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Interactive comment on "Sterol preservation in hypersaline microbial mats" *by* Yan Shen et al.

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This study us a follow-up to two previous papers published on Kiribati hypersaline lake mat ecosystems, published by some of the same authors. While there is no overwhelming consensus from three studies, as to whether steroids are preferentially degraded over other lipid types due to taphonomic bias, the biomarker analyses are of good quality and the overall results are of general interest to organic geochemists and geobiologists.

I have three major comments on this work that I would like the authors to address:

1) Why do the authors assume that the microbial communities, and hence the lipid composition, should be constant over 1500 years of mat growth and burial?

They interpret differences in lipid composition to predominantly taphonomic factors

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. . ..but this is based on an unsubstantiated assumption that eukaryotic contributions to the mat community were fairly constant over depositional history.

The depletion in sterols in deeper layers (in conflict with the results of Shen et al. that showed abundant steroid lipids in all mat layers from another Kirbibati lake) could just as easily indicate a changing mat biological community through time. With higher bacterial contributions to deeper versus shallow layers.

If a "mat-seal" bias was operational and a pervasive diagenetic mechanism for microbial mat remineralization and preservation then why do the results of Shen et al. contradict those found in this investigation?. It seems more likely that the differences in lipid composition represent temporal changes in mat community.

2) Given that Shen et al. could not find kerogen-bound steroids in a previous study using this same Py-GC-MS technique then it becomes suspicious that the pyrolysis method used in not optimized to detect bound steroids in degradation products from "young" mat sediments.

There should be no reason from first principles why bound steroids will not be found given that there is ample proto-kerogen in these mat sediments (given that sequestration will begin very early during diagenesis, see point 3 below)..

This might be due to high baselines in the ion chromatograms that they are searching for steranes and sterenes. Another reason is that Py-GC-MS will produce a complex mixture of unsaturated steroids and sterols bound within polar moieties after bond cleavage, with no good hydrogen donor in the system to cleave these out as steranes.

The authors could perhaps estimate what their detection limit is for detecting kerogen-bound steroids, giving the analytical complexities?

3) I refer the authors to a recent study by Lee et al. (2019) OG, which has only just appeared., in print that showed evidence for early diagenetic incorporation of biomarker lipids by covalent binding into benthic mat sediments from a salt pond Guerrero Negro,

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Mexico . They used sequential chemolysis and HyPy degradation on extracted microbial mat sediments and found evidence for early diagenetic incorporation of a variety of linear, branched and polycyclic lipid skeletons into proto-kerogen on a timescale of only years to decades. The lipids includes bound hopanoids and bound steroids.

So, this supports the idea that HyPy is an effective method for trying to detect bound steroids in mat proto-kerogen due to the I) high sample capacity and ii) use of reducing conditions that yields appreciable steranes and sterene products. It further supports the idea as described in 2) that the Py-GC-MS method used in this investigation is maybe problematic for detecting immature bound steroids from proto-kerogen.

It is surprising since this group has their own HyPy equipment that they choose an online Py-GC-MS method to try and detect kerogen-bound steroids.

The amount of high mw and polar material in pyrolysates from "young" mat sediments. will be appreciable so it is best to choose a method that generates a substantial portion of bound steroids as hydrocarbon products. Even with HyPy, the "polar" fraction dominates the pyrolysate products so this problem will be even more acute with Py-GC-MS performed with an inert gas (rather than high pressure hydrogen and a catalyst as used in HyPy).

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