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Microbial dormancy under freeze-thaw cycling regulates soil biogeochemical responses in alpine meadows

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Predicting cold ecosystem responses is crucial for global climate modeling as climate warming drives profound changes in soil biogeochemical processes. However, large uncertainties in model predictions persist, partially owing to the lack of explicit representation of microbial responses to climate warming in permafrost and seasonally frozen ground. Here, we incorporate the freeze-thaw dynamics and associated microbial adaptation strategy into the Microbial-ENzyme Decomposition (MEND) model. Using a field warming experiment in an alpine meadow with seasonally frozen ground on the Qinghai-Tibetan Plateau (QTP), we calibrated and validated the new MEND model with diverse measurements, including soil carbon (C) and nitrogen (N) fluxes, microbial stoichiometry, and enzyme kinetics. In addition to accurately simulating soil respiration and inorganic N, the model correctly predicted the warming effects on microbial carbon use efficiency (CUE) and enzyme activities. Our findings highlight the importance of microbial dormancy as survival strategies under repeated freeze-thaw stress. We also observed potential regulation of freeze-thaw processes on soil N availability, while long-term projections revealed a substantial reduction in inorganic N, suggesting intensified competition between microbial and plant N uptake under warming. This experiment-model integration framework offers improved predictive capacity for soil biogeochemical feedbacks in cold ecosystems, contributing to more accurate global climate models.