

Fungal networks serve as novel ecological routes for enrichment and dissemination of antibiotic resistance genes as exhibited by microcosm experiments

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Figure S1 Fungal effect on the culturable ARB from the animal manure (M) source, sampled from inoculation point (i) and respective fungal migration front (m). F-5, F-14, and F-16 represent the three selected fungal strains NFC-5, NFC-14, and NFC-16, respectively. Blue bars are total bacteria on R2A without any antibiotic while A, C and K represent ampicillin, ciprofloxacin and kanamycin respectively, applied in medium alone or in combination. *No bacteria were detected at migration point (Mm) for non-fungal treatments.

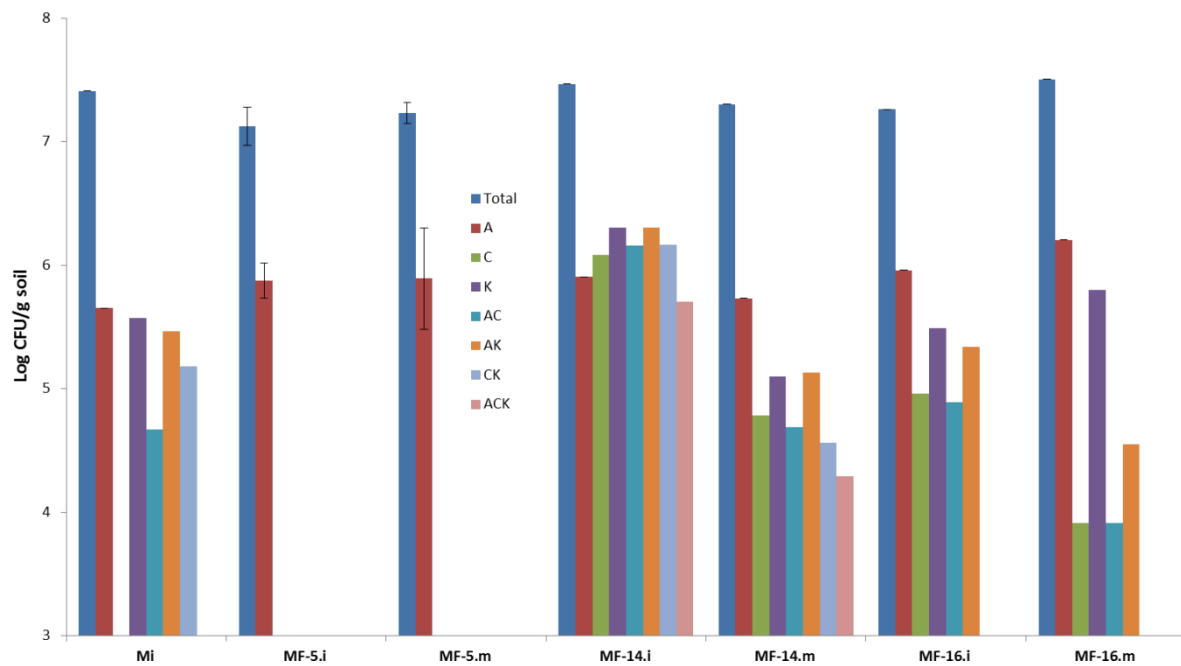


Figure S2 Effect of different fungi on (selected) ARGs abundance, relative to the original W inoculum. F-5, F-14, and F-16 represent the three selected fungal strains NFC-5, NFC-14, and NFC-16, respectively. i and m are the bacterial inoculation point and fungal migration front respectively.

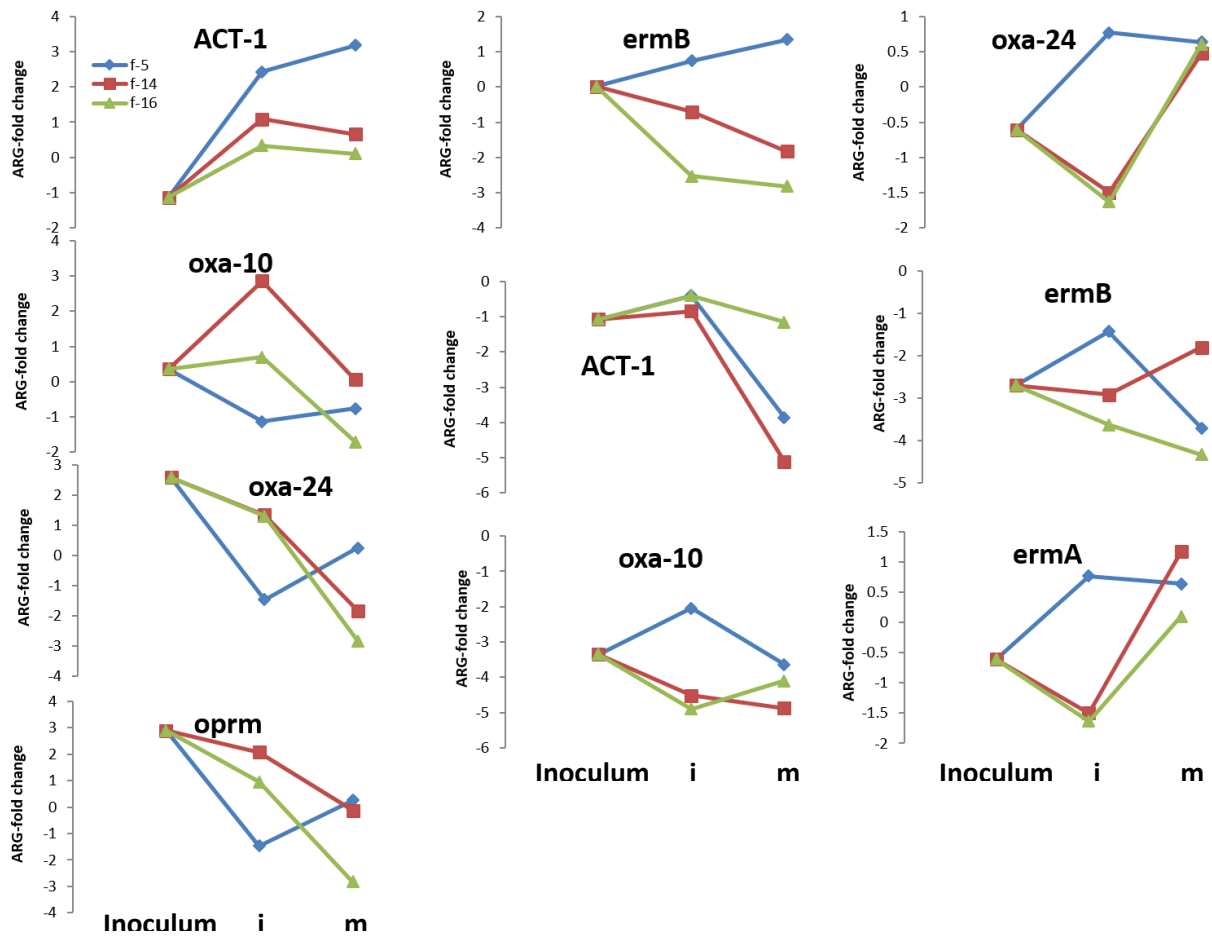


Figure S4 The bacterial 16S rRNA gene abundance in different soil samples affected or not with fungal colonization. M, microbial inoculum originating from manure; W, microbial inoculum originating from sludge/water of waste water treatment plant; i, bacterial inoculation point; m, fungal migration front; 5, 14 and 16 are the selected fungi as in table 1.

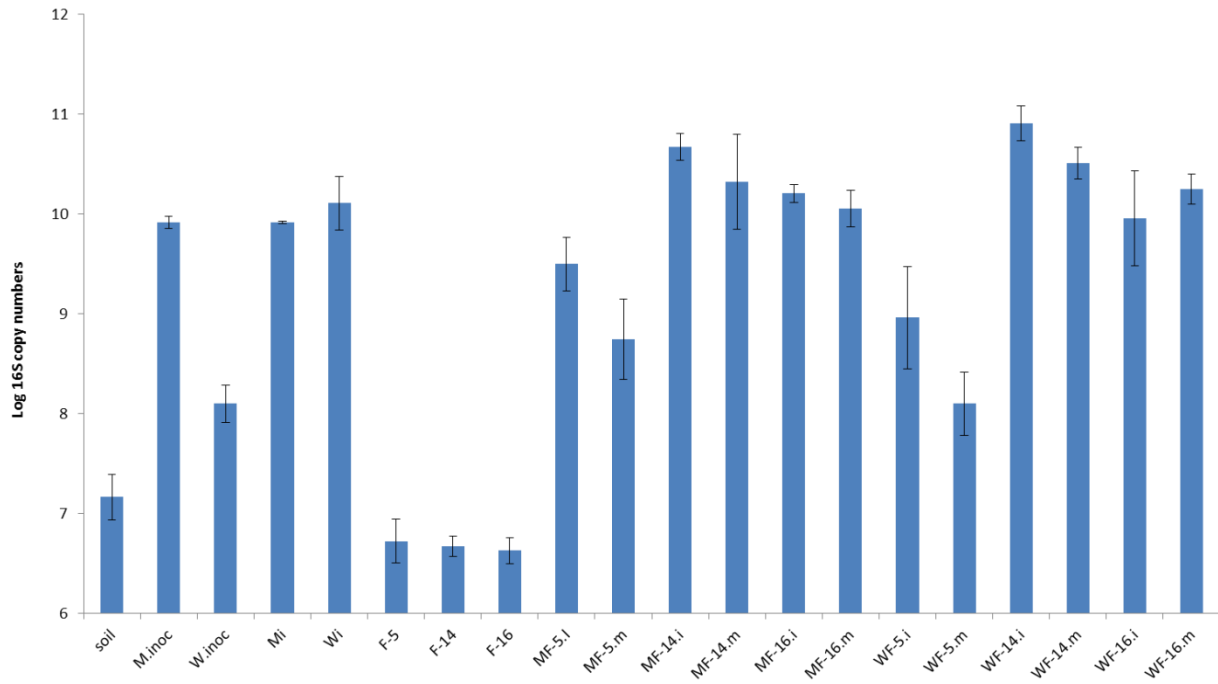


Figure S5 Principle component analysis for bacterial ARGs of W and M source, influenced by fungal colonization. qPCR data for 84 ARGs were used for each treatment to calculate PC1 and PC2. Bi means bacterial inoculum either from manure (M) or waste water (W), i means inoculation point in soil microcosm and m means the fungal migration front.

