Tropentag, September 16-18, 2015, Berlin, Germany

"Management of land use systems for enhanced food security: conflicts, controversies and resolutions"

Evaluation of Biological Nitrification Inhibition (BNI) Capacity in a Biparental Mapping Population of *Brachiaria humidicola*

Jonathan Núñez[1], Ashly Arevalo[1], Danilo Moreta[1], Hannes Karwat[2], Manabu Ishitani[1], John Miles[1], Guntur Subbarao[3], Margaret Worthington[1], Georg Cadisch[2], Idupulapati Rao[1], Jacobo Arango[1]

[1] *International Center for Tropical Agriculture (CIAT), Colombia*

[2] *University of Hohenheim, Inst. of Plant Production and Agroecology in the Tropics and Subtropics, Germany*

[3] *Japan International Research Center for Agricultural Sciences (JIRCAS), Japan*

Abstract

Soil nitrogen (N) loss due to rapid nitrification (oxidation of ammonium to nitrate) is a serious problem with economic and environmental implications. As a result, a large proportion of N fertilisers applied to crops are lost to the environment via nitrate leaching and nitrous oxide emissions. The tropical pasture grass *Brachiaria humidicola* (Bh) exudes organic molecules from roots that inhibit the soil nitrification process. This ability, termed biological nitrification inhibition (BNI), has great potential for restoration of soil fertility, reduction of nitrogen pollution from agriculture, and improvement of nitrogen use efficiency. In the present study, three methodologies were standardised to quantify the intrinsic BNI-potential of plant genotypes. Specifically, BNI-potential was measured in 121 hybrid progeny of a bi-parental population constructed from a cross between Bh germplasm accessions of CIAT 26146 $\times$ CIAT 16888, differing in BNI-potential (medium-high and high, respectively). Root extracts from each hybrid were evaluated for intrinsic BNI-potential using a bioluminescence assay that uses a recombinant Nitrosomonas europaea. The soil incubation method was also employed to measure nitrification rates in soil samples collected from pots where the Bh hybrids were grown for a year. These results were further validated by quantifying nitrifying microorganisms using qPCR, using the amoA gene as a functional marker. We identified groups of Bh hybrids with contrasting BNI-potential based on differences observed in the bioassay, nitrification rates and nitrifier population size. The capacity for BNI in mapping population was normally distributed indicating that the trait is quantitatively inherited. Quantitative trait loci (QTL) mapping resulted in identification of minor QTLs that are associated with BNI capacity. Results from this study indicated that using three different phenotyping methods it is possible to identify promising Bh hybrids to assist the on-going *Brachiaria* breeding efforts. This study also contributed towards establishing correlations among BNI capacity in roots, soil nitrification rates and the amount of nitrifying microorganisms present in the soil.

Keywords: Bioassay, biological nitrification inhibition (BNI), *Brachiaria*, nitrification, nitrogen, phenotyping, QPCR, QTL

Contact Address: Jacobo Arango, International Center for Tropical Agriculture (CIAT), Tropical Forages, A A 6713 Cali, Colombia, NA Cali, Colombia, e-mail: j.arango@cgiar.org