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# Soil physicochemical properties impact more strongly on bacteria and fungi than conversion of grassland to oil palm



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### S.A. Wakelin<sup>a,\*</sup>, E. Gerard<sup>a</sup>, C. van Koten<sup>a</sup>, M. Banabas<sup>b</sup>, M. O'Callaghan<sup>a</sup>, P.N. Nelson<sup>c</sup>

<sup>a</sup> AgResearch Ltd, Lincoln Science Centre, Cnr Springs Road and Gerald Street, Private Bag 4749, Christchurch 8140, New Zealand <sup>b</sup> Papua New Guinea Oil Palm Research Association, Kimbe, West New Britain, Papua New Guinea

<sup>c</sup> College of Science, Technology and Engineering, James Cook University, Cairns, Australia

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#### ABSTRACT

The conversion of grassland to oil palm is expected to increase throughout tropical regions where oil palm grows. Given the extent of land use change, there are concerns associated with impacts on ecosystem function and nutrient cycling. For this work, soil samples were collected in Papua New Guinea from 15 sites with oil palm (planted on grassland) and adjacent remnant grassland. Using DNA-based approaches, bacterial and fungal community composition was assessed in each sample, along with abundance of genes involved in key nitrogen cycling steps: nitrification (bacterial and archaeal *amoA* genes), nitrite reduction (*nirS* gene), and nitrous oxide reduction (*nosZ* gene). Across all microbial properties measured, variation among sites was greater than variation due to land use change. This was driven by among-site variation in soil physicochemical properties, particularly total soil organic carbon content and  $\delta^{13}$ C, electrical conductivity, exchangeable calcium, potassium and magnesium content, and extractable phosphorus content. The results suggest that in this environment, routinely measured soil properties such as soil pH, organic carbon, and exchangeable cation contents may serve as indicators for the effects of land use and management on soil microbial community composition and functioning.

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#### 1. Introduction

Oil palm (Elaeis guineensis Jacq.) is cultivated on more than 17 million ha worldwide (2012 data, FAOSTAT, 2015), and the area is expected to expand until at least 2050 to meet growing demand for palm oil (Corley, 2009). The industry has been expanding at  $610,000 \text{ ha y}^{-1}$  over the last decade (FAOSTAT, 2015), replacing forest, woodland, savannah, and other crops (Gibbs et al., 2010; Carlson et al., 2012). This changing land use poses threats to biodiversity and ecosystem services, particularly where biodiverse and carbon-rich ecosystems such as rainforest are replaced (Tilman et al., 2001; Green et al., 2005; Koh and Wilcove, 2007; Fitzherbert et al., 2008; Turner et al., 2008). Thus grasslands and savannas, which are extensive in the tropics, are seen as desirable locations for future expansion of the oil palm industry (Corley, 2009; Chase and Henson, 2010; Wicke et al., 2011). In the coming decades, large areas of grassland and savanna throughout the tropics are expected to be converted to agriculture (Romero-Ruiz et al., 2012; Castiblanco et al., 2013; Lavelle et al., 2014). Grasslands tend to have high soil organic matter contents and biological

\* Corresponding author. E-mail address: steve.wakelin@agresearch.co.nz (S.A. Wakelin).

http://dx.doi.org/10.1016/j.pedobi.2016.03.001 0031-4056/© 2016 Elsevier GmbH. All rights reserved. activity than other forms of agriculture (Guo and Gifford, 2002; Chen et al., 2010; Murugan et al., 2014), but the effects on soil biology following converting tropical grassland to oil palm have not been assessed.

The diversity and functioning of soil organisms have central roles in ecological processes such as carbon and nutrient cycling and supporting above-ground diversity (Coleman and Whitman, 2005: Roper and Gupta, 1995: Wardle et al., 2004: van der Heijden et al., 2008). Considerable recent research on soil biology under oil palm has focussed on soil fauna (Lavelle et al., 2014; Carron et al., 2015a,b and references therein) and ecology of pathogenic organisms (Sariah et al., 2005; Cooper, 2011), but there have been few studies of soil microbial communities. In the work that has been done, soil microbial diversity and activity have generally been found to be similar under oil palm and forest (Adachi et al., 2006; Lee-Cruz et al., 2013; Nurulita et al., 2015), with most of the variability driven by organic matter inputs or soil organic C (SOC) contents, and soil water (Adachi et al., 2006; Melling et al., 2013). Furthermore, in a recent study by Hamilton et al. (2016), the conversion of forest to oil palm was associated with alteration of the soil N cycle, primarily via decreased nitrification, impacting on N<sub>2</sub> production. These N-cycle disruptions are likely to be closely coupled with shifts in the functional ecology of the soil microbial community.

Within oil palm plantations, soil microbial biomass, activity, and diversity also increase with SOC content, being greatest under the frond pile (the part of the plantation with highest organic matter inputs) and increasing with plantation age or when organic amendments are applied (Lamade et al., 1996; Haron et al., 1998; Situmorang et al., 2014). Soil microbial diversity and activity in tropical grasslands is also related to SOC content, as well as the content of N, P and nutrient cations (Devi et al., 2014; Waring et al., 2014; Lisboa et al., 2014). Grassland and savanna tend to have lower SOC, microbial biomass, microbial activity, and diversity of mycorrhizae than forests (Öpik et al., 2006; Singh et al., 2010; Eaton and Chassot, 2012) and in grasslands those microbial factors are also influenced by grazing intensity and fire (Michelsen et al., 2004; Devi et al., 2014).

Microbial diversity, in the context of structural and compositional shifts among sampled communities, has been used to assess impact of land use change in a wide range of studies (e.g. Bossio et al., 2005; Ding et al., 2013; Suleiman et al., 2013; Lisboa et al., 2014). This information can be assessed against the underlying changes in soil or environmental conditions to determine the primary drivers of change in microbial diversity (Wakelin et al., 2008), and also be used to identify taxa that can be used as indicators for monitoring the impact of land-use change. An associated approach is to characterize changes in the size or composition of components of the microbial community mediating the biogeochemical cycling of major elements (e.g. Wakelin et al., 2013a; Paula et al., 2014). The information gathered from both approaches can provide insights into the capacity of the soil ecosystem to sustain ecosystem processes. In this study, the various abiotic and biotic components of the system are considered together, which considerably strengthens the ability to interpret how land use may influence soil biology either directly (plants and plant inputs as specific drivers of microbial communities) or indirectly (plant-affected or managementinduced changes in soil edaphic properties which then alter microbial communities).



Fig. 1. Locations of the 15 sites in Papua New Guinea from which paired oil palm and grassland samples were taken for soil microbial analysis. Note that sample site 10 was omitted for analysis is this study (absence of grassland land use).

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