
Article:
Blaud, A., Menon, M. orcid.org/0000-0001-5665-7464, van der Zaan, B. et al. (2 more authors) (2016) Effects of Dry and Wet Sieving of Soil on Identification and Interpretation of Microbial Community Composition. Advances in Agronomy, 142. pp. 119-142. ISSN 0065-2113

https://doi.org/10.1016/bs.agron.2016.10.006

Table 1. Soil characteristics of bulk soil samples on a dry mass basis. Mean value ± one standard deviation (n = 3) are shown.

Location	Cropland 48°09'N, 16°41'E	Grassland 48°11'N, 16°44'E
Water content (%)	22.0 ± 2.9	15.8 ± 2.0
Soil pH (H_2O)	7.7 ± 0.14	7.4 ± 0.09
Organic C (%)	2.4 ± 0.36	5.0 ± 0.60
Total N (%)	0.13 ± 0.01	0.33 ± 0.04
C_{org}/N	18.1 ± 1.83	15.0 ± 0.52
$N\text{-}NH_4^+$ (mg kg^{-1})	1.59 ± 0.29	4.77 ± 0.98
$N\text{-}NO_3^-$ (mg kg^{-1})	20.3 ± 3.07	1.5 ± 0.66
$P\text{-}PO_4^{3-}$ (g kg^{-1})	0.35 ± 0.10	0.59 ± 0.04
$CaCO_3$ (%)	19.0 ± 1.90	21.1 ± 1.41
Sand, 63-2000 μm (%)	32.7	8.2
Silt, 2-63 μm (%)	43.8	63.0
Clay, < 2 μm (%)	23.5	28.8

Table 2. Proportion of genes (%) lost in the water during soil fractionation using wet-sieving. The loss of gene number in the water is express as a percentage of the number of the same gene present in 1 g of bulk soil. Mean value ± one standard error (n = 3) are shown. Different letter indicate significant ($P < 0.01$) differences between cropland and grassland for a specific gene.

Gene	Cropland	Grassland
Bacterial 16s rRNA	1.55 ± 0.43	0.75 ± 0.30
Fungal ITS	0.48 ± 0.11	0.71 ± 0.52
nifH	2.31 ± 0.84	1.90 ± 0.85
amoA bacteria	0.33 ± 0.12	2.14 ± 0.63
amoA archaea	0.83 ± 0.09	1.83 ± 0.60
narG	1.16 ± 0.41 A	6.97 ± 0.80 B
nirS	0.85 ± 0.31	0.57 ± 0.17
nosZ	0.45 ± 0.14	0.60 ± 0.18

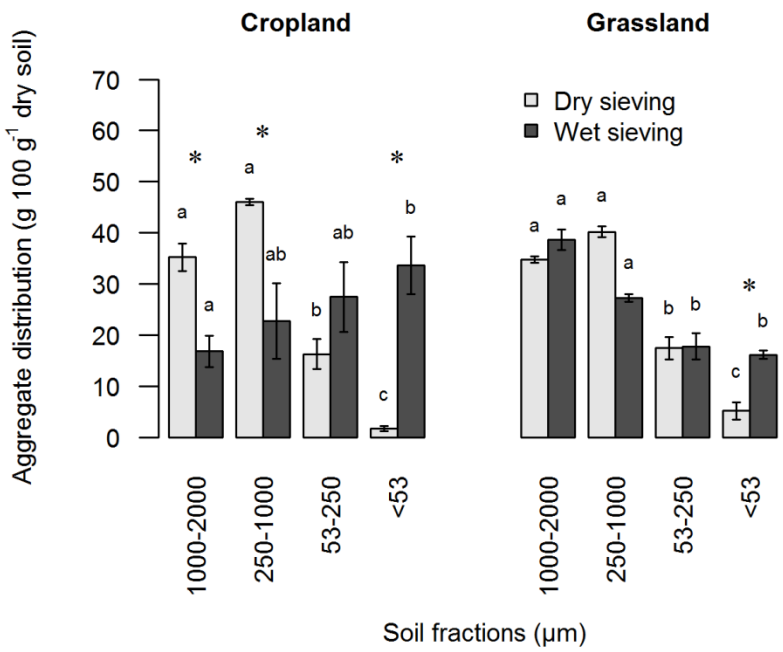

Fig. 1. Weight distribution of soil fractions (g 100 g^{-1} dry soil) obtained by dry- or wet-sieving method of soils from cropland and grassland. Means values ± standard error (n = 3) are shown. * indicates significant ($P < 0.05$) difference between dry- and wet-sieving for a specific soil fraction and site. Different letters indicate significant ($P < 0.05$) difference between soil fractions for a specific sieving method and site.

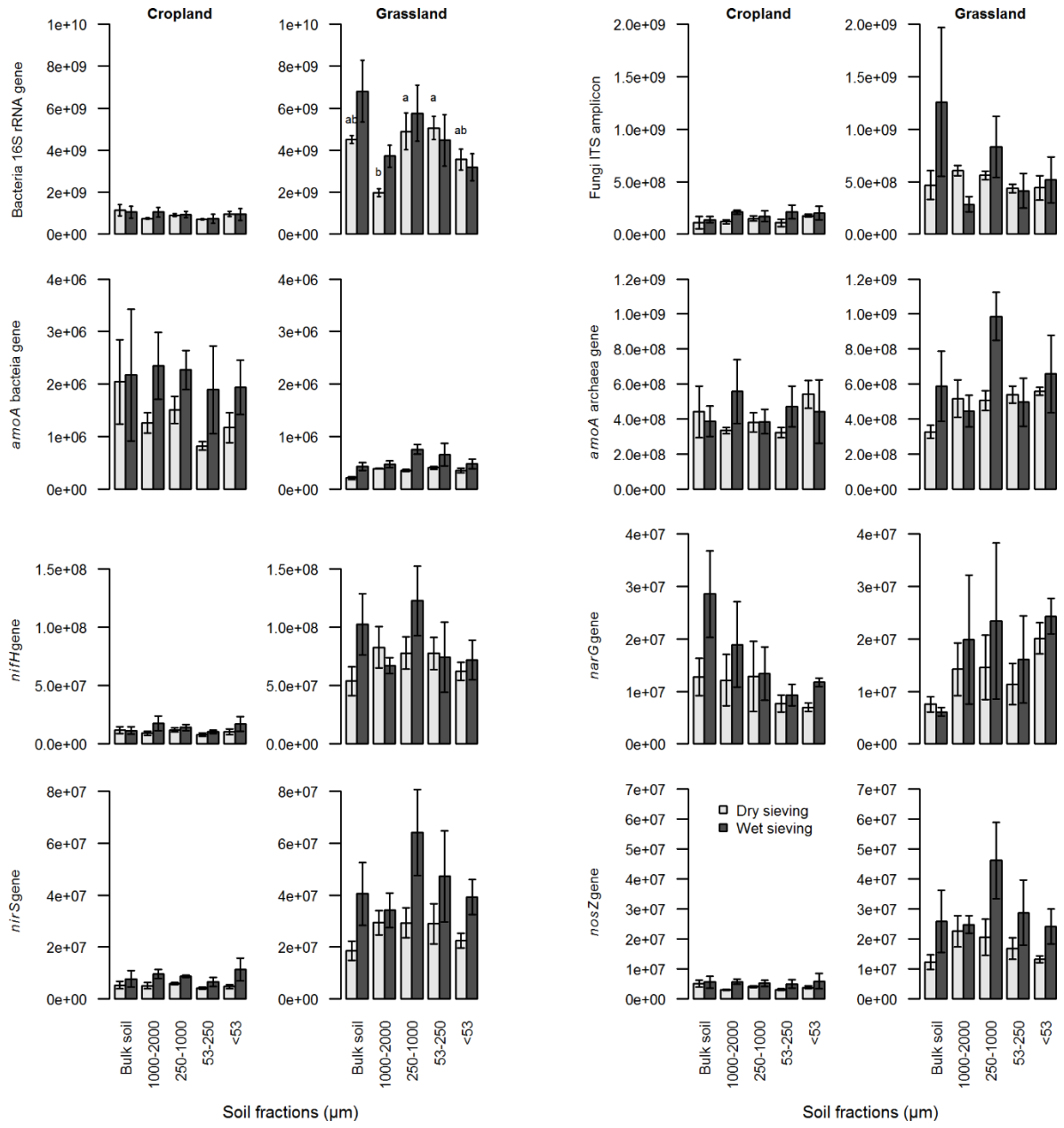

Fig. 2. Variation in gene abundance of bacteria (16S rRNA gene), fungi (ITS amplicon), N fixating (nifH gene), ammonia oxidizing bacteria and archaea (amoA gene), nitrate reductase (narG gene), nitrite reductase (nirS gene) and nitrous oxide reductase (nosZ gene) between four soil fractions obtained by dry- or wet-sieving methods from cropland and grassland. All abundances are expressed on the basis of 1 g of dry mass of soil fraction or bulk soil. Means values ± standard error (n = 3) are shown. * indicates significant ($P < 0.05$) different between dry- and wet-sieving for a specific soil fraction and site. Different letters indicate significant ($P < 0.05$) difference between soil fractions for a specific sieving method and site.

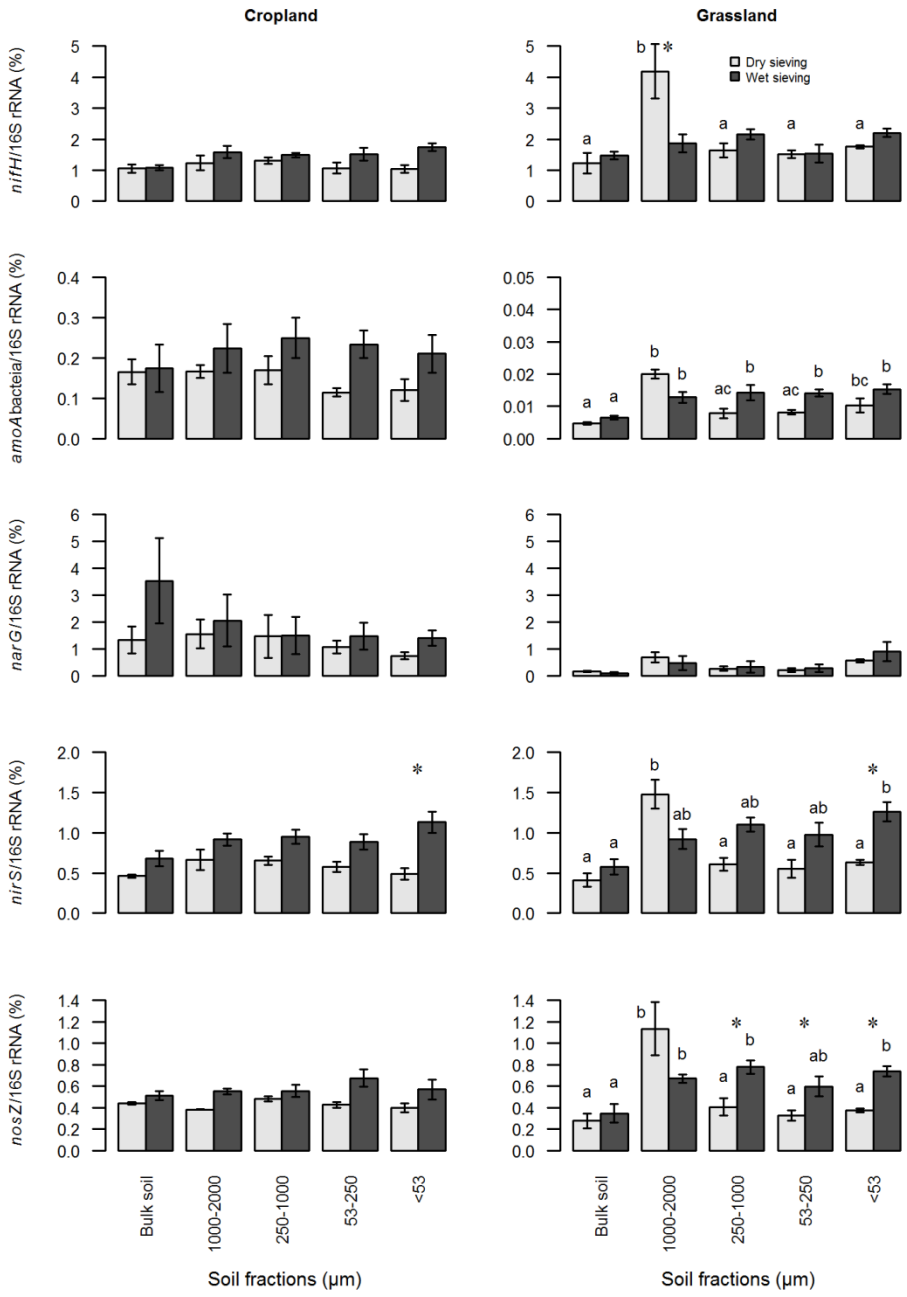

Fig. 3. Variation in N functional gene/bacterial 16S rRNA (%), of the N fixating (nifH gene), ammonia oxidizing bacteria (amoA gene), nitrate reductase (narG gene), nitrite reductase (nirS gene) and nitrous oxide reductase (nosZ gene) between four soil fractions obtained by dry- or wet-sieving methods from cropland and grassland. Means values ± standard error (n = 3) are shown. * indicates significant ($P < 0.05$) different between dry- and wet-sieving for a specific soil fraction and site. Different letters indicate significant ($P < 0.05$) difference between soil fractions for a specific sieving method and site.

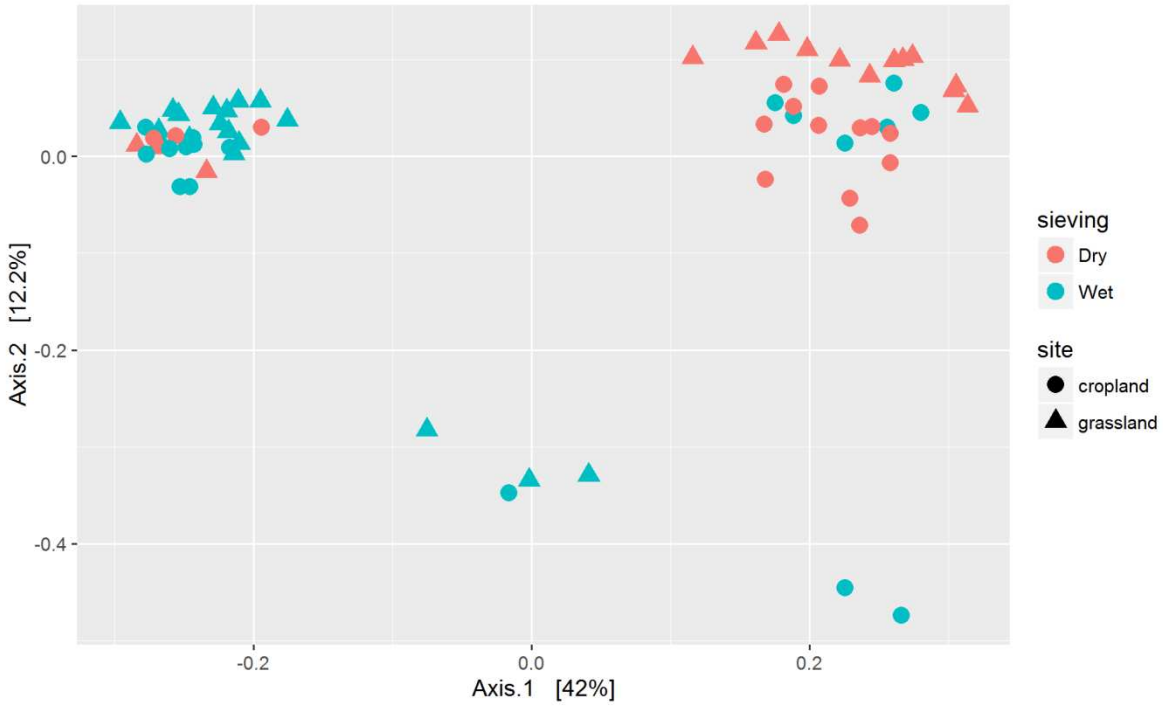

Fig. 4 PCoA of bacterial community of four soil fractions obtained by dry- or wet-sieving method and bulk soil from cropland and grassland. The PCoA was based on relative abundance of OTU and generated using Bray-Curtis distance. The six samples isolated from the rest of the samples correspond to water from the wet-sieving.

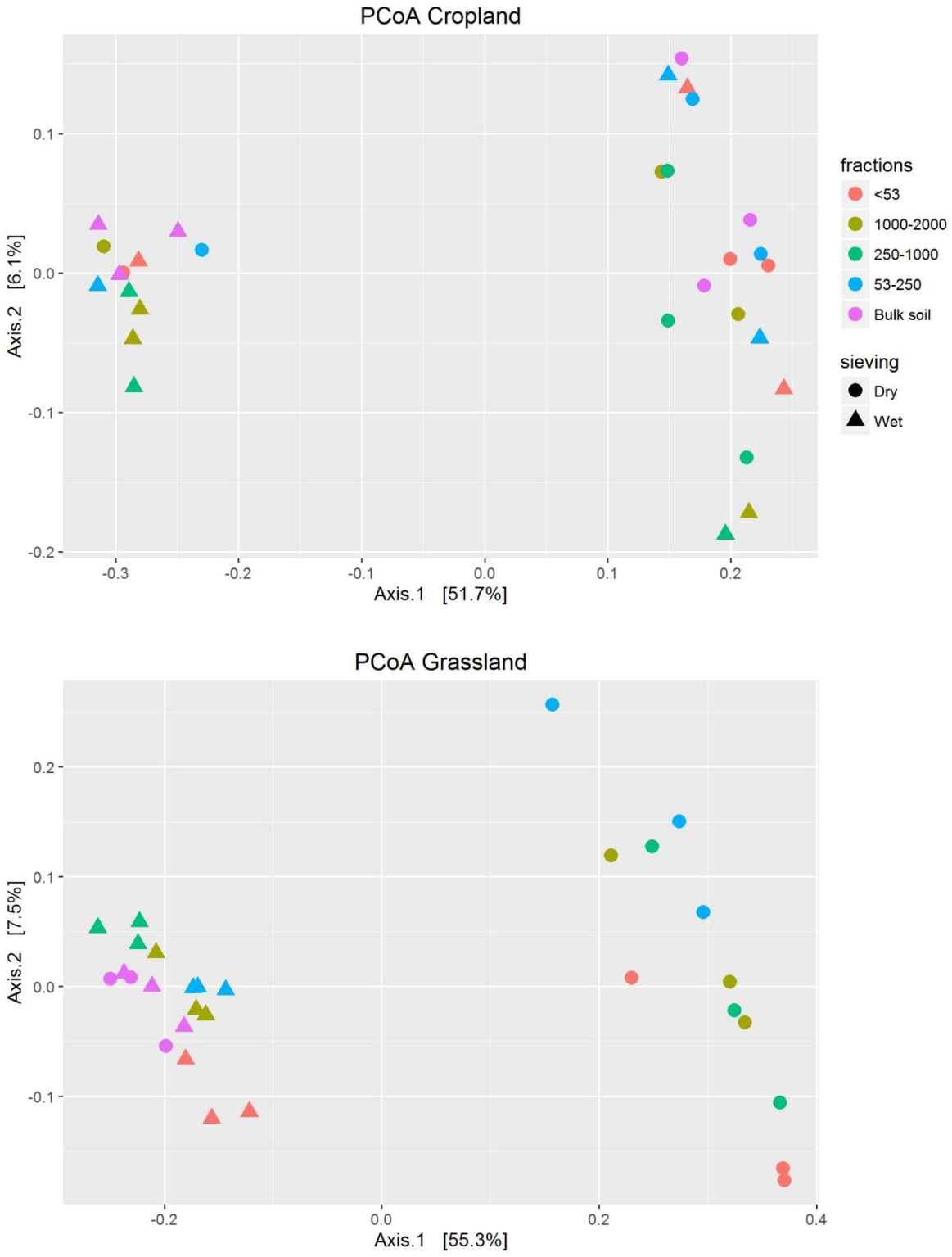

Fig. 5 PCoA of bacterial community of four soil fractions obtained by dry- or wet-sieving method and bulk soil from cropland (top) and grassland (bottom). The PCoA were based on relative abundance of OTU and generated using Bray-Curtis distance.

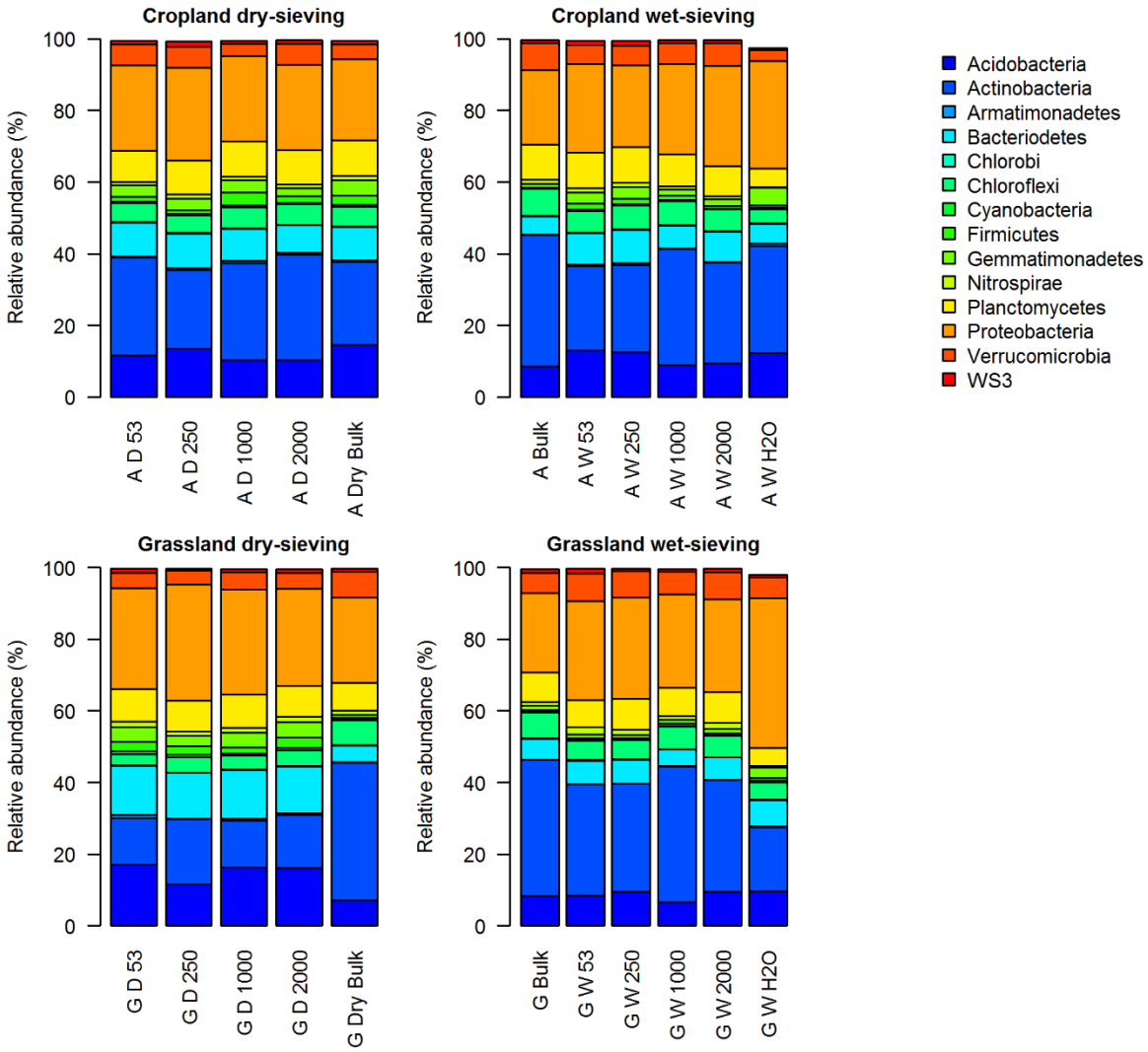

Fig. 6. Relative abundance (%) of bacterial phyla of four soil fractions obtained by dry- or wet-sieving method, bulk soil and water from wet-sieving from cropland and grassland. Means values (n = 3) are shown. Only the dominant phyla (~ > 0.2%) are shown.