Sustainability of intensive rice cropping systems in the tropics from a soil biogeochemical perspective

Wolfgang Reichardt

International Rice Research Institute (IRRI)
Research Center Los Banos
Crop, Soil and Water Sciences Division
MCPP Box 3127, 1271 Makati City, Philippines
Fax: (632)-845 0606
E-mail: W.REICHARDT@CGIAR.ORG

Abstract

In search for potential determinants of sustainable nutrient cycling and supply in tropical rice soils, a set of soil biogeochemical and microbiological analyses was designed to monitor long term field trials in different regions of SE Asia. Considerable pool size changes within and between cropping seasons lend support to a nutrient source and sink model for certain constituents of the soil organic phase. A comparison of an extremely intensive rice cropping system with the extensive traditional Ifugao rice terraces in the Philippines revealed striking differences in the profiles of biogeochemically significant microbial guilds.– Soil microbial analyses offer a decisive advantage in assessing the sustainability of rice soil functions from both an agronomic and an environmental perspective.

Keywords: Rice soil, intensification, sustainability, soil microbiology

Introduction

Both the agroecosystem to be dealt with and the scientific approach applied may lie beyond the mainstream of agricultural research, but they promise to provide a broader foundation for the assessment of sustainability. Nutrient cycling in rice soils is mainly governed by microbial biocatalysts. Yet, so far the key significance of microbial ecology for a mechanistic understanding of soil nutrient supply to the rice crop has attracted only few agronomists. Theoretically, biochemical and microbiological soil analyses have the potential to cover the widest possible scope of research issues ranging from soil nutrient cycling to soil health and ecotoxicology, and, ultimately, from agronomic to environmental sustainability.

Agricultural wetlands in the tropics give examples not only of maximum sustainability over centuries and millennia, but also for extreme intensification with up to three annual crops. Are biogeochemical and microbiological investigations capable of providing new insights into key soil functions of these cropping systems and their sustainability? The two approaches reported here are related to organic nutrient pool dynamics in tropical rice soils, and to diversity shifts in biogeochemical functions of rice soil microbiota.

Study Sites and Methods

Controlled experimental cropping systems have been set up in different regions of tropical Asia to scrutinize regionally favored ways of intensive, yet sustainable soil and crop management. In collaboration with NARS in seven developing countries in S and SE Asia, the International Rice Research Institute (IRRI) in the Philippines has begun to develop basic monitoring programs for long term field experiments in rice soil microbiology. Microbiological and biochemical measures have been elaborated as potential determinants or indicators of tropical rice soil quality and sustainability. These for the most part relatively simple techniques for on-site analyses include: Total soil protein, phospholipid-based soil microbial biomass, total soluble phenolic compounds, respiratory utilization of sole N and C (RUNC) sources (Zak et al., 1994), and enzyme activities of respiratory electron transport systems (ETS). Special off-site laboratory facilities are required for a second set of measures such as radiotracer studies or microbial guild profiles based on either molecular genetics or signature lipid compounds (Reichardt, 1999; Reichardt et al., 2000).

Soil organic nutrient pool dynamics

Declining rice yields in a long-term cropping experiment have been attributed to reduced N use efficiencies (Cassman et al., 1995). These depend on estimates of the indigenous soil N supply (INS). As the bulk of N (>95%) is present in the organic phase of agricultural soils, its

cycling and availability depends largely on biochemical and microbe-dominated processes. In simple nutrient pool models for soil organic nitrogen (Duxbury & Nkambule, 1994) soil microbial biomass ought to play a central role as a dynamic nutrient sink and source (Fig.1). A labile organic N-pool expands as a result of immobilization, and shrinks due to nutrient release that is triggered by processes of remobilization and remineralization (Reichardt et al., 2000).
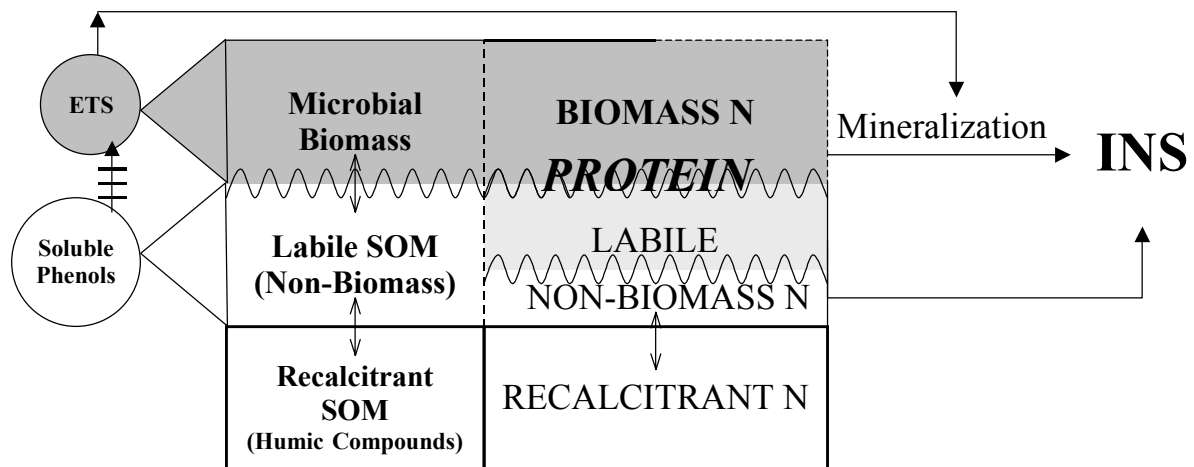

Figure 1. Nutrient Source and Sink – Model based on biocatalytic events in the soil organic matter phase depicting the variable sizes of microbial biomass and soil protein pools, as affected by immobilization and remobilization of N.

Intraseasonal variability of pool sizes has been expressed by coefficients of variance (c.v.) of single measurements of microbial biomass (Wardle et al., 1998). This idea of a linkage between temporal pool size variation and effective nutrient supply was supported by a positive correlation between grain yields and intraseasonal variations of soil microbial biomass in LTCCE plots with optimum N rates (Fig.2).

In LTCCE soil total protein concentrations accounted for 18 – 80% (250 – 1100 kg/ha) of total N. During a monitoring period of three years these concentrations showed considerable and nearly periodic fluctuations (Fig.3). Fertilized plots showed consistently higher protein levels than N omission plots. This indicates a net immobilization of N-fertilizer in the order of 15 to 290 kg/ha of protein-N. Similar to microbial biomass, intraseasonal changes (c.v.) of total soil protein concentrations showed a positive correlation (R= 0.78) with grain yields for a total of eight

cropping seasons on the LTCCE at Los Banos (Fig.4). A similar
relationship was noted for different treatments in a double annual rice
cropping system with crop residue re-incorporation at CLRRI, Omon,
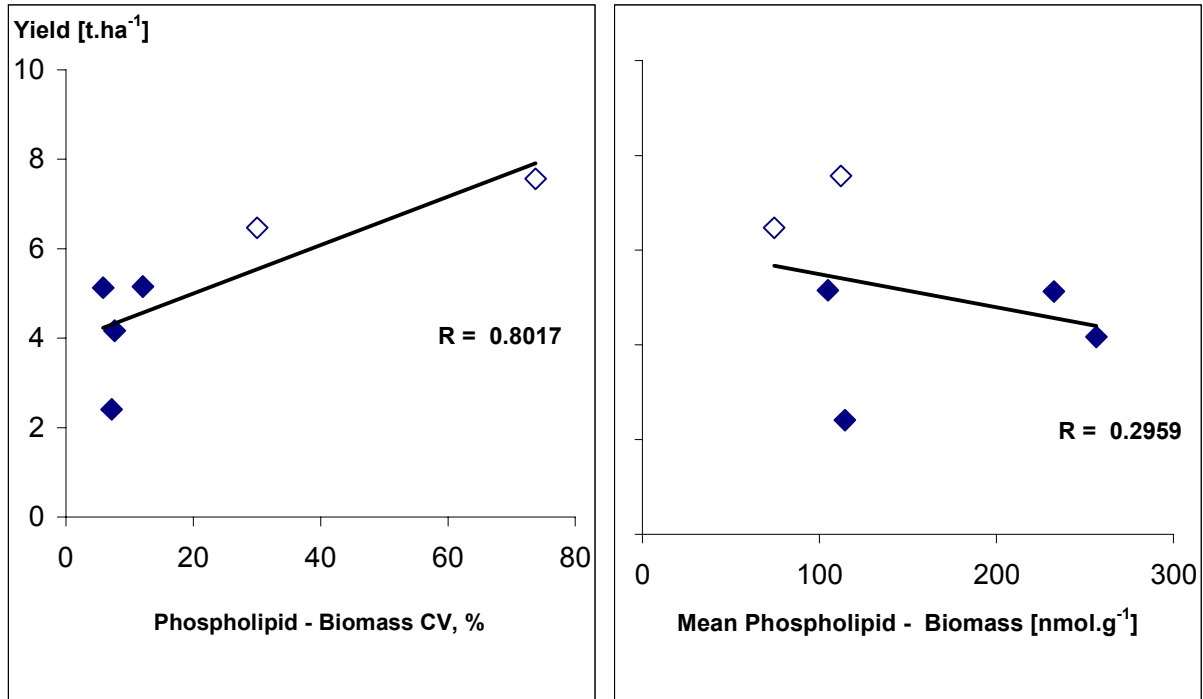Vietnam (Fig.5).

Figure 2. Long term continuous cropping experiment at IRRI: Grain Yields vs PL-based microbial biomass and
intraseasonal variation of the latter, expressed by coefficients of variance (%) (Reichardt et al 2000, in press)
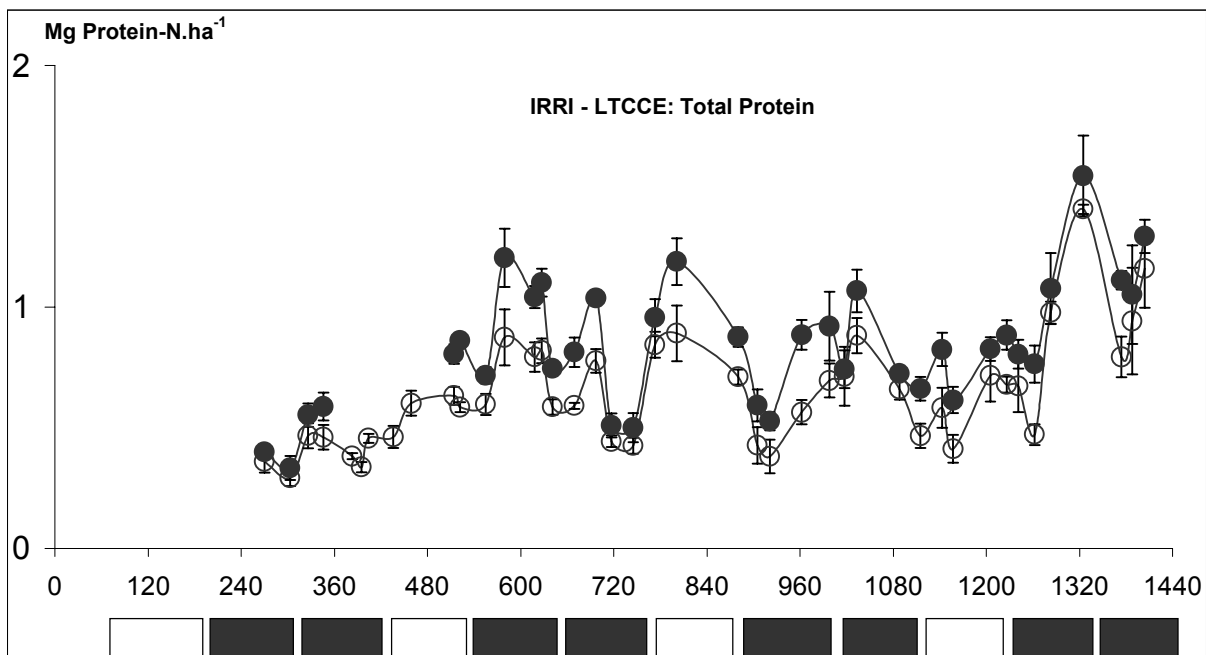

Figure 3. Long Term continuous cropping experiment at IRRI: Total soil protein concentrations in long-term-continuous
cropping experiment at optimum N-rate (●)and at N-omission plots (0) . Dark boxes indicate wet season, light boxes indicate
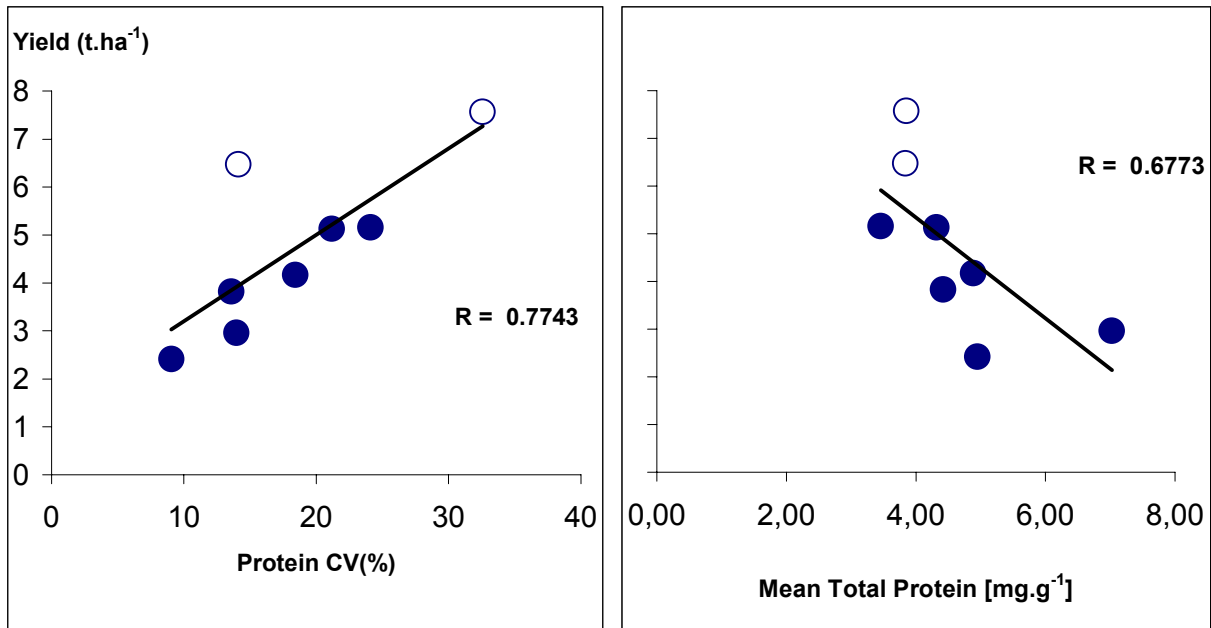dry season. (Reichardt et al 2000, in press)

Figure 4. Long term continuous cropping experiment at IRRI: Grain yield vs total soil protein concentrations and intraseasonal variations of the latter expressed as coefficient of variance (CV, %) (Reichardt et al 2000, in press)
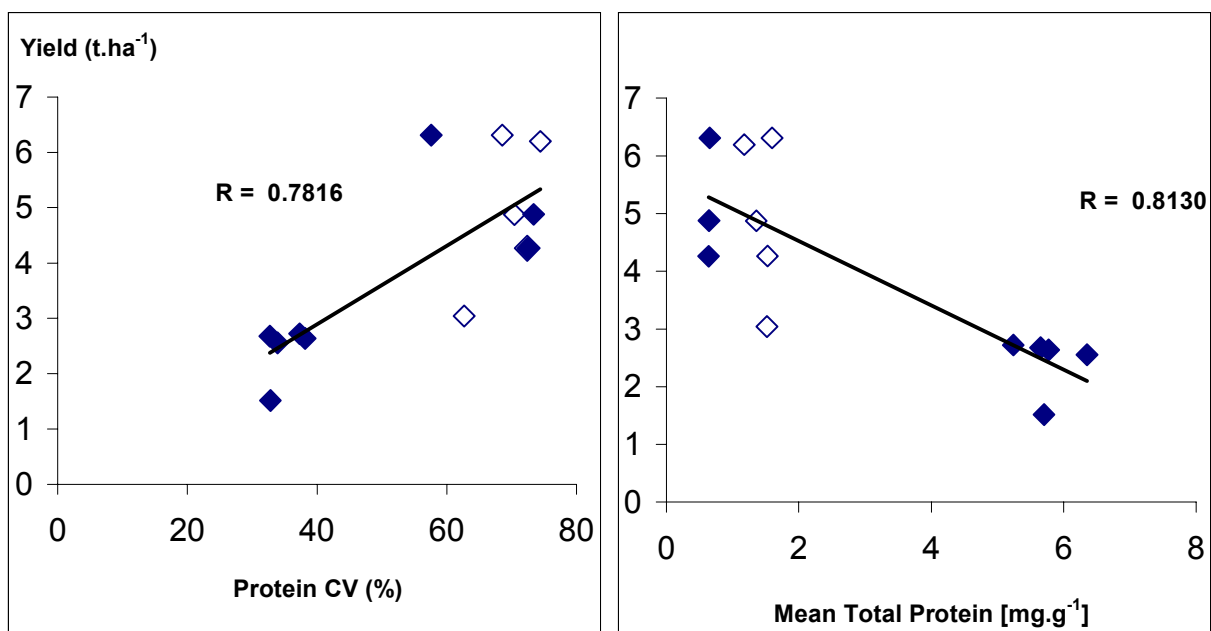

Figure 5. Field experiment at CLRRI, Vietnam: Grain yield vs. total soil proteins and intraseasonal variations of the latter expressed as coefficient of variance (CV, %). (Reichardt et al 2000, in press)

Cell-bound, respiratory processes with an E_h-dependent sequence of terminal electron acceptors account for the mineralization of a considerable, if not the bulk fraction, of labile soil organic matter. As a comprehensive measure, biomass-linked respiratory electron transport system (ETS) activity is most practicable for monitoring bioactivity in

submerged soils (Reichardt et al., 2000). In seasonal patterns obtained from LTCCE, ETS activities peak only during dry seasons in which grain yields tend almost to double (Fig.6). This positive linkage between grain yields and ETS activities suggests rapid remineralization of labile, organically bound plant nutrients with the participation of various, predominantly microbial dehydrogenases (summarized as ETS activities).
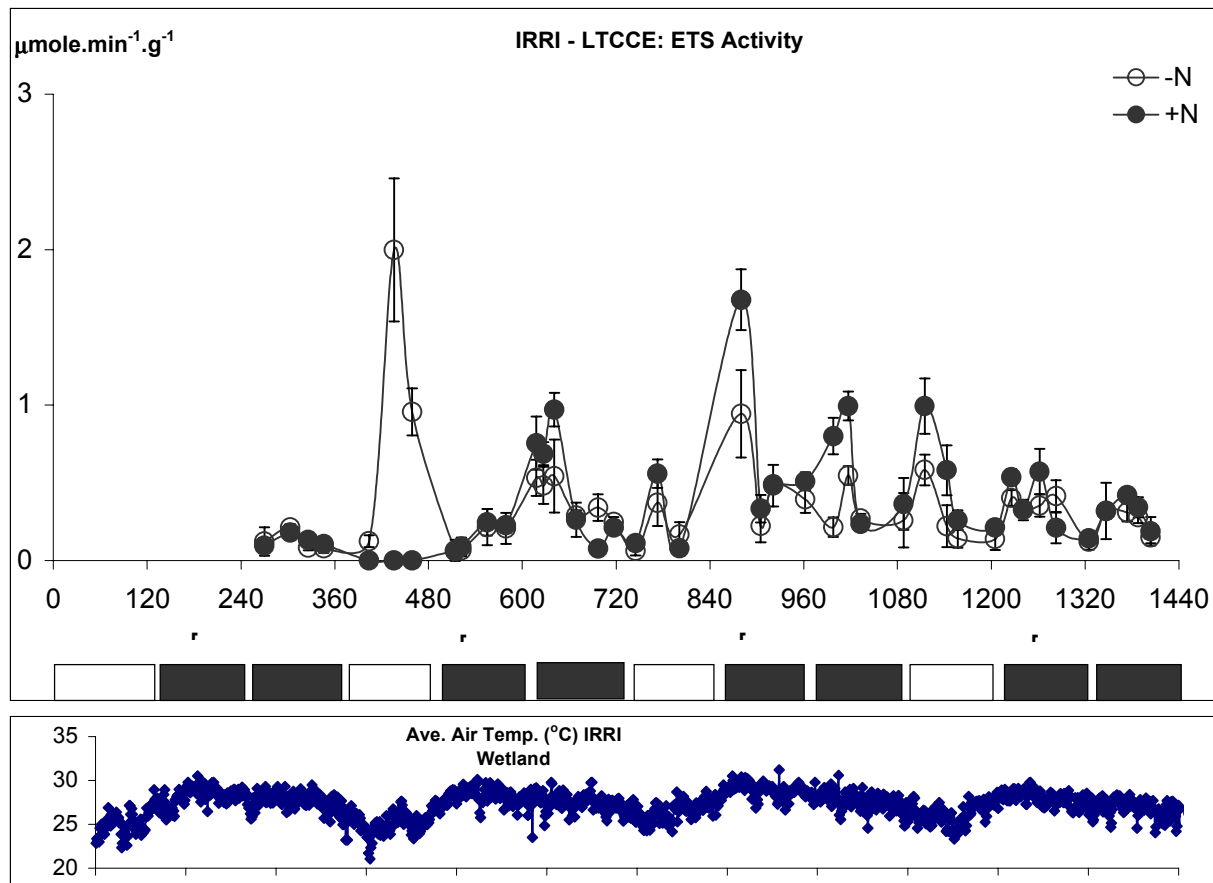

Figure 6. Long term continuous cropping experiment at IRRI: Fluctuations of respiratory ETS activities in soil. Black boxes: Wet season; light boxes: Dry season. (Reichardt et al 2000, in press)

Low ETS activity levels during wet seasons coincided with elevated concentrations of soluble phenolic compounds. In a mechanistic interpretation, phenols accumulating predominantly during wet seasons might have acted as inhibitors or biogeochemical regulators of ETS activity in the soil. In almost permanently flooded rice soils these regulatory effects seem to play a greater role than reported for aerated soils (Bending et al., 1998). Negative correlations between ETS activities

and soluble phenol concentrations confirm that remineralization of labile organic nutrient pools is influenced, if not regulated, by the dynamics of soluble phenols (Fig.7). In a rice cropping experiment at Suphanburi Rice Research Center (Thailand), differential impacts of soil management practices revealed interactive effects between nutrient and pest management.
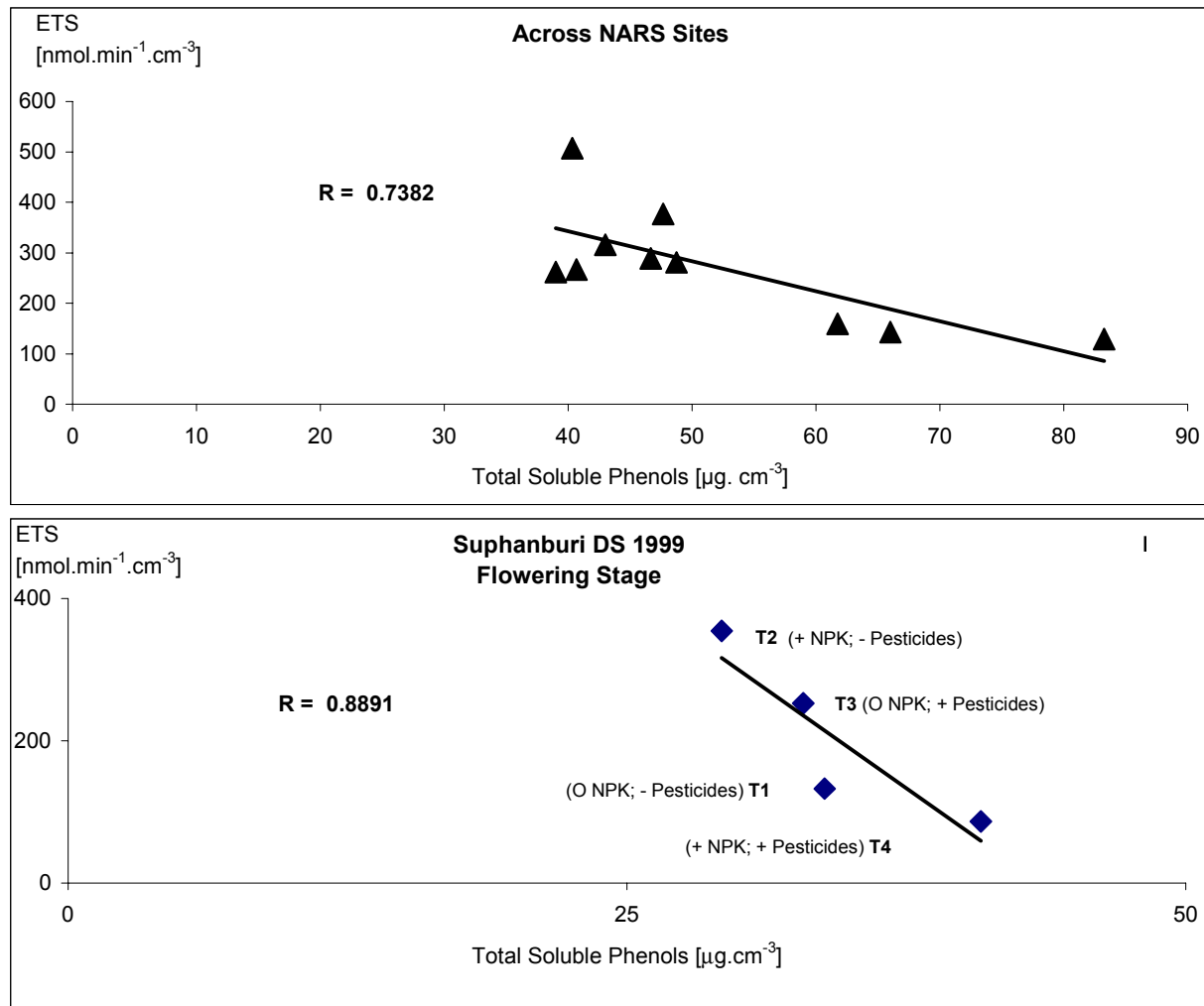

Figure 7. Negative correlations between soluble phenol concentrations and respiratory ETS activities in soils of rice cropping experiments in South East Asia. (Reichardt et al 2000, in press)

Sustainability and profiles of biogeochemical functions

Sustainability of the ancient rice terraces in tropical Asia is already evident by virtue of their persistence over centuries and even millennia. Despite this general evidence it remains to be explored whether intensified management of wetland rice soils following the "green

revolution" in Asia can affect their relatively favorable status. Clues to an answer were expected from a comparison of the "guild" structure of soil microbial communities inhabiting the extremes of traditional low-input and highly intensive rice cropping systems.

Signature lipid compounds (SLC) profiles (Reichardt et al., 1997) revealed profound differences between both systems (Table1).

Table 1. Comparison of soil microbial analyses in extremely extensive and intensive, irrigated rice cropping systems in the Philippines (Reichardt et al 2000, in press)

Measures	Ifugao Terraces	Continuous Triple Cropping Trial	
	Input-Free:	*Use of Agrochemicals:*	
	Recycling of Crop Residues Only	Pesticides[3] Only	Pesticides[3] and Mineral Fertilizers
Microbial Biomass			
as PLFA (nmoles/g)	45$\pm$7 a[1]	20$\pm$4 b	24$\pm$7 b
%C_{bio}/total C[2]	1.18	0.74	0.86
Microbial Community Status (cy/ 7c)	0.22$\pm$0.02 c	0.75$\pm$0.04 b	0.84$\pm$0.05 a
Prokaryotes:Eukaryotes Ratio	7.0$\pm$0.4 c	11.6$\pm$1.4 b	16.0$\pm$2.0 a
Selected PLFA (as % of total)			
Eukaryote SLC			
Fungi (18:2 6)	2.7$\pm$0.3 a	2.0$\pm$0.1 b	1.55$\pm$0.15 c
Protozoa (20:4 6)	0.7$\pm$0.2 a	0.1$\pm$0.2 b	0.0 b
Phototrophic Eukaryotes (20:5 3)	1.3$\pm$0.2 a	0.4$\pm$0.2 b	0.3$\pm$0.0 b
Prokaryote SLC			
Sulfate-Reducing Bacteria			
17:1 6c	0.9$\pm$0.1 b	1.5$\pm$0.0 a	1.4$\pm$0.1 a
i17:1 7c	1.0$\pm$0.1 b	1.6$\pm$0.1 a	1.6$\pm$0.1 a
10me16:0	3.4$\pm$0.5 b	7.0$\pm$0.5 a	7.8$\pm$1.0 a
Methanogens (Diether Lipids)	0.03$\pm$0.01	0.05$\pm$0.02	0.07$\pm$0.03
Methylotrophs I (16:1 5c)	2.0$\pm$0.2 c	2.6$\pm$0.2 b	2.95$\pm$0.15 a
Diversity Based on PLFA			
Richness	52$\pm$4 a	46$\pm$4 ab	45$\pm$4 b
Shannon Diversity Index	2.98$\pm$0.04 b	3.07$\pm$0.03 a	3.04$\pm$0.02 ab
Pielou Evenness	1.74$\pm$0.04 b	1.87$\pm$0.02 a	1.87$\pm$0.02 a
Respiratory Utilization of Carbon Sources			
Richness	225$\pm$7 a	181$\pm$20 b	207$\pm$16 a
Shannon Diversity Index	5.29$\pm$0.05 a	4.94$\pm$0.15 b	5.17$\pm$0.09 a
Pielou Evenness	2.25$\pm$0.01 a	2.19$\pm$0.02 b	2.23$\pm$0.01 a

[1] means of the same letter are not significantly (p<0.05) different (LSD test)
[2] microbial biomass C in % of total C, based on a conversion factor of 100   moles phospholipids per 1 g of   carbon for microbial biomass (Petersen, et al., 1991)
[3] Pesticides include insecticides, fungicides, herbicides and molluscicides.

In the intensive cropping system that is characterized by frequent soil perturbation and agrochemical inputs, biomarkers for prokaryotic microbial guilds with main functions in anaerobic nutrient cycling predominated over eukaryotic fingerprints. Guild profiles of biogeochemical functions in the intensified cropping system were much narrower than in the traditional extensive system. Minimum levels of eukaryote biomarkers in the intensive system coincided also with relatively high phenol concentrations (Table 1). Furthermore, elevated levels of cyclopropane fatty acids in many intensive cropping systems (Fig. 8) indicated a poor metabolic status of their prokaryotic communities.
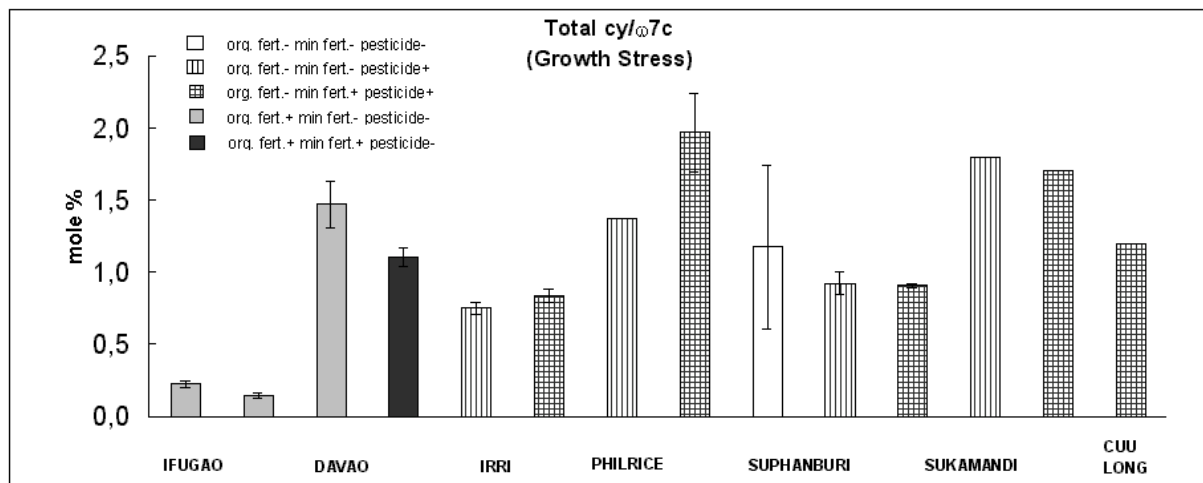

Figure 8. Concentrations of cyclopropane fatty acids as indicators of growth stress in soil microbial communities of several rice cropping field experiments in South East Asia. (Reichardt et al 2000, in press)

Signature lipid compounds [SLC] revealed distinct clusters that allowed to distinguish between the two farming systems. On the other hand, uniform clusters for both systems were obtained with the fast growing (copiotrophic) microbial community segment (RUNC assays, Zak et al., 1994), but only, as long as (mineral) N-fertilizer had been supplied (Fig.9). Enhanced nutrient input into intensive rice cropping systems stimulates fast growing members of the soil microbial community. Yet, elevated levels of nutritional stress indicators (cyclo-propane fatty acids) suggest that intensive growth of microbial populations is not sustained over extended periods of time.
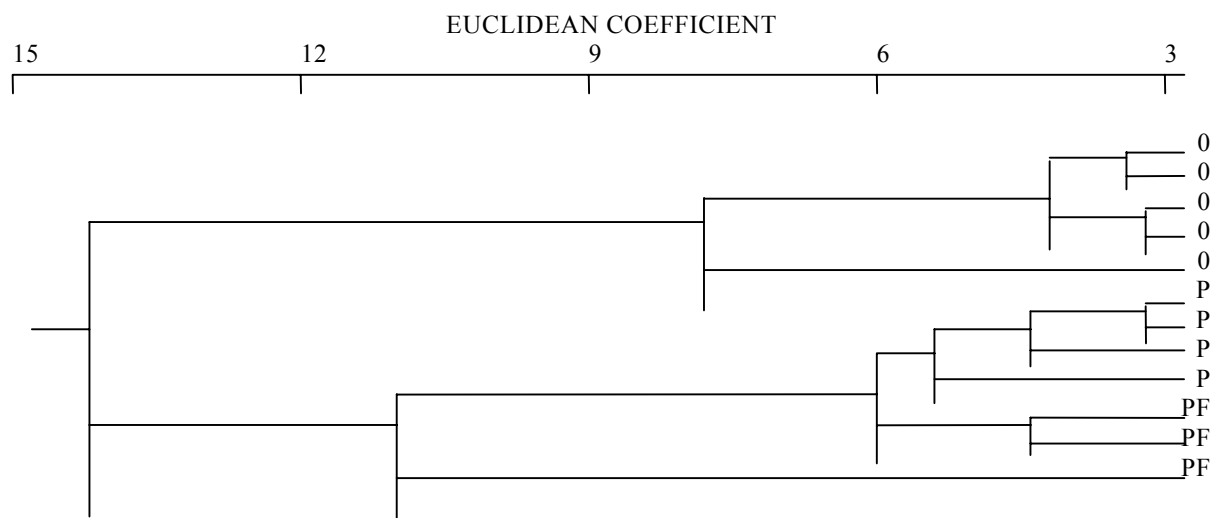
(A)
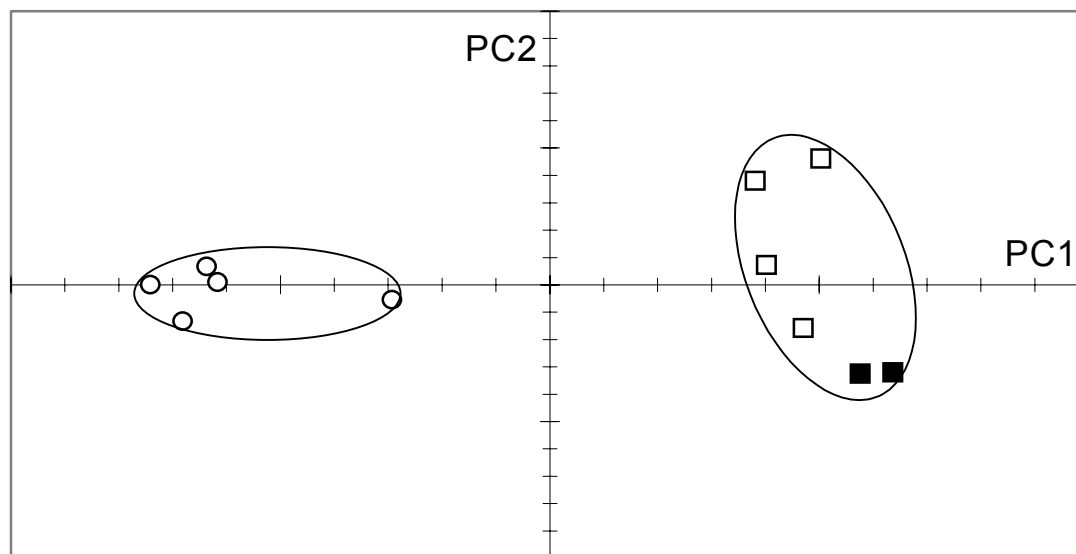
(B)

Figure 9.   (A) Principal component analysis of SLC for soil from rice terraces without agrochemical input (empty circles), and from intensive pesticide-treated long-term cropping experiment without (empty rectangles), and with mineral fertilizer input (filled rectangles; n=2) Principal component fatty acids: 1) 10 me 16:0; 2) i17:0.
(B) Sahn clustering (UPGMA) applied to SLC data from input-free rice terrace (0) and intensive pesticide-treated cropping system split into N-fertilizer omission plots (P) and plots with complete fertilizer and pesticide application (PF).
(Reichardt et al 2000, in press)

Apparently, Biolog-based RUNC assays are more likely to reflect responses of copiotrophic populations to soil management practices. The more comprehensive PLFA profiles, on the other hand, reflect rather site-specific than treatment-specific differences. - Diversity indices based on either SLC or RUNC profiles showed only slight differences and even opposite trends among each other (Table 1). This is not surprizing in view of the absence of an undisputed concept of microbial diversity that is based on biogeochemical functions (Kennedy and Gewin, 1997; Freckman et al., 1997; Ekschmidt and Griffith, 1998).
The choice of the latter is rather arbitrary, depending on the intrinsic objective of a particular investigation.

More recent concepts of resource compartmentalization along major biogeochemical pathways promise to overcome such conceptual bias (De Ruiter et al., 1998). When applied to the described comparison of cropping systems, the combination of almost permanent flooding with intensive agrochemical input and perturbation of the soil can be viewed as a selective force that favors more strictly anaerobic guilds and causes the accumulation of potential ecotoxicants (phenols). Incipient states of declining sustainability would coincide with considerable streamlining and reduction of biogeochemical "energy channels" (De Ruiter et al., 1998). Assuming that energetic organization of microbial communities in these agroecosystems is a prerequisite of their ecological stability, high input rice cropping systems would exhibit a lesser degree of sustainability than the traditional, extensive rice terrace system.

References

BENDING GD, TURNER MK, BURNS IG (1998) Fate of nitrogen from crop residues as affected by biochemical quality and the microbial biomass. Soil Biology & Biochemistry 30:2055-2065

CASSMAN KG, DE DATTA SK, OLK DC, ALCANTARA J, SAMSON M, DESCALSOTA J, DIZON M (1995) Yield decline and the nitrogen economy of long-term experiments on continuous, irrigated rice systems in the trophics. In: Lal R, Stewart BA (eds) Soil Management: Experiments Basis for Sustainability and Environmental Quality, pp 81-219

DE RUITER PC, NEUTEL AM, MOORE JC (1998) Biodiversity in soil ecosystems---the role of energy flow and community stability. Applied Soil Ecology 10:217-228.

DUXBURY JM, NKAMBULE SV (1994) Assessment and significance of biologically active soil organic nitrogen. In: Doran, et al., (eds) Defining Soil Quality for a Sustainable Environments. SSSA 35:125-145

EKSCHMITT K, GRIFFITHS BS (1998) Soil biodiversity and its implications for ecosystem functioning in a heterogeneous and variable environment. Applied Soil Ecology 10:201-215.

FRECKMAN DW, BLACKBURN H, BRUSSAARD L, HUTCHINGS P, PALMER M H AND SUELGROVE PVR (1997) Linking biodiversity and ecosystem functioning of soils and sediments. Ambio 226:556-563

KENNEDY AC, GEWIN VL (1997) Soil microbial diversity: present and future considerations. Soil Science162:602-617

PETERSEN SO, HENRIKSEN K, BLACKBURN TH, KING GM (1991) A comparison of phospholipid and chloroform fumigation analyses for biomass in soil: potential and limitations. FEMS Microbial Ecology 85:257-268

REICHARDT W, MASCARIÑA G, PADRE B, DOLL J (1997) Microbial communities of continuously cropped, irrigated rice fields. Applied and Environmental Microbiology 63:233-238

REICHARDT W (1999) Guide to Soil Microbiological and Biochemical Assays in Long-Term Rice Cropping Experiments. IRRC-RTDP Working Group III. IRRI, Los Banos, Philippines.

REICHARDT W, INUBUSHI K, TIEDJE J. (2000) Microbial processes in C and N dynamics. In: Kirk GJD, Olk, DC (eds) Carbon and Nitrogen Dynamics in Flooded Soils. Manila, Philippines, pp 101-46.

WARDLE DA (1998) Controls of temporal variability of the soil microbial biomass: a global scale synthesis. Soil Biology Biochemistry 30:1627-1637.

ZAK JC, WILLIG MR, MOOREHEAD DL, WILDMAN HG (1994) Functional diversity of microbial communities: A quantitative approach. Soil Biology & Biochemistry 26:1101-1108