

Interactive comment on “Identification of new microbial functional standards for soil quality assessment” by Sören Thiele-Bruhn et al.

Robert Griffith (Referee)

rig@ceh.ac.uk

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This paper discusses new methodologies and opportunities offered by molecular methodologies to provide microbiological indicators for assessing soil quality. In essence, it reports on key issues raised during recent discussions within the International Organization for Standardization (ISO), and identifies the need to focus on soil functions of relevance to ecosystem services as recognised for example in the Millennium Ecosystem Assessment. A key focus of the paper is in highlighting and scoring the potential of qPCR approaches for quantifying functional gene abundances of relevance to providing simple metrics relevant for quantification of biogeochemical fluxes (which are difficult to quantify directly).

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The paper is generally well written, interesting, and delivers on synthesising the current broad status with respect to these issues, and additionally proposes some potentially new indicator approaches which could be implemented. As such, I feel it makes a useful contribution. The paper could be improved by offering more critical analyses of the approaches; as well as authoritatively defining the new science needed to facilitate the implementation of more robust soil microbiological indicators.

Three areas which could be elaborated on further I feel are highlighted below. Perhaps fully covering them in detail extends beyond the remit of this manuscript, so I leave it to the editor to decide whether they should be expanded upon in the article (alternatively I guess these publically viewable comments may constitute a contribution to the “discussion” format of the journal. ...).

1. Indicator targets within the global soil geographic context. The paper briefly mentions this on line 365 (“methods need to be implemented into a framework, which takes into account site-specific conditions”), but offers no specific ways forward for this critical issue. Are elevated abundances of a functional indicator always “desirable”, and how might indicator target values, and indeed the indicators themselves differ for different soil systems? I’m not sure if we even have a good soil classification system or framework that allows us to set regionalised targets for the simple variable of soil carbon, and I sense this is what causes pushback on soil targets from industry and policymakers. Given this, could proposing even more microbiological variables be deemed somewhat premature?

2. Relatedly, what is the evidence that gene abundance relates to functions of relevance to ecosystem services? It is often stated that you cannot infer anything about processes from gene abundance alone, but I feel there is little literature actually specifically addressing this with robust contrasts within an ES indicator context. For example comparative data for ammonia oxidation gene abundances does actually appear to relate to nitrification rates in certain studies, so do we need a critical meta-analyses of this now for a variety of indicators? Again, relating to the point above, do we always

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want high nitrification, high litter decomposition, high enzyme activity etc in all soil systems; and is there any evidence that molecular detection of elevated pathogens reliably informs on plant health...Essentially what do these measures really tell us about desirable ES outcomes, and if there is little information available, then what can be done to progress?

3. Standardisation: essential for policy, but bad for science? Given the paper's policy focus, it appears to heavily endorse standardisation. However molecular ecology is a rapidly growing field, and technologies change (eg sequencing platforms) which causes issues with implementing standardised protocols. Scientific developments must be free to progress in order to develop the deep and often complex understanding of processes required to implement meaningful process indicators. It would be useful to highlight this potentially conflicting issue. . .

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