

[Home](#) > [ETDS](#) > [DISSERTATIONS](#) > [AAI3518252](#)

Off-campus UMass Amherst users: To download dissertations, please use the following link to [log into our proxy server](#) with your UMass Amherst user name and password.

Non-UMass Amherst users, please click the view more button below to purchase a copy of this dissertation from Proquest.

(Some titles may also be available free of charge in our [Open Access Dissertation Collection](#), so please check there first.)

---

## Universidade de Sao Paulo Centro de Energia Nuclear na Agricultura: Soil microbiota related to carbon, nitrogen and greenhouse gas cycles across different land uses in Southwestern Amazonia

---

[View More](#)

[SHARE](#)

---

[Daniel Renato Lammel, University of Massachusetts - Amherst](#)

---

### Abstract

Sustainability is one of the biggest goals of humankind in the new millennium. An increasing global demand on agricultural products stimulates agricultural expansion in Brazil, especially in the Southwestern Amazon, namely in the Cerrado and Amazon biomes. A better understanding of biogeochemical cycles and their influence on natural and agricultural systems is key to achieve environmental sustainability and improve agricultural efficiency. These biogeochemical cycles are driven by microbes, and the aim of this thesis was to correlate microbial functional group abundances with differences in carbon, nitrogen, and greenhouse gas cycles in response to land use changes in Southwestern Amazon soils. This work was performed at the University of São Paulo, Brazil, and at the University of Massachusetts Amherst, USA, while the candidate was enrolled in Ph.D. programs at both universities. The thesis is composed of five studies. The first study shows that land use change from Cerrado and forest to agriculture (soybean, *Glycine max* (L. Merrill), in succession with other crops) or pasture (*Brachiaria brizantha* (Hochst. ex A. Rich.) did not reduce soil microbial diversity but changed microbial structure. The second study, a physico-chemical background for this land use conversion, describes the alteration of C and N stocks, soil chemical parameters, and microbiological parameters such as biomass, biological C stocks, and changes in the abundance of prokaryotes and fungi. In the third and fourth studies microcosm experiments depict how the agricultural change to soybean and *Brachiaria* alter the original microbial structure found in forest or cerrado. These studies focused on abundances of key biogeochemical genes (*amoA*, *nirK*, *nirS*, *norB*, *nosZ*, *mcrA*, and *pmoA*) and

Enter search terms:

  

[Notify me via email or RSS](#)

---

[Browse](#)

[Collections](#)

[Disciplines](#)

[Authors](#)

---

[Author Corner](#)

[For Authors](#)

[Author FAQ](#)

---

[Links](#)

[UMass Amherst Libraries](#)

[UMass Amherst](#)

[Contact Us](#)

correlated gene copy abundances with C, N, and GHG measurements. In the fifth study, *in situ* soil surveys and GHG samplings were used to characterize the changes from forest to pasture (*B. brizantha*, 25 years) or soybean crop system (for 2 years or 25 years in succession). We found correlations between genes and processes, indicating that gene abundances provide important microbial information for the understanding of the targeted biogeochemical cycles. Land use, rather than plant species, promotes alterations in microbial gene abundances and processes. During the survey period, forest exhibited higher microbial activity, resulting in higher nitrate availability and N<sub>2</sub>O emissions. These processes were correlated with higher abundances of process related genes. Nitrate and N<sub>2</sub>O emissions were lower in agricultural and pasture soils. CO<sub>2</sub> emission was higher in the two-year-old soybean plot. The forest and two-year-old soybean plots acted as a sink for CH<sub>4</sub>, while the pasture plots represented a source of it. The results validated the use of gene abundance determination as a valuable tool to better understand C, N, and GHG processes. The genes *nirK*, *nosZ*, and 16S rRNA presented the best correlations with the processes. A larger temporal and spatial analysis is needed to infer statements on the processes' dynamics due to land use change. For the first time gene abundance measurements were used to integrate the C, N and GHG cycles, giving insights into land use changes in Southwestern Amazon. ^

## Subject Area

Biology, Microbiology|Biogeochemistry

## Recommended Citation

Daniel Renato Lammel, "Universidade de Sao Paulo Centro de Energia Nuclear na Agricultura: Soil microbiota related to carbon, nitrogen and greenhouse gas cycles across different land uses in Southwestern Amazonia" (January 1, 2012). *Doctoral Dissertations Available from Proquest*. Paper AAI3518252.  
<http://scholarworks.umass.edu/dissertations/AAI3518252>

This page is sponsored by the [University Libraries](#).

© 2009 [University of Massachusetts Amherst](#) • [Site Policies](#)