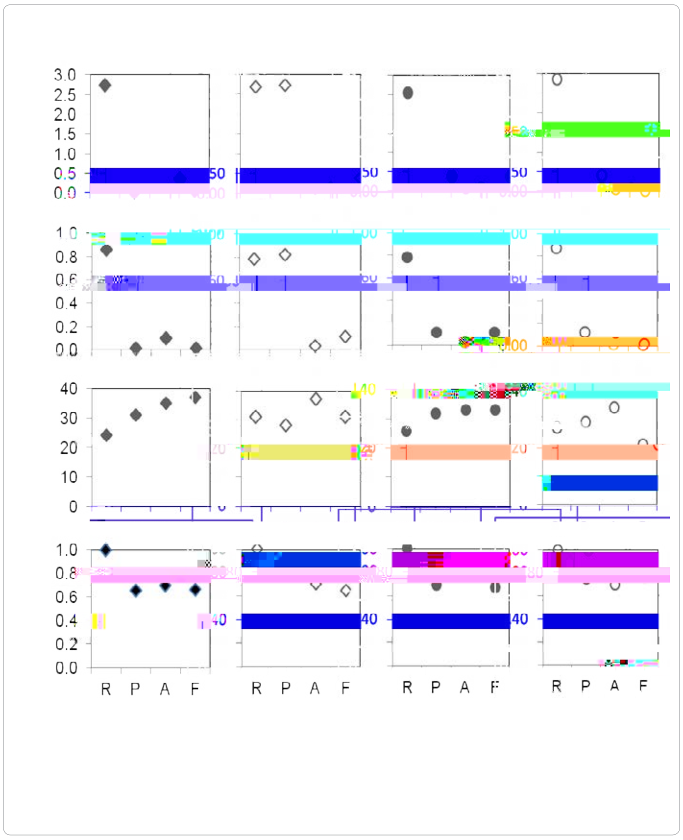
Keywords Municipal wastewater; Habitat media; Ecological index; Community structure

Introduction

The continuing need for robust, sustainable and reliable (bio) technologies that are also characterized by minimal carbon emissions/footprints must be matched by an equally growing and sound knowledge base of the underpinning microbial communities.



In general, the average taxa richness of all inocula increased (27 ± 1.5 to 34 ± 1) through the treatment process indicating a change in the selection pressure [18,19]. The one exception was for the P-inoculum cultured on its respective medium, which decreased from 31 to 28. The Sørensen index of similarity indicated comparable community composition throughout the treatment process and suggested that species abundance only varied at different stages.

Emergent research has been made to culture previously uncultured microbial strains from soil ecosystems with only limited investigations for wastewater management. This is in direct contrast to the multiple molecular-based analyses that have been applied, developed and optimised to characterise the complex microbial communities in different wastewater biotechnologies. Matching and complementing genotypic tools with culture-based (phenotypic) analyses will facilitate: (i) identification of novel strains; (ii) quantification of their upper and lower physiological limits and function characterisation; (iii) culture maintenance of important monocultures/ communities [20]; and (iv) more informed exploitation in wastewater treatment plants for increased efficiency/stability/reliability.

Conclusion

This study exemplified the use of wastewater-based media to culture microbial communities that characterized specific phases of a continuous treatment train. DGGE-based analysis then facilitated measurements of diversity, evenness, taxa richness and similarity between treatment stages. Future work should entail detailed physiological/phenotypic studies of the cultivated strains/communities and, subsequently, sequencing to allow genotypic comparisons with these and uncultured wastewater species in existing databases.

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References

1. Nichols D, Cahoon N, Trakhtenberg EM, Pham L, Mehta A, et al. (2010) Use of ichip for high-throughput in situ cultivation of "uncultivable" microbial species. Appl Environ Microbiol 76: 2445-2450.
2. Liebeke M, Brözel VS, Hecker M, Lalk M (2009) Chemical characterization of soil extract as growth media for the ecophysiological study of bacteria. Appl Microbiol Biotechnol 83: 161-173.
3. Bastida F, Nicolás C, Moreno JL, Hernández T, García C (2010) Tracing changes in the microbial community of a hydrocarbon-polluted soil by culture-dependent proteomics. Pedosphere 20: 479-485.
4. Bucková M, Godocíková J, Zámocký M, Polek B (2010) Screening of bacterial isolates from polluted soils exhibiting catalase and peroxidase activity and diversity of their responses to oxidative stress. Curr Microbiol 61: 241-247.
5. Amann RI, Ludwig W, Schleifer KH (1995) Phylogenetic identification and in situ detection of individual microbial cells without cultivation. Microbiol Rev 59: 143-169.
6. Tyson GW, Banfield JF (2005) Cultivating the uncultivated: a community genomics perspective. Trends Microbiol 13: 411-415.
7. Ritz K (2007) The plate debate: cultivable communities have no utility in contemporary environmental microbial ecology. FEMS Microbiol Ecol 60: 358-362.
8. Sait M, Hugenholtz P, Janssen PH (2002) Cultivation of globally distributed soil bacteria from phylogenetic lineages previously only detected in cultivation-independent surveys. Environ Microbiol 4: 654-666.
9. Chaer GM, Fernandes MF, Myrold DD, Bottomley PJ (2009) Shifts in microbial community composition and physiological profiles across a gradient of induced soil degradation. Soil Sci. Soc. America J. 73: 1327-1334.
10. Bollmann A, Palumbo AV, Lewis K, Epstein SS (2010) Isolation and physiology of bacteria from contaminated subsurface sediments. Appl Environ Microbiol 76: 7413-7419.
11. Bougnom BP, Knapp BA, Elhottová D, Koubová A, Etoa FX, et al. (2010) Designer compost with biomass ashes for ameliorating acid tropical soils: effects on the soil microbiota. Appl. Soil Ecol. 45: 319-324.
12. Muyzer G, De Waal EC, Uitterlinden AG (1993) Profiling of complex microbial populations by denaturing gradient gel electrophoresis analysis of polymerase chain reaction-amplified genes coding for 16S rRNA. Appl. Environ. Microbiol. 59: 695-700.
13. Manefield M, Whiteley AS, Griffiths RI, Bailey MJ (2002) RNA stable isotope probing, a novel means of linking microbial community function to phylogeny. Appl Environ Microbiol 68: 5367-5373.
14. Silva EP, Russo CAM (2000) Techniques and statistical data analysis in molecular population genetics. Hydrobiologia 420: 119-135.
15. Fromin N, Hamelin J, Tarnawski S, Roesti D, Jourdain-Miserez K, et al. (2002) Statistical analysis of denaturing gel electrophoresis (DGE) fingerprinting patterns. Environ Microbiol 4: 634-643.
16. Shannon CE, Weaver W (1949) The Mathematical Theory of Communication. Champaign: University of Illinois Press.
17. Sørensen T (1957) A method of establishing groups of equal amplitude in plant sociology based on similarity of species and its application to analyses of the vegetation on Danish commons. Kongelige Danske Videnskabernes Selskab 5: 1-34.
18. Johnson DR, Lee TK, Park J, Fenner K, Helbling DE (2014) The functional and taxonomic richness of wastewater treatment plant microbial communities are associated with each other and with ambient nitrogen and carbon availability. Environ. Microbiol.
19. Vuono DC, Munakata-Marr J, Spear JR, Drewes JE (2015) Disturbance opens recruitment sites for bacterial colonization in activated sludge. Environ Microbiol .
20. Goodhead AK, Head IM, Snape JR, Davenport RJ (2014) Standard inocula preparations reduce the bacterial diversity and reliability of regulatory biodegradation tests. Environ Sci Pollut Res Int 21: 9511-9521.