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Interactive comment on "Compound-specific ^{15}N stable isotope probing of N assimilation by the soil microbial biomass: a new methodological paradigm in soil N cycling" *by* A. F. Charteris et al.

Anonymous Referee #2

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A compelling premise and promising application for looking at microbial metabolism. However, I think the importance of this paper is overstated at almost every turn. As far as I know, compound-specific measurements of amino-acid d15N aren't new. I think that there is some information missing, particularly relating to the calculation of assimilated N. Fixing these issues will make the paper much stronger in my opinion. I also have a few minor comments on missing details and style. Comments are below.

Introduction: Using quotation marks implies imprecise language and this is a scientific paper. Please avoid using words in quotation marks.

Page 1138, Line 28: The term total hydrolysable AA pool is not defined here. As far as

I know, this is not a commonly used term and should be defined here.

Page 1139, Line 24: How long were soil samples stored before freeze-drying?

Page 1139-1140: It is not clear what the final enrichment of the inorganic and total N pools were for each of the three treatments (NH4, NO3, and Glu-N). Having these data, as well as initial concentrations of NH4, NO3, and AA in the samples prior to treatment, will make it more clear that these are tracer additions of labeled N.

Page 1141: What was the sample size for combustion analysis? A range would be fine.

Equation 6: Looks like this assumes 100% conservation of the label? Since you have %TN and d15N, you should be able to calculate a %recovery of the label. I think this is an important piece of information missing from this manuscript.

Page 1145: Any explanation why, if this is a tracer addition, there is twice as much THAA in the 15N-Glu treatment compared to the inorganic N treatments? Is that all due to the added Glu? If this point is addressed and I missed it, my apologies. Otherwise, it needs to be addressed.

Page 1147: Regarding Figure 3, you need to address how this may not simply be due to differences in label recovery between treatments. What was the %recovery in each treatment? Addressing this will make your conclusions that much stronger.

Discussion: You have a chance in this paper to compare/contrast this method with other methods, namely 15N in total microbial biomass N. If this truly is to be a new paradigm, you must put it in context with the old one.

Interactive comment on SOIL Discuss., 2, 1135, 2015.