Enzymatic biofilm detachment causes a loss of aggregate stability in a sandy soil.

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Final responses + marked-up version

(All named corrections were applied. Fundamental corrections are labeled with [number])

Dear Mr Redmile-Gordon,
first I would like to express my sincere thanks to you for reviewing, especially for your detailed and very helpful suggestions and your forbearance concerning grammatical errors.

Title

[1] Line 1: *Title should change, I suggest: 'Enzymatic biofilm digestion in soil aggregates facilitates the release of particulate organic matter (POM) by sonication'.*
We changed the title as suggested. Thank you very much.

General corrections

[2] Lines 181, 200, 263, 264, 265, 266, 270, 272, 273, 280, 339, 340, 343, 371, 379, 426 and elsewhere: *Renaming of SOC.*
As (1) C is the actual measure and (2) SOC involves DOC, which is rejected during POM extraction, POM and SOC are not suitable to term the C release from aggregates. Instead, "particulate organic carbon" (POC) will be used. This also includes organic molecules, already adsorbed on the HF after ultrasonic treatment. When describing the extracted material as a whole, POM will be used.
[We decided to use the termes LF-SOC and HF-SOC. For our motivation, see [2] in the discussion part.]

Lines 13, 14, 15, 26, 37, 39, 46, 49, 78, 79, 80, 83, 89, 92, 93, 96, 101, 105, 110, 112, 123, 138, 143, 144, 146, 147, 192, 210, 265, 280, 281, 283, 342, 343, 344, 406, 410, 413: *Diverse suggestions to improve orthography, grammar, lucidity and scientific notification.*
All proposals are included. Thanks a lot.

Abstract

Line 24: *delete 'which preserves aggregate structure'.*
"… which preserves aggregate structure, …" was removed, as additional influence on binding mechanisms such as surface charge of POM cannot be ruled out.

Line 30: *This is overly confident and not quite accurate. Is it not true that enzymatic digestion of EPS polymers may have increased the abundance of EPS fragments released upon sonication? Therefore, remove 'our results confirm, that EPS stabilises soil aggregates predominantly by a strong intra-aggregate fixation, and enzymatic biofilm digestion caused a shift of occluded particulate organic matter (POM) to more fragile binding patterns' and replace with 'our results suggest that EPS stabilises intra-aggregate particulate organic matter (POM) within soil aggregates'.*
The samples have a C_{mic} of 0.352 mg g^{-1} dry soil aggregates and a C_{org} of 8.7 mg g^{-1} dry soil. total POC release amounts to 1.8 mg g^{-1} dry soil for E0 and 1.98 mg g^{-1} dry soil for E4 – the difference (0.18 mg g^{-1} dry soil) is half the C_{mic}. Therefore it is (mathematically) possible, that the whole difference in POC release is caused by release of biofilm fragments. The real share is unknown, but the small share of released bacterial DNA as well as visibly increased dark POM release in E4 after sonication reinforce additional non-biofilm POM release. However, we choose the more careful statement as you suggested "our results suggest that EPS stabilises intra-aggregate particulate organic matter (POM) within soil aggregates" and will revisit this in the discussion part.

Introduction

Lines 61-63: *awkward sentence, please rephrase.*
Done: "In addition, carbonates and phosphates as well as microbial precipitates force up aggregation."

Line 82: *replace 'biofilm forming species and habitats:' with 'community composition and environmental cues:'*
Sounds much better. Thank you and done.

[3] Line 108: *Unsubstantiated statement which leaves the reader wondering 'why'. I suspect the authors are drawing on the rationale presented Redmile-Gordon et al. (2014) and suggest this is expanded upon for clarity and to help build justification. Suggest the authors replace 'That is mainly due to methodological reasons' with 'This is mainly due to methodological reasons. For example, Tang et al. (2011) found no link between bacterial EPS extracted using sulphuric acid and aggregate stability. Redmile Gordon et al (2014) subsequently found in a comparison study that the techniques previously used to measure extracellular polysaccharide in soil co-extracted large quantities of 'random' soil organic matter which confounded estimates of EPS production."*
I will add "Though Tang et al. (2011) showed a significant contribution of bacterial growth on aggregate stability, the observations could not definitely be attributed to soil microbial exopolysaccharide production. Redmile-Gordon et al. (2014) subsequently found that the techniques previously used to measure extracellular polysaccharide in soil co-extracted large quantities of 'random' soil organic matter which confounded estimates of EPS production."

Material and Methods

Lines 141-142: *This is not a method to estimate soil microbial biomass, this is respiration, correct accordingly.*
"To estimate the soil microbial biomass" refers to the whole paragraph. For clarification, the paragraph will be reshaped to "To estimate the soil microbial biomass, first 8 x 10 g of soil aggregates have been adjusted to 70 vol% soil water content and incubated for 70 hours

at 20°C in the dark to attain basal respiration. Then, based on DIN EN ISO 14240-2 ..."

Lines 163-172: This section takes some time to understand. Insert "sufficient enzymes were provided to digest the EPS content expected in five scenarios (E0 to E4)"
Line 165: "each" added before "with highest need of enzymatic units for the total biofilm detachment".
Line: 172: "five scenarios were design" is replaced with "sufficient enzymes were provided to digest the EPS content expected in five scenarios:"

Lines 181/193: *… e.g. Cerli et al 2012 do not claim this method quantifies aggregate stability*
Cerli et al. (2012) was replaced by Golchin et al. (1994) as prime reference. Cerli et al. (2012) will appear in the discussion about light fraction release as indicator of aggregate stability.

Line 190: *Why for 30 min? To allow NaPT diffusion?*
"... to allow SPT diffusion into the aggregates" will be added.

Line 195: *50 J ml^{-1} given over what time period?*
Time periods depend on the weight of sample+SPT solution and fluctuate around 1 min 15 sec.

Line 217: *What volume of wash was used as an equivalent for the mass of soil stipulated in the FastDNATM spin kit soil manual? (Can it really be used to extract DNA from a dilute wash and compare with soil?)*
FastDNA™ SPIN KIT (used for liquid samples of 200 µl and pure cultures) and FastDNA TM SPIN Kit for Soil (normally used with "Up to 500 mg of soil sample" and for complicated samples) only differ
(1) in the first buffer,
(2) the point of time for the application of protein precipitation solution (PPS) and
(3) in the last incubation procedure (incubation in DES solution for 5 minutes in a heat block at 55°C after addition of SEWS-M instead of incubation at room temperature before addition of DES). Both methods are very similar. As we did a qualitative comparison of DNA release, variance of DNA release between methods is of minor importance.

Results

Line 268: *Move 'data are shown as mean values and standard deviations of five parallels' to figure caption*
Done.

[4] Lines 274-279: *Incorrect (and potentially misleading) presentation of results. Suggest as replacement: "there was no increase or decrease relative to the control, however, there was a trend for increased POM release with increasing enzyme addition, and the difference between the lowest enzyme addition and the highest was statistically significant as indicated by the Tukey test. This trend was only broken by the control treatment (given no enzymes)" // Unnecessary and confusing statement, we can see the standard deviation and Tukey test results on the figure, better to remove the statement. // Potentially misleading statement, yes, E2 and E3 have no difference compared to the control, but neither do E1 or E4.*
Thank you very much for the proposal. We decided to desist from a specific significance level in the revision of this paper. A p-value of 0.05 is a convention underpinned only by practical but not scientific reason. E.g. visible differences are leveled by using it: E0, E2 and E3 appear to have similar mean values and variance, whereas E1 (p=0.06) and E4 (p=0.15) show visible differences to the control at 50 J/ml. Whereas E1 is not explained by the model and have to be discussed, E4 matches the forecast and is underpinned by the increase in bacterial cell release. That has to be carefully discussed. "There was a trend for increased POC release with increasing enzyme addition, and this trend was only broken by the control treatment (E0, given no enzymes)." [p-values changed due to new

statistical method, see [4-1]]

Lines 284-288: *There has been no physical transfer of organic matter between these analytical pools. A reduced aggregate stability may have for example, or increased release of biofilm fragments retained on the 1.5 µ glass filter, but this is a matter for discussion. It might be more useful to say here that it is reassuring that the SOC remaining in the sediment reflects what would be expected given the quantities extracted at 50 J... but of course it would (because you present relative fractions in preference to absolute concentrations). I am struggling to find a reason to retain this section. I think it better to delete lines.*

Our intention was to express that nearly the whole net POC differences E1-E0 and E4-E0 are related to variations in the HF, but not in fLF, oLF(100) and oLF(150). That will be included in lines 274-297.

[5] Line 289: and Figure 2 These results have already been presented, it is not clear exactly what compounded estimate of error is being given, and besides, data were already presented in figure 1. Remove Figure 2. **Line 290:** This has already been presented, that one can add the non-significant results to the significant, and finds the same thing is nothing surprising or worthy of comment. Delete. **Line 291:** Clumsy sentence and repetition: delete first sentence. **And lines 291-293:** Released POM data may be evidence of this, and may not be - this is a matter for the discussion. Delete these lines.

Lines 289-293 will be deleted. Fig. 2 will be changed to mg POC /g dry soil and shortly described.

[We decided to remove the cumulative diagram. For cumulative LF-SOC, see [5] in the results part.]

[6] Lines 293-296: Delete section starting “The lower aggregate stability is indicated by a steeper gradient and on average in an...”. Replace with “The addition of the highest enzyme concentration (E4) caused the release of about 40% more POM by mild sonication (50J ml-1) than occurred with the addition of the lowest concentration (E1). This was statistically significant at ($p < 0.05$).” end of section.

Thank you very much. “At 50 J ml^{-1} ultrasonic treatment results in an additional POC release of about 10% more POC compared to the control, whereas POC release is reduced by -18% in E1. The addition of the highest enzyme concentration (E4) caused the release of about 1/3 more POM by mild sonication (50 J ml^{-1}) than occurred with the addition of the lowest concentration (E1) ($p=0.003$).

Line 302: *In contrast here I think the relative increase in DNA release is a little understated. Yes it is useful to also give it as a percentage of total DNA extracted from the soil as you have done (Figure 3 - now rename to Figure 2), but perhaps in line 302 replace text "it is increased by about 3.5% to a value of 5.5% in the E4 scenario in comparison to the control” with ‘While there was no difference in DNA concentrations suspended in the wash of control and low enzyme additions, treatment E4 caused an increase to more than double the DNA content of either E0 or E1.”*

Thank you. Replaced by: “While there was no difference in relative DNA release in the wash of control and low enzyme additions, treatment E4 caused an increase to more than double the DNA content of either E0 or E1, which amounts to 5.6% of total DNA”.

Discussion

[7] Lines 324-335: First paragraph disorganised: it is an unpleasant jump to the model in the first sentence. Build up to it. It would be smoother if begin with the main result result, followed by your description of enzyme transport into the unsaturated pore space and discussion of others work E.g. “We found that increasing the quantity of enzymes applied to aggregates led to increased release of POM when aggregates were sonicated. Then describe the pore system (currently lines 325 326), then give your model of explanation “we present a model to explain the observed findings ...”

Thank you. First paragraph was replaced by:

“We found that increasing the quantity of enzymes applied to aggregates led to increased release of POC when aggregates were sonicated. This detachment is explained by the transport of α-glucosidase, β-galactosidase, DNAse and lipase into the unsaturated pore space. Consequently enzymes diffuse into the biofilm matrix, where structural components

like polysaccharides, eDNA and lipids are digested as approved for diverse enzymes and enzyme targets in ecological and medical studies (Böckelmann et al., 2003; Walker et al., 2007). We utilize a simple spacial model to explain the observed findings: The biofilm bridges gaps between primary particles, connects them and builds a restructured pore system inside the aggregate (Fig. 4). As macromolecular biofilm components yield EPS as a viscoelastic structure (Sutherland, 2001), their digestion causes a loss in EPS viscosity and thereby should reduce aggregate stability. The effect is expected to grow with increasing enzyme activity until the whole EPS matrix is dispersed."

Lines 336-337: *Delete the discussion of what is not being discussed.*
Done.

Line 345: 'de facto' is way too strong and encourages the reader think of examples to disprove this over-confident statement. E.g. it could have been caused by cell lysis. Delete 'de facto'.
Done.

Line 352: This is not the only possible explanation and further discussion with relevant literature is required. Might some of the C released from occluded POM and/or biofilm not have been detected in the filtered light fraction? – e.g. may have been present as smaller particulates or DOC? Also, DNA/cells/POM may not have been released without sonication. Include this. Current literature has more to offer. Add "Furthermore, we pre-incubated soils given 0.2 mM NH_4NO_3, and added further NH_4NO_3 with the enzyme application. Redmile-Gordon et al (2015) proposed that low C/N ratios of substrates available to soil microorganisms reduces cell specific EPS production rates, and may trigger microbial consumption of EPS to acquire C for cell-growth. The observations leading to this proposed dynamic were also found by addition of NH_4NO_3. In the present study, NH_4NO_3 was applied with all treatments including the control (which also received no C from enzyme provision). The resulting lowest C/N ratio in the control soils may itself have decreased the EPS, contributing to the higher than expected release of POM from the control soil with sonication at 50 J mL^{-1}, and the break in the trend for increasing POM release with increasing enzyme addition.
[8] We now write: "Decreased POC release in E1 could be explained by pre-incubation of soil aggregates given 0.2 mM NH_4NO_3 and further addition of NH_4NO_3 with enzyme application. Redmile-Gordon et al. (2015) proposed that low C/N ratios of substrates available to soil microorganisms reduces cell specific EPS production rates, and may trigger microbial consumption of EPS to acquire C for cell-growth. The observations leading to this proposed dynamic were also found by addition of NH_4NO_3. In the present study, NH_4NO_3 was applied with all treatments including the control (which also received no C from enzyme provision). The resulting lowest C/N ratio in the control soils may itself have decreased the EPS, contributing to the higher than expected release of POM from the control soil with sonication at 50 J mL^{-1}, and the break in the trend for increasing POM release with increasing enzyme addition."
[9] Further "Probably high enzyme concentrations dissolve biofilm structures that remain part of the coarse POM at low enzyme treatment, which results in underestimation of E4 POC release." was added in this paragraph.

Lines 350-352, 390: *Discussion about link between biofilm digestion and aggregate stability.*
Sentence in lines 350-352 "The incomplete biofilm digestion suggests, that the influence of biofilms on aggregate stability is larger than demonstrated in scenario E4." shifted to a later part of discussion. Previous reference to aggregate stability is replaced by biofilm digestion/POC release context, except in the spacial model.

Line 353: *Replace "The incomplete … ambiguously" sentence with "Nonetheless, biofilm detachment caused by E4 is still likely to be incomplete." And continue with "Slow enzyme diffusion..."*
Line 348-350 is replaced by "Hence, biofilm detachment caused by E4 is still likely to be incomplete." Continued with "Slow enzyme diffusion...".

[10] Lines 352, 356-367: *This paragraph contains some useful information that should be retained for comparison of enzyme quantities added. However, the explanation drawing on enzyme activities in natural*

soils is not clear and needs re-thinking and re-writing. Actually, it seems the argument is flawed. You only observed effects when you increased enzyme activities well above 'natural' levels so on the contrary seems to support the hypothesis that diffusion factors ARE limiting (e.g. sorption to active surfaces). Suggest you cite the excellent review by (Burns et al., 2013) (see section 3.3; page 220).

"Based on our calculations enzyme concentrations of mix E1 should be sufficient for total biofilm digestion within time of application (1h) – as far as there are no other factors reducing enzyme efficiency. As surveys of natural soils show enzyme concentrations up to mix E3 [Cooper and Morgan, 1981; Eivazi and Tabatabai, 1988; Acosta-Martinez and Tabatabai, 2000], such factors might be reasonably assumed. This is underpinned by our results, that show the only increase in POC release in scenario E4 attended by only an incomplete cell release. After addition to the soil sample, enzymes must enter the EPS matrix by diffusion. Therefore it is assumed that parts of the enzymes probably do not reach the biofilm due to inhibited diffusion. Beside diffusion, sorption and decomposition could play a major role in reducing enzyme efficiency. Whereas turn-over rates of soil enzymes are not yet assessed, extended stabilization of active enzymes over time on soil mineral and organic surfaces is reported (Burns et al., 2013). This mechanism could explain immobilization of enzymes off the biofilm and high measured soil enzyme concentrations from literature in face of still existing biofilms. Due to this boundary conditions, quantification of the relation of enzyme concentration and POC release was not possible in this work, although there is a tendency for enhanced POC release." This information will be included in lines 356-367.

Lines 368-370: *It does not reinforce this, and if it does it conflicts with your model. If your model is correct it would only be found'after disruption of aggregates to release the oLF (as you observed at 50 J ml^{-1}; congruent with your model). It could also have been lost as soluble C, as mentioned above in reference to line 352 above. Delete 368 – 370.*

Correct. I referred to a POM occlusion only mediated by EPS, but in the model it seems very implausible to assume occluded POM, that is not bound by physico-chemical interactions. Deleted.

Lines 378-383: *Not statistically significant therefore remove this speculation. Statistically it is built on observations that can be reasonably expected by chance.*

Done.

Line 384 *replace 'cumulation of LF carbon release overall energy level clarifies the alteration of soil aggregate stability' with 'The trend for increased of LF carbon release over increasing enzyme additions demonstrates an alteration of soil aggregate stability'.*

Thank you. Done.

Line 385 *– results repetition. And* **[11] lines 386-389** *Careful, you are discussing SOC (POM) release and aggregate stability as if you measured both independently, and focus drifts. I recommend you instead discuss the connection you propose (POM release being due to digestion of EPS which seems to prevent POM release by sonication alone up to 150 J ml-1 – and after more effectively separated from soil minerals by 50J sonication).*

See "New line of argument" at the end of this document.

Line 395: *Good point re enzyme metabolism, although 1 hour is not a lot of time for it, it would be useful to include a reference for rapid metabolism of enzymes/proteins. Add that the large additions of enzyme-C could be used as a C-source for microbial growth which is known to stabilise soil aggregates, e.g. (Watts et al., 2005). This is why total enzyme-C added should be included in your manuscript (suggest this is added to Table 3).*

[12] "The applied enzymes have no relevant mass input to extractable POM. Even in case of complete adsorption to POM in only one fraction, highest enzyme concentration (E4) would result in additional 13.5 µg enzyme /g dry soil being <0.4% of the smallest extracted POM fraction.

Although enzyme concentration has no influence on extracted POC, addition of enzyme-C could be used as microbial metabolic C-source which is known to lead to soil aggregate

stabilization (Watts et al., 2005; Tang et al., 2011). Soil turn-over rates of enzymes are not assessed (Burns et al., 2013). Fast metabolization of enzymes within 1 hour would hinder quantification of the relation of biofilm digestion and POC release by influencing aggregate stability during the experiment." This content will be connected to point (**Line 352**).

[13] Lines 407, 408: better if you delete 'a 9000 fold of the E1 enzyme activity calculated from actual soil biomass to remove approximately // suggest replace '5.5% of the biofilm and no increase in FLF release, the pooled influence of the disregarded boundary conditions on enzymatic detachment efficiency is large' with '5.5% biofilm removal indicated by DNA measurements coupled with no increase in fLF release, may suggest that the pooled influence of the disregarded boundary conditions on enzymatic detachment efficiency is large'.

As the role of fLF C is discussed regarding lines 368-370, the paragraph is replaced with: "Most of these restrictions are owed to the high complexity of the soil ecosystem. Enzymes were applied in concentrations four orders of magnitude higher than calculated from actual C_{mic} and even 1-2 orders of magnitude higher than values from literature. Considering maximum 5.5% biofilm removal indicated by DNA measurements may suggest that the pooled influence of the disregarded boundary conditions on enzymatic detachment efficiency is large." Orders of magnitude are still noted to illustrate the probable range of influence of the disregarded boundary conditions.

[14] Lines 410-413: *delete 'nonetheless' // replace 'Loss of aggregate stability' with 'Release of entrapped POM' // replace 'stabilisation' with 'stabilising' // Citation needed: suggest after 'stabilising agent of soil aggregates' to insert 'as discussed in a comprehensive review by Or et al. (2007)'. // Subsequent sentence, why limit to just natural ones? I suggest you replace 'Aggregate stability is influenced by the digestion of EPS components. Adapting this relation to natural soil ecosystems,"' with 'The apparent loss of aggregate stability caused by the digestion of EPS components in the present study suggests biofilm relevance in soil ecosystems.' And finish the discussion there.*

Paragraph replaced with "These results give insight in fundamental processes underlying aggregate stability. Release of occluded POM coupled with increased bacterial DNA release after treatment with high enzyme concentrations underpin the assumption that biofilm is a stabilising agent of soil aggregates as discussed in a review by Or et al. (2007). The apparent loss of aggregate stability caused by the digestion of EPS components in the present study suggests biofilm relevance in soil ecosystems e.g. in terms of soil-aggregate related functions like soil water dynamics, mechanical stability as well as rootability."

Conclusion

[15] Lines 414-417, 419-420, 422-423, 425, 425-427, 427, 431: *Move this final part to the start of conclusions: "Our results suggest a change of biofilm composition due to a shift ..." //* Already discussed, is weak, better to delete. // delete "and thereby enhances aggregate stability". Already discussed and now superseded by your two important sentences above this (first one suggested to be taken from discussion, lines 414 – 417). // Delete 'fLF' (these abstract technical distinctions are not appropriate for this statement). Continue with the condition i.e. "not to an increase in fLF release without physical disruption of aggregates by sonication." // replace SOC with POM (should already be defined) 427 delete the sentence starting "The bacterial DNA..." as discussed already; this does not withstand logical critique. // 'microbial communities' already are for various reasons, I think you mean the biofilm or EPS, EPS being relevant even when no biofilm can be observed … suggest you replace 'communities' with 'EPS dynamics'.

New conclusion: "It was shown that EPS is a factor of aggregate stability. Our experimental results suggest that extracellular polymeric substance (EPS) contributes to occlusion and attachment of particulate organic matter (POM) in soil aggregates. The application of a highly concentrated mix of α-glucosidase, β-galactosidase, DNAse and lipase is related to a detachment of POM from a stable to a more fragile binding structure, but not to an increase in POM release without physical disruption of aggregates by sonication. The pattern of measured POC release and additional bacterial DNA release points to an intra-aggregate fixation of POM by enzyme targets. A loss of EPS integrity

could therefore cause a detachment of soil organic matter, not only in the laboratory but also in natural soil ecosystems. Our results further suggest that a change of biofilm composition probably due to a shift in microbial population structure may alter soil aggregate stability. On macro-scale this could affect soil compactibility, erodibility, water transport, retention and aeration regime, rooting depth and the occlusion of soil organic carbon. This, in conclusion, invites to behold soil EPS dynamics as a factor of sustainable land use.” [changed wording, same content]

Figures and Tables

Figure 4: edit caption – you are not showing ‘biofilm structure’ – this is ‘aggregate structure’ replace accordingly.
Caption changed to “Proposed model of aggregate structure: ...”

Table 3: Add quantity of enzyme-C added to enable judgement of substrate utilisation by soil microbial biomass.
Quantities added.

Table 3: column E0: should the q value not be zero? Otherwise why are the enzyme activities different from column E1?
Yes. Thanks.

Furthermore ...

… there are also some points I have to answer back.

Line 38: *insert ‘and’ before ‘is an integral’*
That doesn't fit in this place.

Line 56: *delete '.'*
There is an end of sentence and the references are related to the whole paragraph.

Line 173: *use large ‘C’ for carbon*
c in c_{cell} means “concentration”

Line 409: *Insert sentence: ‘Conversely, or in addition to the above, complete biofilm removal may have been achieved, however as the model (figure 4 – now figure 3) proposes, POM would not be released until the retaining aggregates were disrupted by disruptive physical forces such as those caused by sonication.’ (Kaiser and Berhe, 2014)*
As only 5.5% of the bacterial DNA are removed after enzymatic treatment, it seems implausible to expect complete biofilm detachment. Further, point (**Lines 368-370**).

New line of argument

Line of argument will be restructured in the following way (e.g. to avoid repetitions): Discussion of POM release (increase in E4, decrease in E1, tendency, p-values but no significance level) – discussion of bacterial DNA release – discussion of of the relation of both (EPS as enzyme target) – discussion of the explanatory power of (small) POM release and of its usability for aggregate stability measurement in similar soil samples – “A more quantitative analysis of the relation of enzymatic EPS detachment and POM release would require more replicate samples and probably inclusion of soils from different land use. However, this was beyond the scope of the present study.”

Best regards,

Frederick Büks

Enzymatic biofilm detachment causes a loss of aggregate stability in a sandy soil.

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Dear Referee2.
Thank you very much for reviewing. In the following I will try to answer your important comments and to clear the objections.

1.a. *Section 2.2: confusingly written maths section*
Pooling of equations to a single one is a space saving way to show these manifold steps of converting concentrations of biofilm components to the final value of needed enzyme units. I will place each single step in the supplements. The paragraph beginning in line 163 will be revised to clarify the following: Literature show a wide range of enzyme-target concentrations in different soils. As we do not know target concentrations of our soil (due to a lack of extraction methods), we considered the largest published concentrations to find existing effects. Further as target molar masses vary as well, here we choose the smallest mass. Both conduce to a “worst-case” point of view with maximum enzyme targets.

[16] 1.b. *Section 2.2: poor justification of numbers used: Eg the supposed soil bulk density number seems odd, as this can be measured for field core samples and be recreated to field soil density. Otherwise explain the assumption for this particular experiment as normal dried and sieved soil without repacking does not get to this density.*
Different samplings during the field experiment showed soil bulk densities of 1.4 g/cm^3. These values are normal for a sandy silt (Su3) [Chaudhari et al., 2013], that is used in this experiment.
For scenario E1 soil bulk density is irrelevant because c_{cell} and therefore target maxima were estimated from c_{mic}. For scenario E2 and the following we measured a minor soil bulk density in a sample of soil aggregates (~1.15 g/cm^3). On the other hand, biofilm populations are mentioned to be mainly located in soil aggregates [Nunan et al., 2003]. Therefore – following our “worst-case”-approach – we used the bulk density of the original soil to estimate maximum target values.

1.c. *Section 2.2/2.3: poor justification of numbers used: The ‘scenarios’ have been explained (though could be improved in clarity) but do not actually contain any information regarding the technical set up.*
How much enzyme activity units were applied?
Enzyme units are listed in table 3.
What was the level of purity of the enzyme preparations?
Enzyme purity is guaranteed by the producer (data sheets of product numbers Sigma-Aldrich: G0660, G5635, L0382 and D5025).
How where the enzymes added? Was there mixing involved?
Enzymes were added as described in section 2.4. Enzyme solutions were vortexed and than added to aggregate samples as described in section 2.4.

There is a severe lack of information, especially as the whole manuscript depends on contact of these enzymes with EPS materials. How have the authors assured that these enzymes have reached the materials

processed further?
Contact of enzymes and EPS on the micro-scale were not demonstrated directly. Contact of enzymes to EPS can be assumed as the whole enzyme solution was absorbed by the soil aggregates. Fine pores (already filled with ARW from pre-incubation) in contrast need to be supplied by diffusion, that is probably inhibited. However, enzymes are able to diffuse into the EPS within 1 hour, as described by Böckelmann et al. (2003). Thus, observed effects are not quantitative, but qualitative. We tend to express the more cautious position "Enzymatic treatment causes an increased release of POM after sonication" to include uncertainties about enzyme contact to targets.

1.d. *Section 2.2/2.3: the E4 scenario seems to suggest a large excess of enzymes was applied. How have the authors ensured that such a large excess is not damaging to resident live microbial cells? E.g. a large excess of lipase may affect the membrane integrity of cells. This may in turn impact on DNA quantification without actually directly affecting soil aggregate stability.*
Cell membranes are built of phospholipids. We used purified lipase from porcine pancreas. Lipases are cutting fatty acids off e.g. glycerol, but are unable to cut fatty acids from phospholipids (as phospholipases do).

1.e. *Section 2.3: information/studies on basal respiration at 30C/37C, the temperature of the actual experiments performed, are missing.*
Respiration data are collected at 20°C in another experiment using the same soil, where basal respiration was reached after 2 days. Therefore we concluded 3 days as sufficient to reach basal respiration at even higher temperatures.

[17] 1.f. *Section 2.4: this experiment was performed on a separate soil incubation experiment within kit tubes. The experiment should however have been performed on subsamples taken from the experiment in 2.2/2.3 as the conditions in (closed?) kit tubes are very different from regular soil incubations. The authors attempt to link the results from both experiments, which in my opinion is not warranted as the experiments have been performed under different conditions.*
A direct subsampling from the aggregate stability experiment to perform the DNA experiment was rejected due to its destructive capability regarding aggregates. In turn, temperature, substrate, pH and water content of the tube experiment were similar to the incubation of samples for the measurement of aggregate stability. Further differences were disregarded. As part of our hypothesis, the link between both increase in POM release and bacterial cell release can explained causally.

1.g. *Section 2.4: for especially scenario E4, with an apparent excess of enzymes including DNase, I am surprised to see the authors report successful DNA purification. How have the authors achieved DNA purification in the presence of excess DNase? Idem for the scenarios with lower amount(s) of DNAse added?*
During incubation DNAse only digest free DNA but not DNA within bacterial cells of the biofilm. Later the pooled wash solution contains most of the DNAse. After centrifugation, this solution was discarded, whereas the bacterial pallet was resuspended in 200 µl ARW. At this stage, bacterial cells are still intact and immune to DNAse, whereas DNAse is diluted and hindered by high buffer ion concentrations. After mechanical cell lysis PPS (Protein Precipitation Solution) was added leading to e.g. precipitate DNAse. All steps of DNA extraction were conducted on ice to strongly reduce enzyme activity.

[see 4] 2.a. *The results of soil stability/SOM measurements indicate that none of the 'scenarios' are significantly different from the control experiment. The only significant difference the authors report concerns between treatment results, which leaves me wondering about the relevance of the whole study.*
Even if there is no significant difference in aggregate stability, unfulfilled expectations (as e.g. a dramatic loss in aggregate stability after enzymatic treatment) do not minder the relevance of a study. In addition – without any attempt to prettify our results – p-values <0.05 as the limit for significance is a convention. From my point of view there is a tendency of increasing POM release (p=0.1, 5 parallels) in E4, and a tendency to

decrease (p=0.06, 5 parallels) in E1 compared to the control. The first one fits to our model, the second one does not. Both tendencies are visible and have to be explained under the restriction of being small.

[see 5] **2.b.** *The results shown in Figure 2 have been reported without statistical analyses on significant difference. Please include statistical analyses on significant difference between control and treatments. The figure's error bars of the control and the experimental treatments could suggest that differences between control and treatment scenarios are unlikely to be significant, leaving doubt about the experiment's relevance and study design.*
Good idea. I will do this. Thereby, y-axis of figure 2 will be converted to mg POC /g dry soil.

2.c. *Figure 3 is missing a control on DNA present in the added enzyme mixtures. Can the authors ensure that the DNA extracted and amplified is not derived from the enzyme preparations added? Especially scenario E4 might lead to addition of a lot of DNA.*
We do not have this data. ARW for stock solutions and dilutions include ultrapure water and were autoclaved. Remaining free DNA strand amount is assumed to be far below soil DNA concentration and most probably digested by DNAse in stock and dilutet solutions. Further possible DNA additions were similar between variants and related to blind values.

2.d. *Figure 3: In contrast to the above, DNase is added in the scenarios, which should then lead to degradation of DNA present in the samples. Can the authors therefore please clarify the puzzling details of this experiment?*
Until mechanical cell lysis, extracellular DNA including eDNA from EPS is digested by DNAse. As mentioned in 2.c. small amounts of additional DNA are supposed to be irrelevant and the bulk of free DNA is rejected by washing. E4 shows the highest DNA release, although undigested biofilm in low enzyme treatments could increase DNA-concentration via centrifugation to the pallet. That could probably point to an underestimated additional DNA release in E4. It underlines the only qualitative approach of this experiment.

2.e. *Figure 3: Can the authors please provide (control) data on (expected) cell lysis from treatments, esp E4? This will enable untangling of results due to lysis and any EPS - biofilm effect on soil aggregation.*
DOC release from bacterial cells due to enzymatic treatment and ultrasonication was not quantified. This DOC is most probably removed by repeated washing during density fractioning. Measuring the distribution of remaining bacterial DOC among fLF, oLF and HF is impossible by method. However, visibly increasing POM release in E4 (see Line 30, Final response to Marc Redmile-Gordon) points to a negligible effect of bacterial DOC sorption on measured C.

[see 4] **3.a.** *The significant in – between - treatment results are given too much focus and attention, especially in the knowledge that none of the treatments were significantly different to controls. The majority of the conclusions drawn are not supported by the actual data provided.*
and 3.b. *Line 390 '... our results give a qualitative evidence for the influence of biofilms on aggregate stability...' This conclusion is not supported by the data provided.*
See point 2.a. We propose careful line of argument including a statement of insignificance and a discussion of tendencies in face of p-values nearby p=0.05.

3.b. *Figure 4: this diagram can be omitted.*
As figure 4 illustrates the model, we prefer to retain it.

Best regards,
Frederick Büks

[1] Enzymatic biofilm digestion in soil aggregates facilitates the release of particulate organic matter by sonication

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Abstract.

The stability of soil aggregates against shearing and compressive forces as well as water caused dispersion is an integral marker of soil quality. High stability results in less compaction and erosion and has been linked to enhanced water retention, dynamic water transport and aeration regimes, increased rooting depth and protection of soil organic matter (SOM) against microbial degradation. In turn, particulate organic matter is supposed to support soil aggregate stabilization. For decades the importance of biofilm extracellular polymeric substances (EPS) regarding particulate organic matter (POM) occlusion and aggregate stability has been canonical because of its distribution, geometric structure and ability to link primary particles. However, experimental proof is still missing. This lack is mainly due to methodological reasons. Thus, the objective of this work is to develop a method of enzymatic biofilm detachment for studying the effects of EPS on POM occlusion. The method combines an enzymatic pre-treatment with different activities of α-glucosidase, β-galactosidase, DNAse and lipase with a subsequent sequential ultrasonic treatment for disaggregation and density-fractioning of soils. Particulate organic matter releases of treated samples were compared to an enzyme-free control. To test the efficacy of biofilm detachment the ratio of bacterial DNA from suspended cells and the remaining biofilm after enzymatic treatment were measured by quantitative real-time PCR. Although the enzyme treatment was not sufficient for total biofilm removal, our results indicate that EPS may attach particulate organic matter (POM) within soil aggregates. The tendency to additional POM release with increased application of enzymes was attributed to a slight loss in aggregate stability. This suggests that an effect of agricultural practices on soil microbial populations could influence POM occlusion/aggregate stability and thereby carbon cycle/soil quality.

1 Introduction

Soil organic matter (SOM) comprises 50% (~1,700 Gt, including peat) of the near-surface terrestrial carbon budget, compared to ~813 Gt bound in the atmosphere (Lal, 2008). Beside carbon storage and its influence on the atmospheric CO_2 balance, manifold ecological soil functions are mediated by different SOM types like dissolved organic matter (DOM), particulate organic matter (POM), molecular organic matter of organo-mineral associations, colloidal organic matter and coprecipitated molecular organic matter (Kalbitz et al., 2000; Weng et al., 2002; Pokrovsky et al., 2005; Eusterhues et al., 2008). For example, POM is a structural component of soil aggregates, a nutrient source and provides surfaces for microbial growth (Chenu and Stotzky, 2002; Bronick and Lal, 2005). Parts of the POM are occluded within soil aggregates (Six et al., 2002). Physical isolation protects POM against microbial degradation (Six et al., 2002; Lützow et al., 2006) and maintains its ecological functions, while on the other hand this POM is thought to promote soil aggregation (Bronick and Lal, 2005). Therefore, many benefits of soil POM are linked to soil aggregate stability.

The stability of soil aggregates against shear and compression forces *(Skidmore and Powers, 1982)* as well as disaggregation caused by water (Tisdall and Oades, 1982) is an integral marker of soil quality (Bronick and Lal, 2005). Since aggregate stability implies pore stability, it results in less soil compactibility (Baumgartl and Horn, 1991; Alaoui et al., 2011) and a more dynamic water transport regime in the macropores that reduces erosion caused by surface runoff (Barthes and Roose, 2002). Other benefits in comparison to compacted soils are a higher aeration (Ball and Robertson, 1994) and lower penetration resistance (Bennie and Burger, 1988) causing increased rootability and rooting depth (Bengough and Mullins, 1990; Taylor and Brar, 1991). In addition, micropores within the aggregates enhance water retention.

The occlusion of POM within soil aggregates depends on the properties of the aggregated components. The mineral part of the solid soil matrix is composed of siliceous sand, silt and clay particles, oxides and hydroxides of Fe, Al and Mn as well as diverse minor minerals. Sticking together, pervaded and coated with multivalent cations and organic constituents like soluble metabolic products, humic substances, black carbon and other POM, macro-aggregates (>250 µm) are formed by direct coagulation or built of micro-aggregates (<250 µm). (Bronick and Lal, 2005; Brodowski et al., 2006; Lützow et al., 2006) The structure-bearing primary particles, precipitates and adsorbed molecules cohere by physico-chemical interactions between (i) permanent charge of mainly the clay mineral fraction, (ii) multivalent cations with small hydrate shells such as Ca^{2+}, Fe^{3+} and Al^{3+}, (iii)

variable charges of various minerals and SOM and (IV) variable and permanent dipoles of different soil components. Also carbonates, phosphates and other microbial precipitates force up aggregation and occlusion of POM. (Jastrow and Miller, 1997; Bronick and Lal, 2005)

In addition, since a few decades biological structures like bacterial colonies, bacterial pseudomycelia, algae, fungal hyphae and their exudates (e.g. glomalin), roots and soil fauna are accepted as a major factor of soil aggregation (Tisdall, 1991; Oades, 1993; Wright and Upadhyaya, 1998; Brown et al., 2000; Chenu and Stotzky, 2002; Rillig, 2004; Bronick and Lal, 2005). Furthermore the role of extracellular polymeric substance (EPS) of bacterial biofilms as an adhesive between soil particles is seen to be of importance (Baldock, 2002; Ashman et al., 2009).

Physical and chemical properties of soil mineral and organic matter allow to hypothesize a simple spacial model of the inner geometry of soil aggregates, that includes biofilms as links between primary particles (Fig. 1).

The biofilm itself is a viscous microenvironment mainly built up of 90-97% water (Zhang et al., 1998; Schmitt and Flemming, 1999; Pal and Paul, 2008). The remaining dry mass contains differing ratios of polysaccharides, extracellular DNA (eDNA), proteins and lipids besides 10-50% cell biomass (More et al., 2014). In contrast to 'biofilm', EPS terms the extracellular polymeric matrix excluding cells. Extracellular polysaccharides cause the EPS structural stability by means of entanglement and Ca^{2+} bridging between molecules. So does eDNA (Das et al., 2014). Proteins function as enzymes and structural links stabilizing the polysaccharide matrix, while lipids act as biosurfactants for bacterial attachment on surfaces. (Flemming and Wingender, 2010)

The composition of EPS is highly variable depending on community composition and environmental cues (Table 1): Redmile-Gordon et al. (2014) measured a natural habitat extracellular polysaccharide concentration of 401 µg g^{-1} dry soil in grassland and 169 µg g^{-1} in fallows. Diverse single- and multi-species biofilms show a proportion of polysaccharides on dry EPS of up to 95% (Pal and Paul, 2008; More et al., 2014). Different single- and multi-species biofilms in laboratory cultures and natural soils have a dry EPS eDNA content up to 10% (More et al., 2014). For forest soils values of 1.95 up to 41.1 µg g^{-1} dry soil are known (Niemeyer and Gessler, 2002; Agnelli et al., 2004). Extracellular DNA concentration of other diverse soils ranges between 0.03 and 200 µg g^{-1} dry soil (Niemeyer and Gessler, 2002; Pietramellara et al., 2009), whereas concentrations in soils explicitly used for agriculture are unknown. Extracellular matrix protein concentration was measured at 163 µg g^{-1} dry soil in grassland and 43 µg g^{-1} dry soil in fallow (Redmile-Gordon et al., 2014), but can contribute the largest fraction of EPS dry mass, e.g. 60% (More et al., 2014), and even up to 75% in *P.*

putida biofilms in laboratory cultures (Jahn et al., 1999). The typical proportion of lipids in the EPS dry-mass of different non-soil biofilms amounts up to 10% (More et al., 2014). Sparse molar mass data from different environments comprise $0.5x10^6$ to $2x10^6$ Da for polysaccharides (Flemming and Wingender, 2010), $7.75x10^4$ to $2.32x10^7$ Da for eDNA (DeFlaun et al., 1987) and 750 to 1,500 Da for lipids (Munk, 2008).

The extracellular matrix is not only exuded by soil bacteria and archaea, but also by fungi and algae. It is engineered by grazing protozoa and small metazoa as well as microbial extracellular enzymes. (Battin et al., 2007; Flemming and Wingender, 2010)

The activity of EPS degrading enzymes in natural soils spans up to two orders of magnitude: The α-glucosidase and β-galactosidase acitivity of various soils ranges from 0.00011 U g^{-1} to 0.0011 U g^{-1} and from 0.00017 to 0.0094 U g^{-1}, respectively (Eivazi and Tabatabai, 1988; Acosta-Martinez and Tabatabai, 2000). The lipase activity in coarse mineral soils shows values from 0.3 U g^{-1} in a sandy soil (Cooper and Morgan, 1981) to 2.09 U g^{-1} in a Luvisol (Margesin et al., 2000) and up to 5 U g^{-1} in a Leptosol (Margesin et al., 1999). Data for eDNAse activity in soils are not available.

Not much is known about the contribution of EPS to POM occlusion and aggregate stability in relation to other aggregate stabilizing factors. That is mainly due to methodological reasons: [3] Though e.g. Tang et al. (2011) showed a significant contribution of bacterial growth on aggregate stability, the observations could not definitely be attributed to soil microbial exopolysaccharide production. Redmile-Gordon et al. (2014) subsequently found that the techniques previously used to measure extracellular polysaccharides in soil co-extracted large quantities of ’random’ soil organic matter which confounded estimates of EPS production. Owing to the widespread interest in the role of biofilms on soil fertility, the objectives of this work are (i) to design a selective method for enzymatic biofilm detachment with minor impact on other types of aggregate bonds and (ii) to apply the method to an agricultural soil to provide indications of the influence of biofilm cohesion on POM fixation, which is expected to contribute to aggregate stability (Six et al., 2004).

The method combines a modified enzymatic pre-treatment (Böckelmann et al., 2003) with α-glucosidase, β-galactosidase, DNAse and lipase, a determination of the DNA ratio of sessile to suspended cells after enzymatic treatment and an ultrasonication of soil aggregates followed by density-fractioning and soil organic carbon (SOC) measurement (Kaiser and Berhe, 2014). The ultrasonication/density-fractionation separates SOC into three operational solid fractions: non-occluded free light fraction SOC (fLF-SOC), aggregate-embedded occluded light fraction SOC (oLF-SOC) and colloidal as well as (macro)molecular SOC, which is not detachable from mineral surfaces by the chosen

fractioning method and subsumed under heavy fraction (HF-SOC) (Kaiser and Berhe, 2014).

We hypothesize that a destabilization of the EPS matrix occurs during enzymatic treatment. This should result in an increased cell detachment from aggregates. We also expect an increased fLF-SOC release from destabilized aggregates compared to the control and a shift of the oLF-SOC ratio from higher to lower binding strength (represented by ultrasonic energy levels) that is interpretable as alteration of soil aggregate stability.

2 Materials and methods

2.1 Soil properties and microbial biomass

Well aggregated silty sand (Su3) of a plowed topsoil from a cropland near Berge (Brandenburg/Germany) was air-dried and sieved to obtain a particle size of 0.63 to 2.0 mm containing mainly macro-aggregates. The aggregates have a pH_{CaCl2} of 6.9, C_{org} of 8.7 mg g^{-1} and a carbonate concentration of 0.2 mg g^{-1}.

To estimate the soil microbial biomass, first 8 x 10 g of soil aggregates have been adjusted to 70 vol% soil water content and incubated for 70 hours at 20°C in the dark to attain basal respiration. Then, based on DIN EN ISO 14240-2 half of the samples were fumigated with ethanol-free chloroform in an evacuated desiccator for 24 h, whereas the other half remained untreated. Afterwards chloroform was removed and both halves were extracted with 40 ml of 0.5 M K_2SO_4 solution by 30 min of horizontal shaking and filtered through 0.7 µm glass fiber filters. The DOC concentrations of all filtrates were measured by a TOC Analyzer (TOC-5050A, Shimadzu). 176 ± 22 µg microbial carbon g^{-1} dry soil (C_{mic}) were derived from the difference between DOC concentrations of fumigated and non-fumigated samples multiplied by a conversion factor of 2.22 (Joergensen, 1996). Soil bacterial biomass was derived from C_{mic} as 352 ± 44 mg kg^{-1} assuming 0.5 as a ratio of C_{mic} to total cell dry mass (Bratbak and Dundas, 1984).

2.2 Detachment scenarios

Four degradative enzymes were selected on the basis of soil pH and temperature used for catalytic unit definition (T_{def}): α-glucosidase from *S. cerevisiae* (Sigma-Aldrich, pH_{opt} 6 to 6.5, T_{def}=37°C, product number G0660) hydrolyzes terminal α-1,4-glycosidic linkages in polysaccharides as β-galactosidase from *E. coli* (Sigma-Aldrich, pH_{opt} 6 to 8, T_{def}=37°C, product number G5635) does with β-glycosidic bonds. Lipase from porcine pancreas (Sigma-Aldrich, pH_{def} 7.7, T_{def}=37°C, product number L0382) splits fatty acids from lipids via hydrolysis, but do not digest phospholipids, which are part of bacterial membranes. DNAse I from bovine pancreas (pH_{def} 5, T_{def}=25°C, product number D5025) breaks the phosphodiester linkages between nucleotides of DNA as an endonuclease. Proteases were not used because of their promiscuity and therefore incalculable influence on the other applied enzymes.

Literature shows a wide range of target concentrations related to these enzymes in different soils. As we do not know target concentrations of our soil (due to a lack of

extraction methods), we considered the largest published values (Table 2) of EPS content (ξ_{EPS}^{max}) and enzyme target dry mass contents (ξ_{target}^{max}) from literature. Further, as bacterial dry mass (ξ_{cell}^{min}) and target molar masses (M_{target}^{min}) vary as well, here we choose the minimum percentage and the smallest mass, respectively. These values conduce to a "worst-case" point of view with a maximum of enzyme targets. Any other boundary conditions such as ion activity, diffusion rates or metabolization of enzymes by soil organisms were disregarded.

Calculated by Eq. (1)

$$Unit_{target} = \frac{c_{cell} \cdot q \cdot \xi_{EPS}^{max} \cdot \xi_{target}^{max} \cdot m_{sample}}{\xi_{cell}^{min} \cdot M_{target}^{min} \cdot t} \quad (1)$$

with variables listed in Table 2 and Table 3, sufficient enzymes were provided to digest the expected EPS concentration in five scenarios: In the E1 scenario c_{cell} was given by the results of fumigation-extraction. In the E2 scenario a bacterial dry mass of 500 g m^{-2} in the upper 30 cm is considered, which is assumed to be the maximum for middle and northern European soils (Brauns, 1968). [16] Supposing a soil bulk density of 1.4 g cm^{-3}, a c_{cell} of 1190.5 µg g^{-1} dry soil is given. Although the soil bulk density of the soil aggregate samples is ~1.15 g/cm^3, we decided to use the soil bulk density of the original soil, which is in the normal range of sandy silk soil (~1.40 g/cm^3) (Chaudhari et al., 2013). This is due to the fact that biofilm populations are mentioned to be mainly located in soil aggregates (Nunan et al., 2003) and accords to the "worst-case"-approach. The E3 scenario uses a 100-fold excess (q=100, Table 3) of the enzyme activities applied in the E2 scenario, whereas the E4 scenario contained the 2,820-fold, which is slightly higher than activities used in Böckelmann et al. (2003). Enzyme-free samples (E0) were used as a control.

2.3 Release of POM carbon

Fifteen g of air-dried soil aggregates were incubated in 5 replicates per scenario with 3.4 ml of highly concentrated artificial rainwater (ARW: 0.2 mM NH_4NO_3, 0.3 mM $MgSO_4$ x $7H_2O$, 0.5 mM $CaCl_2$ x $2H_2O$, 0.5 mM Na_2SO_4, 15 mM KCl, pH 5.7) for 3 days at 20°C in the dark to establish basal respiration and avoid slaking in the following preparation steps. After incubation 2.5 ml of ARW containing enzymatic units according to Table 3 were added to the samples. By means of a following incubation at 37°C, enzymes were let to work near their catalytic optimum for 1h, which is proven to be sufficient for biofilm degradation (Böckelmann et al., 2003). After this enzymatic pretreatment, 67.2 ml of 1.67 g

cm^{-3} dense sodium polytungstate (SPT) solution were added resulting in a density cut-off of 1.6 g/cm^3, and samples were stored for 30 minutes to allow SPT diffusion into the aggregates. Then samples were centrifuged for 26 min with 3,569 G. Sodium polytungstate solution with floating fLF was filtered through an 1.5 µm pore size glass fibre filter to capture LF particles. Afterwards following Golchin et al. (1994) aggregate samples were consecutively disaggregated in four steps by application of each 50 J ml^{-1} of ultrasonic energy (Branson© Sonifier 250) for 1 min 15 sec. The energy output was determined by measuring the heating rate of water inside a dewar vessel (Schmidt et al., 1999). Every treatment cycle consisted of ultrasonication, centrifugation for 26 min with 3,569 G and filtering of SPT solution through an 1.5 µm pore size glass fibre filter to capture the LF. Afterwards the LFs and the remaining soil matrix ('sediment', consisting of oLF bonded >150 J ml^{-1} and the HF) were frozen, lyophilized, ground and dried at 105°C. Total amount of fraction carbon was determined using an Elementar Vario EL III CNS Analyzer and the absence of carbonates was proved, respectively.

2.4 Release of bacterial DNA

The release of bacterial cells into the solution was quantified using a FastDNA™ SPIN Kit for Soil and quantitative real-time PCR.

Therefor 45 µl of ARW were added directly to 0.1 g of air-dried aggregates. The samples were sterilely incubated in duplicate at 20°C for 3 days in the dark in a closed FastPrep Lysing Matrix E tube during run to basal respiration. Then 30 µl of ARW containing enzymatic units according to Table 3 were distributed equally to the aggregates' surfaces. The samples were incubated for 1 h at 37°C in a heating block, cooled down on ice to decrease enzyme activity and washed three times in 1 ml of ARW not by shaking but gently rotating along the tube's longitudinal axis to separate detached and planktonic cells from the soil matrix. Supernatants of all three washing steps were removed carefully with a pipette, pooled and centrifuged at 13.000 G for 15 minutes at 4°C. Then the supernatant was discarded, the pallet resuspended in 200 µl ARW and transfered to another FastPrep Lysing Matrix E tube. Both soil and washing ARW samples were extracted and purified at 4°C following the FastDNA™ SPIN Kit for Soil manual. All DNA samples were stored at -20°C for further use. [17] A direct subsampling from the aggregate stability experiment was rejected due to its destructive capability regarding aggregates. Temperature, substrate, pH and water content of the DNA experiment were similar to the incubation of samples for the measurement of aggregate stability. Further differences (e.g. soil volume) were disregarded.

Amplification of 10-fold diluted DNA samples was performed using a C1000 Touch Thermal Cycler (BioRad). According to the reference for SG qPCR Master Mix (Roboklon) thermocycling comprised an initial denaturation at 95°C for 10 min as well as 55 cycles of 15 sec of denaturation at 95°C, 20 sec of annealing at 49°C and 30 sec of elongation at 72°C. The reaction mix contained 1 µl PCR-H_2O, 12.5 µl SG qPCR MasterMix, each 0.75 µl of a 20 µmol l^{-1} solution of the universal bacterial primers 63f (5'-CAGGCCTAACACATGCAAGTC-3') and 341r (5‘-CTGCTGCCTCCCGTAGG-3‘) (Muyzer et al., 1993; Marchesi et al., 1998) and 10 µl template DNA. *Escherichia coli* 16s DNA solution containing 10,000 copies $µl^{-1}$ was used as qPCR standard in steps of tenfold diluted concentration from 10^6 to 10^2 copies $µl^{-1}$.

2.5 Statistics

[4-1] For evaluation of the light fraction SOC (LF-SOC) release, mean values as well as standard deviations were calculated. Parallels of each variant were positively tested to provide normal distribution and evidence of variance homogeneity (Shapiro Wilk test, Levene test, both $p>0.05$, data not shown). One way analysis of variance (ANOVA) was applied followed by Tukey test to clarify significant ($p<0.05$) differences in LF-SOC release between variants of each energy level. Results of bacterial DNA release were presented as duplicates.

3 Results

3.1 Release of POM carbon

The relative LF carbon release from soil aggregate samples after different enzymatic treatments is shown in Fig. 2. The proportionate C of each captured fraction is defined as C_{frac} C_{Σ}^{-1}, in which C_{frac} is the release of LF-SOC per energy level or – in case of the sediment – the organic carbon remaining in the soil matrix. C_{Σ} is the total SOC of all separated LFs and the sediment.

Averaging all treatments, around 79% of C_{Σ} remain in the sediment, whereas the bulk of LF-SOC is released as weakly bound oLF (50 J ml^{-1}) and fLF. Only around 4.5% of C_{Σ} is detached at 100 J ml^{-1} and 150 J ml^{-1}.

None of the enzymatic treatments altered the quantity of fLF-SOC released in the absence of sonication (0 J ml^{-1}).

[4, 6] In contrast, visible differences to the control were shown for E1 (decrease, p=0.34) and E4 (increase, p=0.42) at mild sonication (50 J ml^{-1}), whereas E2 (p=1.00) and E3 (p=1.00) are very similar to the control. The difference between E1 and E4 was statistically significant (p=0.01) as indicated by the Tukey test, and the addition of the highest enzyme concentration (E4) caused the release of about 63% more oLF-SOC than occurred with the addition of the lowest concentration (E1).

Released LF-SOC at 100 and 150 J ml^{-1} is not different among treatments. Only the E2 scenario shows any tendency of increased oLF-SOC release at 100 J ml^{-1} compared to the other treatments (p=0.07 compared to E3).

The sediment represents the SOC remaining unextractable at ≤150 J ml^{-1} and accordingly shows a trend to decrease with increasing enzyme activity. In relation to the control, nearly the whole alteration in the oLF-SOC releases of E1 and E4 at 50 J/ml as well as E2 at 100 J/ml comes from the sediment fraction, but hardly from the other LFs. However, opposite reallocation of SOC between fractions due to converse physico-chemical effects can only be observed in sum. Therefore alterations must be considered as net C transfer between stability fractions.

[5] Cumulating LF-SOC releases of all energy levels, E1 shows a reduction by 16% compared to the control (3.3% of C_{Σ}), whereas E4 was increased by 10% (2.2% of C_{Σ}). The strongest enzymatic treatment (E4) caused the release of about 58% (0.49 mg/g dry soil) more cumulated LF-SOC than occurred with scenario E1.

3.2 Release of bacterial DNA

The relative DNA release after enzymatic treatment, as pictured with the treatments E0, E1 and E4 in Fig. 3, is defined as the ratio of extracted DNA from suspended bacterial cells (DNA_{susp}) to the sum of DNA extracted from suspended and sessile bacterial cells and the remaining EPS (DNA_{Σ}) multiplied by 100. While there was no difference in relative DNA release in the wash of control and low enzyme additions, treatment E4 caused an increase to more than double the DNA content of either E0 or E1, which amounts to 5.6% of total DNA. This increase is caused by both an increase in released bacterial DNA from suspended bacterial cells and a decrease in eDNA remaining in washed soil.

4 Discussion

[7] We found that increasing the quantity of enzymes applied to aggregates led to increased release of LF-SOC when aggregates were sonicated. This detachment is explained by the following mechanism: The enzyme mix flows into the unsaturated pore space. From there α-glucosidase, β-galactosidase, DNAse and lipase diffuse into the biofilm matrix, where structural components like polysaccharides, eDNA and lipids are digested as approved for diverse enzymes and enzyme targets in ecological and medical studies (Böckelmann et al., 2003; Walker et al., 2007). We propose a simple spacial model to explain the observed findings: The biofilm bridges gaps between organic and mineral primary particles, connects them in addition to other physico-chemical bondings and builds a restructured pore system inside the aggregate (Fig. 1). As macromolecular biofilm components yield EPS as a viscoelastic structure (Sutherland, 2001), their digestion causes a loss in EPS viscosity and thereby should reduce forces involved in the occlusion of POM. The effect is expected to grow with increasing enzyme activity until the whole EPS matrix is dispersed.

[2] In the following, LF-SOC is interpreted as SOC from released POM, since the share of both adsorbed DOM and colloids on captured dry mass is considered to be negligible after SPT treatment. Furthermore, LF-SOC transferred from the sediment fraction to light fractions due to enzymatic treatment is also interpreted as POM, as in contrast mineral associated organic matter of the HF is not assumed to be extractable at the applied energies (Cerli et al., 2012).

[4] In accordance with the model, measured oLF-SOC releases indicate a trend for increased POM release with increasing enzyme addition (Fig. 2). The E4 scenario shows that relative oLF-SOC release increased by 63% (5% of C_{Σ}) compared to E1 at 50 J ml^{-1}, but its release is similar to the mean of the other treatments at 0 J ml^{-1}, 100 J ml^{-1} and 150 J ml^{-1}. Noticeable deviations of E1 and E4 from the control do not match the usual significance criteria ($p<0.05$). However, the increase of the relative oLF-SOC release in the E4 scenario compared to the control is predominantly related to an equally lower C content of the sediment but no decrease in the 100 J ml^{-1} and 150 J ml^{-1} fractions. That points to a strong (oLF >150 J ml^{-1}) intra-aggregate fixation of POM due to enzyme targets, which is weakened by enzymatic treatment.

The relation of LF-SOC release with enzymatic biofilm digestion is supported by the comparison of bacterial DNA releases between the treatments (Fig. 3). This indicates that applied enzymes are targeting biofilm components and release bacterial cells: The E4 scenario shows EPS digestion and additional cell release leading to a doubled relative

DNA release compared with the control and E1. However, considering that most of the soil bacteria are expected to live in biofilms (Davey and O'toole, 2000), the total DNA release of only 5.6% in the E4 scenario is too low for total biofilm digestion. Hence, biofilm detachment caused by E4 is still likely to be incomplete and the increased oLF-SOC release of E4 only results from a partial soil biofilm detachment. We conclude a slight influence of enzymatic treatment on the occlusion of POM at enzyme concentrations exceeding natural concentrations. This conforms to results of Böckelmann et al. (2003), which indicate that a treatment with enzyme concentrations of near that of E4 is sufficient to destabilize biofilms within 1 hour.

[10] The incomplete biofilm detachment can be explained by the reduction of enzyme activity due to interaction with the soil matrix. Based on our calculations enzyme concentrations of mix E1 should have been sufficient for total biofilm digestion within time of application (1h) – as far as there are no other factors reducing enzyme efficiency. As surveys of natural soils show enzyme concentrations up to mix E3 (Cooper and Morgan, 1981; Eivazi and Tabatabai, 1988; Margesin et al., 1999; Acosta-Martinez and Tabatabai, 2000; Margesin et al., 2000), such factors might be reasonably assumed. After addition to the soil sample, enzymes must enter the EPS matrix by diffusion. Therefore parts of the enzymes probably do not reach the biofilm due to inhibited diffusion. Beside diffusion, sorption and decomposition could play a major role in reducing enzyme efficiency. Whereas turn-over rates of soil enzymes are not yet assessed, extended stabilization of active enzymes over time on soil mineral and organic surfaces is reported (Burns et al., 2013). This mechanism could explain immobilization of enzymes off the biofilm and high measured soil enzyme concentrations from literature in face of still existing biofilms. After penetration of biofilms (macro)molecules interfere with EPS components depending on molecular size, charge and biofilm structure (Stewart, 1998; Lieleg and Ribbeck, 2011) which is strongly influencing decay rates of enzymes. Due to these boundary conditions, quantification of the relation of enzyme concentration and POM carbon release was not possible in this work.

[4] The trend for increased POM release with increasing enzyme addition was only broken by the control treatment. Whereas E4 matches the forecast of releasing more POM than the control, scenario E1 shows a reduced release by -2.8% and the DNA release remains unchanged compared to the control. This decrease in the 50 J ml^{-1} fraction is related to an increase in the sediment fraction and cannot be explained by the model (Fig. 1). [8] Probably it could be explained by pre-incubation of soil aggregates given 0.2 mM NH_4NO_3 and further addition of NH_4NO_3 with enzyme application: Redmile-Gordon et al. (2015)

proposed that low C/N ratios of substrates available to soil microorganisms reduce cell specific EPS production rates, and may trigger microbial consumption of EPS to acquire C for cell-growth, which could weaken the biofilm. The observations leading to this proposed dynamic were also found by addition of NH_4NO_3. In the present study, NH_4NO_3 was applied with all treatments including the control (which also received no C from enzyme provision). Enzyme C in E1 to E4 could be used as microbial C source. The addition of SOC is known to lead to soil aggregate stabilization (Watts et al., 2005; Tang et al., 2011) and withdraw the effect of reduced C/N ratio. In contrast, the retention of the lowest C/N ratio in the control soils may itself have sustained EPS consumption and repressed reconstruction of the EPS, contributing to the higher than expected release of POM from the control soil with sonication at 50 J mL^{-1} and the break in the trend for increasing POM release with increasing enzyme addition. However, decay rates of enzymes in soil are unknown but needed for a more accurate estimation of enzyme C as a fast energy and carbon source.

[11] Under certain conditions POM carbon release is indicative for soil aggregate stability. Generally, aggregate stability is characterized by determining the reduction in aggregate size after application of mechanical force. The commonly used methods are dry and wet sieving. However, the destruction of soil aggregates by ultrasonication has an advantage over these methods, which is the quantification of the applied energy (North, 1976). It is used for studying reduction of aggregate size (Imeson and Vis, 1984) as well as detachment of occluded POM carbon (Golchin et al., 1994). Kaiser and Berhe (2014) reviewed 15 studies using ultrasonication of soil aggregates in consideration of its destructiveness to the soil mineral matrix and occluded POM. They found destruction of POM at applied energy levels >60 J/ml, destruction of sand-sized primary particles at >710 J/ml and of smaller mineral particles at even higher energy levels. We used this method of gentle POM detachment from soil aggregates to measure the oLF-SOC release as a result of mechanical force and linked it to aggregate stability. Since Cerli et al. (2012) have shown that the release of free and occluded light fractions strongly depends on soil properties like mineralogy, POM content, composition and distribution, this method is restricted to comparison of soils being similar in these properties. Having regard to this restriction, the trend for increase of oLF-SOC release over increasing enzyme additions demonstrates an alteration of soil aggregate stability.

Although our results give a slight evidence for the influence of biofilms on aggregate stability, they have to be recognized with restrictions to full quantifiability: (1) The enzyme concentration hypothetically needed to disperse the whole soil sample EPS matrix depends on diverse boundary conditions like the concentration of enzyme targets,

environmental conditions such as pH, temperature as well as ion activity and delay factors such as low diffusion, kinetic influence or metabolization of enzymes by soil organisms. (2) Underlying enzyme kinetics were measured by the producer using pure targets for unit definition, while biofilm targets are much more diverse and soil matrix could interfere. (3) Alternative enzyme targets might be reasonably assumed within the complex chemism of the soil matrix. Released organic cytoplasm molecules of lysed cells can be excluded to be an additional enzyme target due to their low concentration. On the other hand, enzyme specificity to EPS targets in face of the organic soil matrix is unbeknown. (4) [9] The decrease of extracted POM mass due to biofilm erasement from surfaces is suggested to be low, but could cause underestimation of POM release especially in scenario E4. In contrast, a direct contribution of enzyme C to the POM carbon release can be refused. [12] Even in case of complete adsorption to the POM of only one fraction, the highest enzyme concentration (E4) would result in additional 13.5 µg enzyme /g dry soil being <0.4% of the smallest extracted POM fraction (Table 3). (5) Regarding DNA release measurement as well, data are semi-quantitative, since quantification of the detachment effect is limited by a potential adherence of detached cells to soil particles after washing (Absolom et al., 1983; Li and Logan, 2004). Thus, cell release could be underestimated as biofilm detachment increases.

[13] Many of these uncertainties are owed to the high complexity of the soil system. Enzymes were applied in concentrations four orders of magnitude higher than calculated from actual C_{mic} and even 1-2 orders of magnitude higher than values from literature. Incomplete biofilm removal indicated by the release of maximum 5.5% DNA from the soil matrix may suggest that the pooled influence of the disregarded boundary conditions on enzymatic detachment efficiency is large.

[14] However, these results give a first though still vague insight in fundamental processes underlying POM occlusion. A slight release of occluded POM coupled with increased bacterial DNA release after treatment with high enzyme concentrations underpin the assumption that biofilm is involved in POM occlusion being a stabilizing agent of soil aggregates as proposed in a review by Or et al. (2007). The apparent increase of POM carbon release caused by the digestion of EPS components suggests biofilm relevance in soil ecosystems e.g. in terms of soil-aggregate related functions like soil water and C dynamics, mechanical stability as well as rootability. However, the statistical power of this introductory work is low and a more quantitative analysis of the relation of enzymatic EPS detachment and POM release would require deeper knowledge of enzyme dynamics in soil, more replicate samples, additional enzyme concentrations and probably inclusion of

soils from different land use. However, this was beyond the scope of the present study.

5 Conclusions

[15] Extracellular polymeric substance (EPS) was shown to be a promising candidate factor of aggregate stability. Our experimental results suggest that EPS contributes to occlusion and attachment of particulate organic matter (POM) in sandy soil aggregates. The application of a highly concentrated mix of α-glucosidase, β-galactosidase, DNAse and lipase is related to a slight detachment of POM from a stable to a more fragile binding structure, but not to an increase in POM release without physical disruption of aggregates by sonication. The pattern of measured light fraction soil organic carbon (LF-SOC) release and additional bacterial DNA release points to an intra-aggregate fixation of POM by enzyme targets. A loss of EPS integrity could therefore cause a detachment of soil organic matter, not only in the laboratory but also in tilled soils. Our results further suggest that a change of the biofilm composition probably due to a shift in microbial population structure may alter soil aggregate stability. On macro-scale this could affect soil compactibility, erodibility, water transport, retention and aeration regime, rooting depth and the occlusion of soil organic carbon. This, in conclusion, invites to behold soil EPS dynamics as a factor of sustainable land use.

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Author contribution

The experiments were designed, carried out and data were evaluated by F. Büks. The manuscript was prepared by F. Büks with contributions from M. Kaupenjohann.

Data availability

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Tables

Table 1: Concentrations and molar masses of biofilm stabilizing macromolecules (polysaccharides=PS, eDNA, lipids and proteins) in different environments.

Conc.	**Proportion**	**Molar mass**	**Comment**	**Reference**
µg $(g\ soil)^{-1}$	µg $(100\ µg\ EPS)^{-1}$	Da		
PS				
169			µg g^{-1} bare fallow	[Redmile-Gordon et al., 2014]
401			µg g^{-1} grassland	[Redmile-Gordon et al., 2014]
	95 %		% of EPS dry-mass	[More et al., 2014]
	40-95 %		% of EPS dry-mass	[Pal and Paul, 2008]
		$2x10^6$		[Chenu and Roberson, 1996]
		$0.5\text{-}2x10^6$		[Flemming and Wingender, 2010]
eDNA				
2.2-41.1			µg g^{-1} forest soil	[Agnelli et al., 2004]
0.08			µg g^{-1} Luvisol	[Niemeyer and Gessler, 2002]
1.95			µg g^{-1} forest podzol	[Niemeyer and Gessler, 2002]
0.03-200			µg g^{-1} unnamed soil	[Pietramellara et al., 2009]
	10 %		% EPS dry-mass	[More et al., 2014]
		$7.75x10^4\text{-}2.32x10^7$	estuarine and oceanic environments	[DeFlaun et al., 1987]
Lipids				
	10 %		% of EPS dry-mass	[More et al., 2014]
		750-1500		[Abröll and Munk, 2008]
Proteins				
43			µg g^{-1} bare fallow	[Redmile-Gordon et al., 2014]
163			µg g^{-1} grassland	[Redmile-Gordon et al., 2014]
	< 75 %		% of *Ps. Putida* biofilm	[Griebe and Nielson, 2000]
	60 %		% EPS dry-mass	[More et al., 2014]

Table 2: Variables used for the calculation of enzyme Units needed for biofilm target decomposition and scenario parameters shared by all variants, [a] More et al., 2014; [b] Pal and Paul, 2008; [c] Flemming and Wingender, 2010; [d] Abröll and Munk, 2008; [e] DeFlaun et al., 1987.

c_{cell}	[µg g^{-1}]	bacterial dry mass per g dry soil
q	[-]	enzyme concentration multiplier
ξ_{EPS}^{max}	[-]	maximum ratio of EPS dry mass per total biofilm dry mass ($\xi_{EPS}^{max} = 0.9^{[a]}$)
ξ_{target}^{max}	[-]	maximum ratio of enzyme target per EPS dry mass ($\xi_{polysaccharides}^{max} = 0.95^{[b]}$, $\xi_{lipids}^{max} = 0.1^{[a]}$ and $\xi_{eDNA}^{max} = 0.1^{[a]}$)
m_{sample}	[g]	sample mass
ξ_{cell}^{min}	[-]	minimum ratio of bacterial dry mass per total biofilm dry mass ($\xi_{cell}^{min} = 0.1^{[a]}$)
M_{target}^{min}	[µg µmol^{-1}]	minimum molar mass of enzyme target ($M_{polysaccharides}^{min} = 0.5\,x\,10^{6[c]}$, $M_{polysaccharides}^{min} = 700^{[d]}$, $M_{eDNA}^{min} = 7.75\,x\,10^{4[e]}$)
t	[min]	incubation time

Table 3: Specific scenario parameters of the variants E0, E1, E2, E3 and E4.

		E0	E1	E2	E3	E4
c_{cell}	[µg g^{-1} dry soil]	352	352	1191	1191	1191
q	[-]	1	1	1	100	2,820
$U^{max}_{a-glucosidase}$	[U g^{-1} dry soil]	0.00000	0.00010	0.00034	0.03393	0.95683
	[µg g^{-1} dry soil]	0.00000	0.00080	0.00272	0.27144	7.65464
$U^{max}_{b-galactosidases}$	[U g^{-1} dry soil]	0.00000	0.00010	0.00034	0.03393	0.95683
	[µg g^{-1} dry soil]	0.00000	0.00020	0.00068	0.06786	1.91366
U^{max}_{lipids}	[U g^{-1} dry soil]	0.00000	0.00754	0.02551	2.55102	71.93876
	[µg g^{-1} dry soil]	0.00000	0.00038	0.00126	0.12551	3.59694
U^{max}_{eDNA}	[U g^{-1} dry soil]	0.00000	0.00007	0.00023	0.02304	0.64973
	[µg g^{-1} dry soil]	0.00000	0.00004	0.00012	0.01152	0.32487

Figures

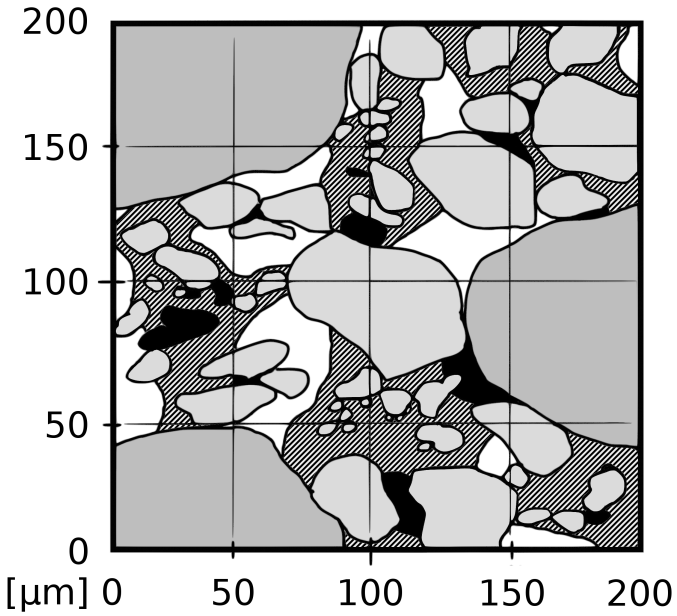

Fig. 1: Proposed model of aggregate structure including biofilms in a soil aggregate: Sand and silt (both grey) and organic particles (black) stick together by physico-chemical interactions and are bridged by EPS (striped), which additionally stabilizes the soil aggregate structure and the pore space (white).

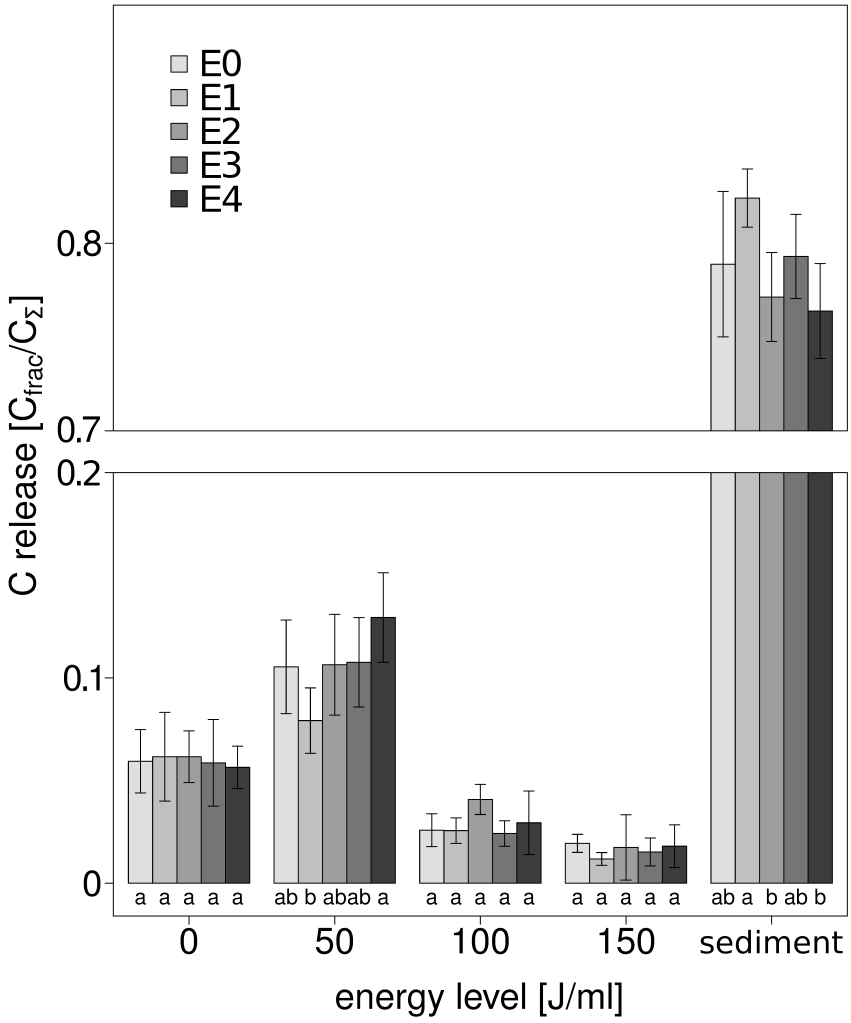

Fig. 2: Relative POM carbon release of treatments (E0, E1, E2, E3, E4) at different energy levels (0, 50, 100, 150 J ml^{-1}, sediment), illustrated by Tukey test characters (a, ab, b). Data are shown as mean values and standard deviations (n=5).

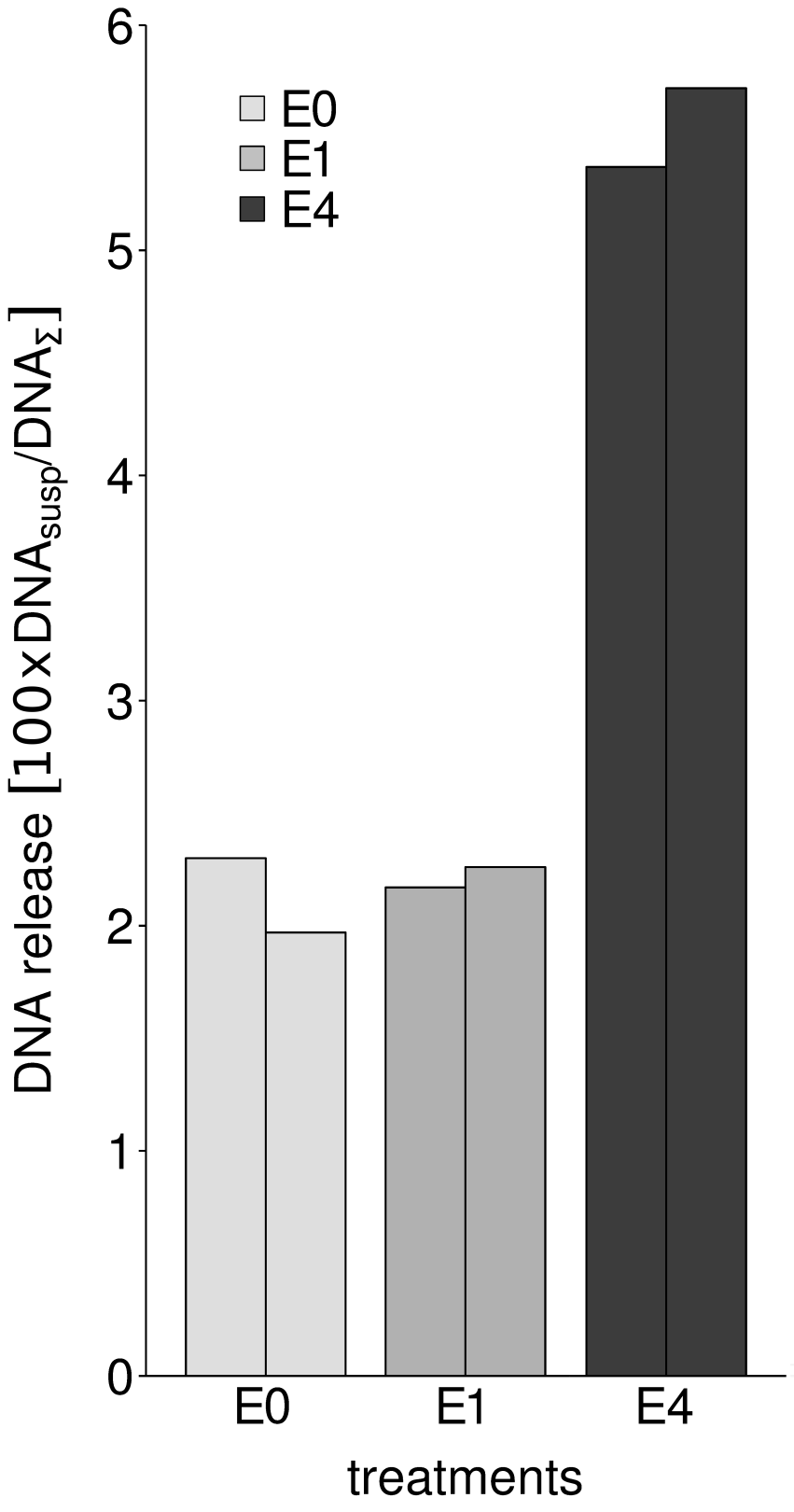

Fig. 3: Relative bacterial DNA release from soil aggregates after treatments E0, E1, and E4 defined as 100x ratio of bacterial DNA from suspended cells (DNA_{susp}) to total bacterial DNA from suspended cells, sessile cells (DNA_{Σ}) and the EPS remaining upon the soil matrix.