

Dear authors,

thanks for preparing a revised version of your manuscript addressing reviewers' comments. The new version addresses these comments well, but there still remains a few places where grammar still needs to be improved. I marked in the attached document places where grammar should be revised.

More importantly, I encountered a problem in the interpretation of the correlations of the posterior parameter values. These correlations are an indication of problems of poor-identifiability of the model with respect to the available information for parameterization. I discuss this problem in a previous paper (Sierra et al. 2015, <https://doi.org/10.1016/j.soilbio.2015.08.012>). Please see the references I mention in this publication where the problem is discussed in more detail, and make changes to the interpretation of your correlations. You interpret them as complex connections among process, but this interpretation is wrong. Fortunately, your correlations are not so high, so the identifiability problem is not severe, but the issue needs to be discussed nevertheless.

Reply:

Sorry for the grammar issues and they are now revised. Also thanks for pointing out the parameter correlation issue. We believe this is not a unique characteristic of present model or present data used in our study, but instead rather a general phenomenon for detailed process-based modeling studies. We therefore have removed the previous wrong interpretation and added a revised discussion in section 4.2 to address this better. As following:

“Most of our constrained parameter distributions are not sharply peaked, but instead rather flat and few parameters show high covariance (Fig. 6, Fig. 7, Fig. 8 and Fig. 9). This is, however not a unique characteristic of the CoupModel or current used data constraints and indeed, has been previously demonstrated in numerous studies with ecosystem models of similar complexity (e.g., He et al., 2016; Klemetsson et al., 2008; Wang et al., 2001). This on one hand, generally reflects the equifinality of models (Beven, 2006), where multiple parameter sets can lead to equally well representations of the system. On the other hand, it also indicates poor identifiability of the calibrated parameters with respect to the available information for parameterization. Here, we again show that given the same data constraints, the parameter identifiability decrease with increasing model complexity (Sierra et al., 2015). In our study, the correlation between the humus decomposition coefficient, K_H and the fraction of C that is allocated to the rooting zone, F_{ROOT} , is smaller when ECM are modeled explicitly than implicitly (Fig. 9). However, the correlations between the ECM fungal litter rate and ECM fungal N uptake rates, and that between fungal N uptake rates, $NORG_{RATE}$ and the microbial C/N ratio, CN_{MIC} (Fig. 9) further indicate these ECM fungal parameters in the more complex “explicit” model cannot be well identified without adding new dataset as additional constraints. One of the major challenges of explicitly including ECM in ecosystem models is the still sparse information about ECM, e.g., unknown turnover of ECM mycelia (Ekblad et al., 2013). Previously reported turnover rates of newly formed mycelia vary from days to weeks, even up to 10 years (Staddon et al., 2003; Wallander et al., 2004), mostly due to the high variability in ECM species and structures (see review by Ekblad et al., 2013). Additionally, root turnover rates can also vary considerably between species, soils, and climate zones (Brunner et al., 2012). Thus far, very few studies have reported parameterization of C and N cycling for ECM in boreal forests. The present model calibration thus provides a key set of ECM parameters that can be further tested by field observations, and more importantly, can act as a prior for future ECM modeling studies.”