Errata for Acta Universitatis Agriculturae Sueciae 2006:39

Paper I

Page 9, 10. Outlook: "In common with DGGE, it [TRFLP] gives a description of the species composition and [in addition] an estimate of the relative abundance of taxa in the sample, based on the abundance of different restriction fragments detected by laser-induced fluorescence on an automated gene sequencer"
Comment: The relative abundance of restriction fragments should be interpreted with caution when translating the TRFLP profiles into relative abundance of taxa in environmental samples.

Paper II

Page 35, Materials and methods: "Ribosomal T-DNA-transformed carrot roots" should be "Ri T-DNA-transformed carrot roots“ (Ri T-DNA = Root inducing transfer-DNA)

Paper III

Page 9, Figure legend (Fig. 2): ”glycogen (δ 8.43)” should be ”glycogen (δ 5.33)”

Paper IV

Page 9, line 7: ”GMA” should be ”FYM”

Page 9, Table 2 should be:

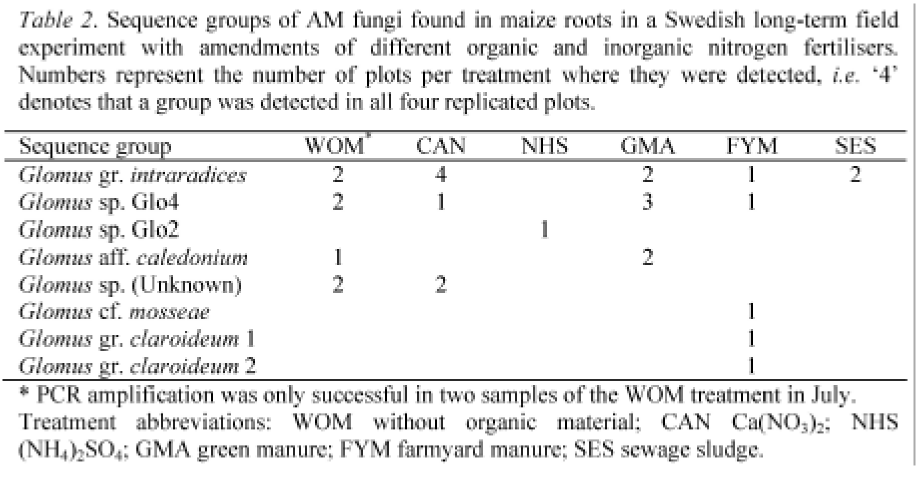

Table 2. Sequence groups of AM fungi found in maize roots in a Swedish long-term field experiment with amendments of different organic and inorganic nitrogen fertilisers. Numbers represent the number of plots per treatment where they were detected, *i.e.* ‘4’ denotes that a group was detected in all four replicated plots.

Sequence group	WOM*	CAN	NHS	GMA	FYM	SES
Glomus gr. *intraradices*	2	4		2	1	2
Glomus sp. Glo4	2	1		3	1	
Glomus sp. Glo2			1			
Glomus aff. *caledonium*	1			2		
Glomus sp. (Unknown)	2	2				
Glomus cf. *mosseae*					1	
Glomus gr. *claroideum* 1					1	
Glomus gr. *claroideum* 2					1	

* PCR amplification was only successful in two samples of the WOM treatment in July.
Treatment abbreviations: WOM without organic material; CAN $Ca(NO_3)_2$; NHS $(NH_4)_2SO_4$; GMA green manure; FYM farmyard manure; SES sewage sludge.

Page 10, Table 3: "% imilarity" should be "% similarity“