuscript is a good and inspiring read. Unfortunately some doubts on the experimental design and the drawn conclusions of the study arise while reading and cloud the pleasure remarkably. The absence of hypotheses is puzzling, especially since the chosen ecological model of very young soils, only a few decades after glacier retreat, should have led to several hypotheses around the topic of temporal dynamics of C and N accumulation and the involved microbial functional traits, thresholds or tipping points in the system regarding soil development etc. A study only aspiring an objective of "identifying processes" but not having any assumptions on which processes it should look, is probably not meeting contemporary standards of good scientific communication anymore.

Thanks for your comment. In order to clarify the objectives of the study, we have reformulated the corresponding part in the introduction. In addition, we changed certain passages in the text that refer to "processes".

"We hypothesize that prokaryotic microorganisms initiate/drive soil properties changes (e.g. soil organic carbon accumulation, weathering) within decades after deglaciation. To test our hypothesis, we related the investigated soil properties to microbial community structure and microbial abundances in the recently (< 50 years) deglaciated foreland and compared it with an older soil located behind a lateral moraine (> 70 years) of the Ecology Glacier." (L. 78ff)

We updated the Conclusions section of our manuscript addressing the hypothesis, and a potential setup and study design to further study the investigated processes.

"However, we conclude that prokaryotic microorganisms initiate measurable changes of soil properties such as pH at a very early stage (within decades) before the soil surface is colonized by pioneer plants or soil horizons other than C horizons are detectable, and thereby promote weathering processes." (L. 426ff)

"To further verify our conclusions and illuminate the microbial processes driving soil formation, in future studies multiple comparable setups (freshly deglaciated material vs. older, more matured soil close to the foreland) could be studied and include metagenomic and metatranscriptomic analyses." (L. 428)

Further, the experimental design is challenged by a very low repetition number (only one field repetition per age class). In Antarctica, harsh conditions melt down iniotially planned sampling schemes for sure, but only 4 soils in single replication in close vicinity to a research station, at least raises the question, why there was not a valid experimental design possible.

In this study, we do not present four age classes represented by one profile each. By sampling three profiles in close proximity in the recently deglaciated area we tried to capture the potential heterogeneity of these soils, and compare these younger soils with an older soil just behind the lateral moraine.

To clarify this, we rephrased a sentence in the Introduction section:

"To capture the heterogeneity of the soil landscape, three soils in close proximity (maximum distance of 150 m) formed on the same substrate and in a similar topographic position but with differing vegetation cover were sampled. These soils, which represent a recently deglaciated area, were compared with an older soil that had formed on a similar substrate that had been deglaciated for at least 70 years." (L. 81ff)

Additionally, we rephrased a sentence in the Material and Methods section:

"The profiles KGI A, B, and C are located within 150 m distance on the same substrate deglaciated since 1979." (L. 117)

In addition, by changing the date we corrected a related mistake in the caption of Fig. 1:

"A, B, and C are located in the glacier foreland deglaciated since 1979."

The authors additionally should make the age determination of their sites much more transparent as well as the data of vegetation on the sites should be reported in full detail. For instance, the authors discuss the role of vegetation for the microbial community in their manuscript, but write simply "mosses, 5% coverage" in the table. This is an almost useless information, as some Antarctic moss species are nourished by aeolian input without interfering much with the soil, while other moss species deeply penetrate into soil with their rhizoids.

Many thanks for this comment. Additional ^{14}C datings were done.
To determine the age of the soil organic carbon, two samples with the highest SOC contents were chosen for AMS ^{14}C dating (KGI C 0 – 1 cm in the glacier foreland and KGI D 0 - 3 cm from behind the lateral moraine). KGI C 0 – 1 cm was the only sample from the foreland with detectable SOC. The samples were pre-treated with the acid/alkali/acid method and the alkali soluble organics (also known as the humin fraction, i.e. the oldest portion of soil organic matter) and were measured by Beta Analytic, Inc. in Florida, USA.

KGI C (Beta – 570459); IRMS $\delta^{13}C$: -27.9 ‰
(92.2%) 1992 - 1995 cal AD (-43 - -46 cal BP)
(3.2%) 1957 cal AD (-8 cal BP)

KGI D (Beta – 570458) IRMS $\delta^{13}C$: -26.1 ‰
(95.4%) 1954 - 1956 cal AD (-5 - -7 cal BP)

The results show with a probability of 92.2% that the humin fraction of soil organic matter in profile KGI C was formed after the melting of the glacier in 1979, whereas the humin fraction of the upper 3 cm in profile KGI D (with a probability of 95.4%) is dated 1954 - 1956 cal AD.

The SOC in the lower part of the KGI D may even be older. Therefore, the SOC at KGI D was already formed at a time when the present foreland of the Ecology Glacier and with this the sites of KGI A, B, C were still under the glacier.

We included these results in a table in the supplementary (Tab. S1) and integrated the new information on the potential age of the sites in 3.1 Soil classification and soil properties in the Results section:

"^{14}C dating showed that the humin fraction of soil organic matter in profile KGI C was formed after the melting of the glacier in 1979 (92.2% 1992 - 1995 cal AD (-43 - -46 cal BP); 3.2% 1957 cal AD (-8 cal BP)), whereas the humin fraction of the upper 3 cm in profile KGI D is much younger (95.4% 1954 - 1956 cal AD (-5 - -7 cal BP)) (Tab. S1)." (L. 187)

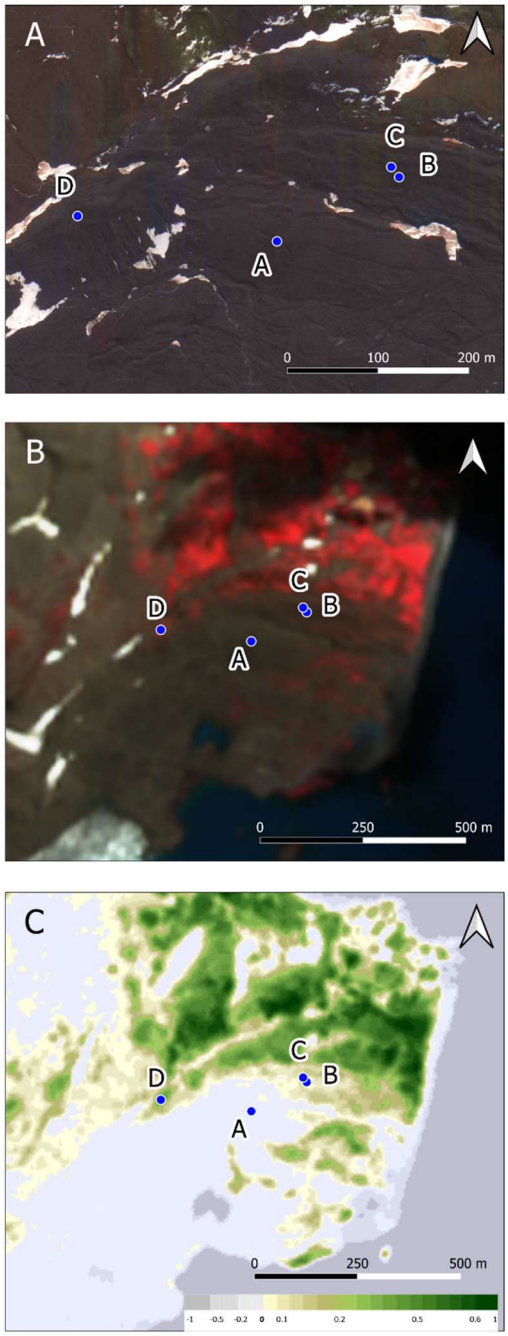
With this first rough listing of plants and the degree of coverage we wanted to test whether different degrees of coverage are reflected in changes of soil properties. We discussed the influence of increasing/decreasing vegetation coverage on microbial communities in lines 304ff. Much to our regret, we are not able give a more detailed description of the vegetation, because we had no botanist in our group. We are aware that a detailed description of the vegetation would help to better understand the mechanisms of soil processes associated with specific plants (e.g. different moss species). However, this was not the aim of this study and we do not discuss this issue. To answer this question would have required a different sampling approach (1 cm depth increments in the upper 10 cm), which would have been plant species specific. This can be a next step and should be part of the goals of our next field trip. Again, many thanks for this comment.

Additionally, it is highly unlikely, that only one species of lichens occurs, which suggests erratic identification. The age dating of the sites is the crucial issue for the study. The appearance of both higher plants native to Maritime Antarctica already on the second youngest soils is directly leading to the question if the dating was done correctly, since this appearance is either limited to highly developed soils or ornithogenic soils. As the soil parameters suggest a young soil, not having enough N for maintaining populations of higher plants on the long run, it is very likely, that these encounters are due to the frequently seen bird dropping effect (excrements containing seed of Deschampsia or Colobanthus stage the appearance of these plants for a season or two, until the N from the excrement is used up). A coverage of 10% of higher plants on such young soils suggest a high frequency of bird visits, which was excluded by the authors, as this would largely question the results of a real soil development situation of the microbial community, as higher plants alien to the respective community would have been introduced.

Bird droppings cannot be excluded, but we suspect the influence to be small: The P contents in the profiles KGI A, B, and C are low and very similar for all depths. A high frequence of bird visits including the bird droppings, as you suggest, would also lead to an increase of the P content at least in the upper cm of these soils. We included a table with RFA data to the supplement (Tab. S2). Please also note, *Deschampsia antarctica* and *Colobanthus quitensis* use mycorrhiozal fungi (ascomycete fungi), to "...facilitate the acquistion of organic nitrogen as early protein breakdown products" (Hill et al. 2019). This means that they do not need N from bird droppings to colonize new areas. Thus, the pedogenic data (particularly pH and SOC) reflect a "real soil development" as we already have discussed in the manuscript.

With the given data all this stays mere speculation, of course. To solve this issue, at least a much better map of the sites, ideally a satellite map showing the features of the sites as well as their surroundings, along with a concise description of the found vegetation should be offered by the authors, please.

We added a new figure (Figure 2) containing three satellite maps: One with very high resolution, one with false colours to visualize the vegetation and one with the ndvi to indicate the presence of chlorophyll. All remaining figures move one number further with their numbering.



We added the caption of Figure 2:

"(A) High resolution satellite image from 06.11.2016 (Map data © 2016 Google). (B) False colour Sentinel-2 image from 19.01.2020 (red = band 8, green = band 4, blue = band 3) for enhanced visualisation of the vegetation. (C) Normalized Difference Vegetation Index (NDVI),

dimensionless with positive values indicating healthy vegetation and negative values indicating the presence of open water bodies. Contains modified Copernicus data." (L. 725 - 728)

Additionally, we added some information in the Materials and Methods section:

"Figure 2B, which shows increasing plant-coverage with an increasing red coloration, shows no vegetation at KGI A, little vegetation at KGI B and C and a higher vegetation coverage at KGI D. Conversely, image 2C shows highest values of chlorophyll at KGI D, substantially less chlorophyll at KGI B and C and no chlorophyll at KGI A."

Regarding the description of the vegetation; please see our answer to your comment above.

If possible some proof of the assumed age, for instance by a combination by 14C and 15N analyses of the soils, showing the age of organic carbon and the source of N (fixed from air or carried in by birds?) would help explain this very rare combination of observed features reported here. These aspects should be discussed in detail, too.

Thank you for the suggestions.

Please note our answer to the first comments regarding age determination.

As explained in the answer to an above comment, due to similar P contents at all depths of profiles A, B, C it is assumed that bird droppings are not of major importance at these sites and therefore no ^{15}N analyses were carried out.

Regarding the DNA-based identification of bacteria it stays largely unclear to the reader where the usually pretty high number of unidentified OTUs (so to say the bacteria not yet known to science) in soils of Maritime Antarctica has gone. The abundance graph reads as if the authors could attribute every single OTU to a phylum.

Originally, completely unassigned OTUs have been identified, but were very low in their abundance and summarized with other low abundant phyla under the term "Others" in Figure 3.

As suggested by Reviewer 1, the sequencing data was reanalysed by using the amplicon sequence variant (ASV) approach. Similar to the OTU analysis, this approach resulted in low abundances of completely unassigned sequences (minimum: 0.01 % in KGI A 10 – 20 cm; maximum: 0.28% in KGI A 0 – 1 cm). Low abundances of unassigned reads are common in recent literature (0.28 % of the total data set of Meier et al., 2019; 1.1 % of the total data set in Kim et al., 2019). The very low abundance of unassigned sequences does not mean that an identification to genus/species level for the remaining sequences was possible, though. Many of the OTUs/ASVs shown in Fig. 5, which represent the most abundant reads in the data set, were just classified to the order or family level.

Since both reviews wondered about this very topic, two tables were added to the supplement as suggested by Reviewer 1: Table S4 shows the "fate" of the raw data, and Table S5 shows the resulting ASV table. This time, both tables also include the positive as well as the negative control. We hope the increased transparency is helpful for the evaluation of our sequencing data.

In the discussion, as already indicated by the missing hypotheses, the reader misses a true discussion of the "identification of processes" promised in the objectives. Not even the "influences of microorganisms on soil formation" promised by the title were discussed in detail, what anyway would have been impossible by a study leaving the fungi completely aside.

Thank you. Please note our previous comment on the hypothesis.

To account for the missing fungi, we propose to change the title to "Influence of prokaryotic microorganisms on initial soil formation along a glacier forefield on King George Island, maritime Antarctica".

After what is discussed in the paper, this study is more investigating the influence of vegetation on the bacterial community of young soils in Maritime Antarctica. A big step towards the originally intended process elucidation of soil formation would be for instance a detailed discussion on the functional traits and abundances of bacteria involved in e.g. C and N accumulation or weathering processes. In the current form, the study is a family list of bacteria of four Antarctic soils, trying to mimic process identification by naming rather weak coincidences. There is surely more to it.

Thank you for your suggestions.

Since we have not included metagenomics or metatranscriptomics in our study, only limited conclusions can be drawn about the occurrence or frequency of different functional characteristics. On the other hand, we discuss the functions and potential effects on the soil environment based on the taxonomy of certain observed taxa, e.g. microorganisms potentially linked to weathering processes (L. 394 – 397) or the degradation of organic compounds (L. 265 – 269 ; L. 410 – 414). However, we agree that such aspects can be discussed in more detail, especially after reanalysis of our sequencing data using the amplicon sequence variant approach. Therefore, we broadened the discussion and included more information on the potential involvement of different prokaryotic groups in certain aspects of soil formation and rephrased the general statement on the observed composition of the community on a phylum level:

"In accordance with observations in other Antarctic habitats (e.g. Ganzert et al., 2011, Yan et al., 2017; Meier et al, 2019), the investigated soils were characterized by highly diverse microbial communities including Acidobacteriota, Bacteroidota, Verrucomicrobiota and especially high abundances of Actinobacteriota and Proteobacteria, which are known to thrive in recently deglaciated soils and facilitate a multitude of different phototrophic, photoheterotrophic and chemolithotrophic processes (Rime et al., 2016; Wei et al., 2016; Garrido-Benavent et al., 2020).

Additionally, we modified the part discussing the missing indication of "obvious" prokaryotic organisms associated with phototrophic carbon fixation:

"However, our dataset showed only low abundances of prokaryotic organisms most probably associated with phototrophic carbon fixation, such as the Cyanobacteria-related Tychonema. Low abundances of Cyanobacteria in recently deglaciated areas are not an uncommon observation in Antarctic soil environments (Ji et al., 2016; Garrido-Benavent et al., 2020).In addition to the low abundances of Cyanobacteria, other bacterial groups might be involved in

248 phototrophic carbon fixation, such as Chloroflexi (Lacap et al., 2011). Moreover, based on the
249 on the amount of chloroplast-related sequences in our dataset, this process is at least partly
250 facilitated by eukaryotic organisms such as algae in the early stage of soil development." (L.
251 288ff)

252

253 We also added additional information on the influence of microorganisms on weathering
254 processes:

255 "By performing enzymatically catalysed reactions, processes reducing the pH and the
256 production of complexing agents (Mavris et al., 2010; Styriakova et al., 2012; Ahmed and
257 Holmström, 2015) microorganisms are able to substantially promote weathering processes
258 (Schulz et al., 2013)." (L. 391)

259

260 As mentioned above, microorganisms can facilitate processes that lower the local soil pH,
261 thereby promoting weathering processes. In the absence of vegetation, we observed a
262 decreased soil pH in the upper centimetres of the KGI A soil profile, which can therefore be
263 linked to microbial metabolism (L. 412 – 414). This pH reduction pH should increase as soon
264 as the soils are colonized by plants, since microorganisms are able to degrade organic
265 compounds and organic acids could be released into the surrounding soil (L. 267 – 269). This
266 effect can be seen in the pH reduction in relation to increasing plant coverage from KGI A (pH
267 6.8), KGI B (pH 6.6) to KGI C with a pH of 5.4 in within the first centimetre.

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Table S1: Radiocarbon dating results obtained on the humin fraction of soil organic matter from two sites at the Ecology Glacier, King George Island.

Profile	Depth [cm]	Horizon	Material	pMC [%]	δ13C (‰)	cal BP (1σ)	cal CE (1σ)	Lab-Nr.
KGI C	0 – 1		soil organic matter, humin fraction (alkali soluble organics)	112.55 ± 0.42	-26.1	-44 to -45 cal BP	1993 - 1994	Beta-570459
KGI D	0 - 3	Ah	soil organic matter, humin fraction (alkali soluble organics)	100.62 ± 0.38	-27.9	-5 to -6 cal BP	1954 - 1955	Beta-570458

Table S2: Major elements by XRF of four soil profiles from King Georges Island, Antarctica. All data given in weight percent. LOI (loss on ignition) determined at 1000°C. For location of the profiles, see table 1.

Profile	Depth	SiO_2	Al_2O_3	Fe_2O_3	MnO	MgO	CaO	Na_2O	K_2O	TiO_2	P_2O_5	LOI	Sum
	[cm]	%											
KGI A													
	0-1	49,43	0,93	19,39	8,53	0,20	3,38	5,85	3,13	1,16	0,24	7,46	99,85
	1-10	48,98	0,94	19,30	8,48	0,20	3,15	5,72	3,00	1,18	0,25	8,39	99,73
	10-20	49,25	0,91	19,26	8,26	0,19	3,03	5,95	3,04	1,19	0,25	8,30	99,78
	20-40	49,73	0,93	19,12	8,54	0,20	3,11	6,26	3,41	1,16	0,24	7,12	99,96
KGI B													
	0-1	49,80	0,95	18,77	8,72	0,21	3,26	6,31	3,74	1,14	0,27	6,28	99,59
	1-10	49,72	0,94	18,95	8,71	0,21	3,29	6,29	3,65	1,12	0,26	6,87	100,14
	10-20	49,92	0,93	18,85	8,69	0,21	3,18	6,34	3,76	1,15	0,27	6,36	99,81
	20-80	49,66	0,94	18,83	8,73	0,20	3,25	6,51	3,71	1,14	0,26	6,43	99,83
KGI C													
	0-1	48,43	0,85	18,65	8,30	0,20	3,47	6,23	3,62	1,05	0,27	8,73	99,94
	1-10	49,45	0,94	18,91	8,76	0,20	3,22	6,24	3,63	1,09	0,28	6,88	99,75
	10-20	49,66	0,95	18,91	8,89	0,21	3,09	6,29	3,69	1,13	0,29	6,68	99,94
	20-40	49,73	0,94	18,90	8,67	0,19	3,10	6,30	3,73	1,17	0,29	6,35	99,52
KGI D	0-3	44,39	0,79	17,47	7,75	0,17	3,40	5,88	2,98	1,12	1,04	14,6	99,76
	3-15	48,84	0,82	19,22	8,06	0,18	3,54	6,30	3,53	1,19	0,35	7,84	100,01
	15-27	49,85	0,80	19,28	7,81	0,19	3,50	6,80	3,79	1,15	0,21	6,54	100,05
	27-60	49,24	0,82	19,30	8,04	0,20	3,56	7,01	3,71	1,08	0,19	6,49	99,80

Table S4: Number of sequencing reads after each processing step.

sample	input	filtered	denoised	merged	Non-chimera	0.01% cutoff
	number of reads					
KGI_A_0_1_a	823555	760184	744842	728869	722825	706168
KGI_A_0_1_b	416652	386897	378089	368092	365389	359124
KGI_A_0_1_c	923881	848435	824280	799372	786254	772324
KGI_A_1_10_a	473836	436670	427179	416676	413400	410050
KGI_A_1_10_b	234950	218204	212241	204825	203788	201502
KGI_A_1_10_c	352840	330275	323230	316343	314148	311452
KGI_A_10-20_a	36923	33865	29718	26130	25958	25922
KGI_A_10-20_b	18966	17275	14209	12268	12259	12252
KGI_A_10-20_c	25875	23729	19871	17313	17308	17300
KGI_A_20_40_a	905510	839764	828694	814373	808267	790148
KGI_A_20_40_b	846168	790425	779458	764252	758482	737591

KGI_A_20_40_c	893543	830439	821643	808578	801514	778446
KGI_B_0_1_a	802491	738909	726606	711994	705038	683957
KGI_B_0_1_b	767042	707072	685728	660207	650385	634947
KGI_B_0_1_c	776140	717207	691876	662511	644483	630913
KGI_B_1-10_a	870220	801229	775510	742168	726536	700009
KGI_B_1-10_b	763113	708362	698110	683584	679585	655095
KGI_B_1-10_c	984339	904070	867753	821445	790478	763807
KGI_B_10_20_a	902645	835484	829409	818332	809608	796113
KGI_B_10_20_b	50853	47043	41987	37904	37729	37613
KGI_B_10_20_c	45144	41598	36756	32746	32618	32557
KGI_B_20_80_a	797077	739614	734477	727607	713996	706767
KGI_B_20_80_b	666167	617867	613646	605338	594001	587915
KGI_B_20_80_c	59859	55236	50726	47120	46730	46649
KGI_C_0_1_a	748549	692351	673800	648601	635472	605915
KGI_C_0_1_b	896152	828214	784842	728938	687678	661043
KGI_C_0_1_c	780292	724237	701902	672607	650189	619970
KGI_C_1_10_a	1072129	979738	941569	893583	866371	830430
KGI_C_1_10_b	796453	734715	714128	686413	675197	651021
KGI_C_1_10_c	945868	879402	852158	818052	799307	765149
KGI_C_10_20_a	914463	847130	837834	821943	814309	788037
KGI_C_10_20_b	724047	663724	657595	646501	642849	625122
KGI_C_10_20_c	379777	348578	342785	334296	331763	325740
KGI_C_20_40_a	805325	743983	737314	727505	720592	705527
KGI_C_20_40_b	883724	818626	808175	789997	782377	762057
KGI_C_20_40_c	651443	603352	595920	583664	578353	564023
KGI_D_0_3_a	779880	715854	698512	675201	664504	626027
KGI_D_0_3_b	787246	723529	685098	643359	617163	586001
KGI_D_0_3_c	898392	826444	770393	701924	643856	619137
KGI_D_3_15_a	815335	754410	739659	718535	709893	677501
KGI_D_3_15_b	950935	871121	850341	820666	806893	766920
KGI_D_3_15_c	930601	858951	806053	732072	650658	627047
KGI_D_15_27_a	913147	851119	839448	822669	812036	784157
KGI_D_15_27_b	1074041	989909	980950	964946	953467	917368
KGI_D_15_27_c	869976	799507	791364	777160	770119	749250
KGI_D_27_60_a	740686	687100	681491	671687	666209	645648
KGI_D_27_60_b	768476	714698	707202	695134	689840	671215
KGI_D_27_60_c	852927	790621	782334	769492	763600	737767
Negative control	11045	9999	9955	9899	9899	9819
Positive control	651120	590140	589778	585268	585268	585250

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