



Quantification of 16S gene and its relation with the CO₂ emission and soil properties in areas under management of sugarcane (*Saccharum* spp.)

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A diversity of microorganisms has an essential role in the recycling of soil chemical elements, controlling, for example, the dynamics of carbon decomposition and stabilization, and consequently the patterns of soil CO₂ emission. In this sense, the objectives of this study were: (i) to estimate and compare the genetic diversity of microorganisms in soils under different sugarcane (*Saccharum* spp.) managements using molecular techniques based on metagenomic studies, and (ii) investigate the relationship of soil CO₂ emission (FCO₂) with microbiological results and soil chemical and physical properties in the evaluated managements. This study was conducted in agricultural areas located in southern Brazil, in which the following sugarcane managements were used: green and burned residues management, a sugarcane area under reform, and a native forest (used as a reference of the original soil condition). FCO₂, soil temperature, and soil moisture were measured over 10 days, and at the end of the measurements soil samples were taken in order to determine the physical and chemical soil properties. The determination of the diversity of soil microorganisms was carried out by means of molecular techniques based on 16S rRNA gene sequencing. The highest mean value for FCO₂ ($3.25 \mu\text{mol m}^{-2}\text{s}^{-1}$) was observed in the sugarcane area under reform, and the lowest values (1.85 and $1.27 \mu\text{mol m}^{-2}\text{s}^{-1}$) were observed respectively in the green residue management and native forest areas. This same pattern was also observed when the 16S gene was quantified. In this case, the largest number of copies of this gene was found in the sugarcane area under reform (4.3×10^{10} copies of 16S rRNA gene per gram of dry soil), and its smallest number of copies was found in the green residues management area (1.7×10^{10} copies of 16S rRNA gene per gram of dry soil). The largest number of copies of the 16S gene associated to the highest values of FCO₂, both observed in the sugarcane area under reform, could be related to the biomass and microbial activity increasing, which are directly related to a good soil fertility conditions and agricultural practices (liming and harrowing), such as the area under reform evaluated in this study. This fact was confirmed by the positive correlation ($r = 0.98$; $p < 0.0001$) observed between FCO₂ and the number of copies of the 16S gene. FCO₂ was also related to the soil moisture ($r = -0.22$; $p < 0.05$) in the area of green residue management, and to the soil temperature ($r = 0.28$; $p < 0.05$), bulk density ($r = -0.48$; $p < 0.05$), micropores ($r = 0.21$; $p < 0.05$) and air-filled pore space ($r = 0.60$; $p < 0.0001$) in the sugarcane area under reform, indicating that FCO₂ is related to the amount of microorganisms advantaged by the soil chemical conditions, as well as its physical properties (higher aeration).