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Longitudinal Gradients in Tree Stem Greenhouse Gas Concentrations Across Six Pacific Northwest

August 2020

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U.S. DEPARTMENT OF ENERGY

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This report describes one study that was completed as part of the project titled "*A critical gap in our ability to quantify and model earth system interactions—Development of a global, mechanistic understanding of methane emissions from trees.*"

Greenhouse gases undergo continuous cycling between the atmosphere and ecosystems due to a wide variety of biological and non-biological processes. While terrestrial plants are well known for their ability to remove carbon dioxide from the atmosphere to perform photosynthesis, they can also play a role in moving other gases from soils to the atmosphere. This study investigates the abundance of the major greenhouse gases—carbon dioxide (CO_2), methane (CH_4), and nitrous oxide (N_2O)—within the trunks of live and dead trees in coastal forests around the Pacific Northwest. We found that carbon dioxide was in high abundance in the tree trunks due to tree physiology, while methane was almost always above atmospheric levels within the tree trunks likely as a result of transport from soil porewaters. Tree trunk methane levels decreased towards the river mouth—where it meets the ocean—as water in the soil had higher salt content that limits methane production. Patterns in nitrous oxide levels were less clear than the other greenhouse gases.

Results from this study build upon a recently growing body of work examining how trees influence greenhouse gas cycles beyond carbon dioxide. Greenhouse gas emissions from herbaceous plants have been extensively studied in wetlands, and tree stems have long been known to contain elevated concentrations of GHGs, particularly carbon dioxide (CO_2). However, it is only in recent years that emissions of major GHGs beyond CO_2—i.e., CH_4 and N_2O—from tree stems have been recognized as a potentially significant component of global GHG budgets. There are two proposed sources for GHGs found within and emitted from tree stems: 1) production of GHG within the tree through microbial or plant physiological pathways (i.e., autochthonous), and 2) the transport of soil-produced GHG through roots to the tree stem (i.e., allochthonous). While the flux of CO_2 from tree stems is well documented in the context of measuring respiration rates, where and when these sources of CH_4 and N_2O dominate remain largely unresolved.

Though many studies have documented tree stem emissions, most are relatively limited in tree type (e.g. single species, living or dead trees only), geographic area, sample size, and type of GHG measured. The extent of tree emissions across ecosystems is still a fundamental question, and, as such, examining a broad range of tree species across different regions and ecosystem types is crucial. Measuring multiple GHGs further facilitates a comparison of their different possible sources. Tree stem flux measurements are inherently variable, similar to direct flux measurements from soils and surface waters, due to both analytical techniques and high spatiotemporal variability. As such, linking fluxes to the GHG pathways described above has been a large challenge.

Examining tree stem GHG concentrations rather than fluxes may remove at least one layer of complexity (i.e., gas diffusivity for a given stem) that will allow a closer examination of the mechanisms driving GHG emissions and distribution across spatial gradients. While the instantaneous relationship between stem concentration and emissions is not well established, there is some evidence that concentrations and emissions are correlated over larger spatial and temporal scales and other studies have modeled emissions based on concentration data. Focusing on concentrations instead of fluxes in this study allowed us to conduct a much larger sample size—an order of magnitude higher than most other tree GHG studies—across an entire region to provide insight into spatial variability. In this study, we therefore set out to conduct a broad regional survey of tree stem GHG concentrations in the temperate Pacific Northwest, a

region not covered in current tree stem GHG literature. Live and standing dead trees of five species common to the region were sampled for dominant CO_2, CH_4, and N_2O). At each coastal forest site (Figure 1), canopy-dominant tree species were sampled along a longitudinal river gradient ranging from upstream reaches without salinity intrusion into soils and near the river's mouth where salinity was detected in soil pore water samples. These are the second measurements of tree stem GHGs in saline environments, and the first in a temperate system, to our knowledge. In addition to establishing a broad regional survey of species and sites in the Pacific Northwest, we also assessed how tree stem GHG concentrations varied by tree characteristics (e.g. diameter, basal area increment, age, health status, taxonomic group [angiosperm vs gymnosperm]), site characteristics (e.g. porewater GHG concentrations, soil salinity), and season (summer/winter).

In total, 246 trees (122 in the winter and 124 in the summer) were sampled across the six sites.. There was a high degree of variability in tree stem gas concentrations among trees. However, pCO_2 consistently far exceeded atmospheric concentrations across all sampling sites. pCO_2 concentrations averaged 20,230 ± 1,562 ppm—approximately 50x atmospheric concentration—but ranged from 1,625 to 302,000 ppm throughout the entire study domain. All sites sampled additionally had above atmospheric concentrations of pCH_4, though it was more variable than for pCO_2. pCH_4 was on average 28x atmospheric concentration (53.5 ± 11.1 ppm), with tree stem CH_4 concentrations ranging from 1.66 to 1,735 ppm. pN_2O was slightly below atmospheric concentration on average (0.299 ± 0.024 ppm), ranging from 0.02 to 5.26 ppm. This maximal N_2O value is equivalent to ~15x atmospheric concentration. There was no significant correlation ($p<0.05$) between CO_2-CH_4, CO_2-N_2O, nor CH_4-N_2O. Soil porewater salinity varied, as expected, between brackish and fresh plots at sites. Soil porewater salinity at fresh sites was 0 PSU for all rivers, and salinity at brackish sites averaged 8.3 ± 1.5 PSU, though porewater at some mouth sites reached up to 24.3 PSU. CH_4 concentrations in stems of live trees varied by location along each river gradient, i.e., at the mouth of the river compared to upstream of the head of tides and/or saline soil porewaters. CH_4 was higher in live trees at fresh plots than in live trees at the brackish plots ($p<0.05$). There was not a significant difference between locations along the river continua for pCO_2 or pN_2O ($p>0.05$).

Overall, our results indicate a linkage between soil porewater and tree stem pCH_4 along coastal gradients, whereas tree stem pCO_2 was linked more closely to tree characteristics, and drivers of tree stem pN_2O were unclear. Measurements of tree stem GHGs across broad spatial and temporal scales—including along gradients in hydrological conditions and soil porewater chemistry—will facilitate a clearer understanding of the mechanisms involved in tree stem GHG fluxes and enable more precise considerations of the role of tree stem greenhouse gas fluxes in ecosystem models. Future studies should focus on developing a clearer understanding of the drivers of variability across trees and ecosystem types. Quantification of related processes will underpin new conceptual and predictive models of C and N exchange and transformation through water, soil, plant, and atmosphere at all scales.

As a follow on to this study, we performed a similar round of sampling campaigns on the East coast, where we found a linkage between O_2 and CH_4 levels within the tree stem and soils (Norwood et al., in review). We also found that genomic markers for methanogenesis and methanotrophy both correlate with stem CH_4 emissions in temperate hardwood forests, providing quantitative evidence of internal CH_4 production in some trees (Brewer et al., in prep).

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