

## Short communication

## Soil microbial communities along the route of a venturesome cycling trip

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## ABSTRACT

The purpose of the present study is not solely scientific but arose from a rare fusion of art and science during a venturesome bicycle trip from Austria (Europe) to Laos (Asia). The artist Wolfgang Burtscher produced every-day dirt tire imprints on papers (*tripmarks*) to document his journey ([www.tripmarks.at](http://www.tripmarks.at)). Contributing to public awareness in this International Year of Soils 2015 we took a closer look at the dirt forming these pieces of art, namely to investigate the inherent microbial life. As such, we benefited from minute soil samples along a global transect, which permitted the classical hypothesis on microbial cosmopolitanism to be evaluated. DNA from 0.1 g soil was extracted and amplified with specific primers for fungi and actinobacteria to obtain denaturing gradient gel (DGGE) fingerprinting patterns. Spatial variables were generated by applying trend surface analysis and principal coordinates of neighbour matrices. Canonical correspondence analysis was also used to check for driving factors.

Our results show that microbial variability is primarily being influenced by environmental rather than spatial patterns. Clearly distinct communities in the soils of distant sampling sites were formed for actinobacteria but not for fungi. Furthermore, cosmopolitan phylotypes with relative abundances as high as 80.5% (fungi) and 74.0% (actinobacteria) were detected. These findings show that Eurasian soil microbial communities follow environmental rather than spatial constraints. For the artist, these results emphasize the broad diversity of microorganisms present on his tripmarks joining the facet of the beauty and variety of life with his dirty tire imprints.

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## 1. Introduction

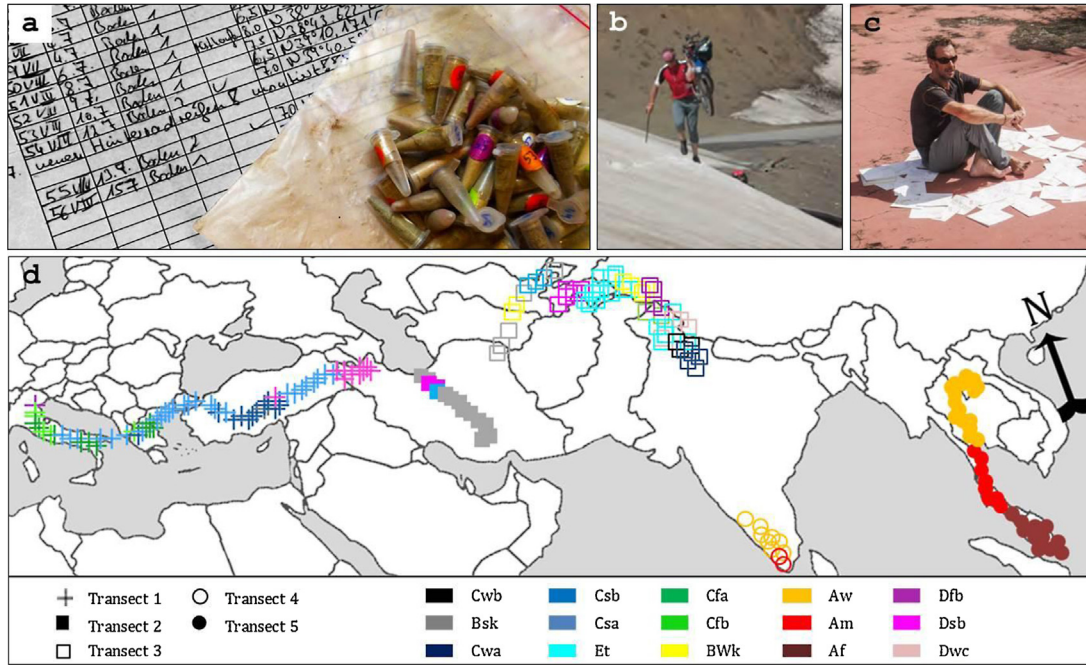
Since the dogma of *everything is everywhere, but the environment selects* was formulated in the early 20th century (Baas Becking, 1931; Beijerinck, 1913), several studies showed evidence of a microbial cosmopolitanism (Fenchel and Finlay, 2004; Finlay, 2002). It is supposed to be due to passive dispersal, dormant life stages and short generation times. Though, it has also been shown that there exist relationships between certain microbial groups or species and environmental parameters (Fierer and Jackson, 2006; Griffiths et al., 2011). However, modern molecular and fingerprinting techniques that permit a circumstantial depiction of community variations led to a debate about the correctness of the above mentioned statement (Green and Bohannan, 2006), claiming that the species are distributed following certain spatial patterns. However, theories and assumptions of global distribution patterns are still unclear, as sampling efforts on a global scale are high and data analyses complex. To dig deeper into the influence of space on

microbial communities, space can be used either as a predictor or a co-variable in such statistical models (Dray et al., 2006), affecting ecological patterns and processes at different scales (Legendre and Legendre, 1998).

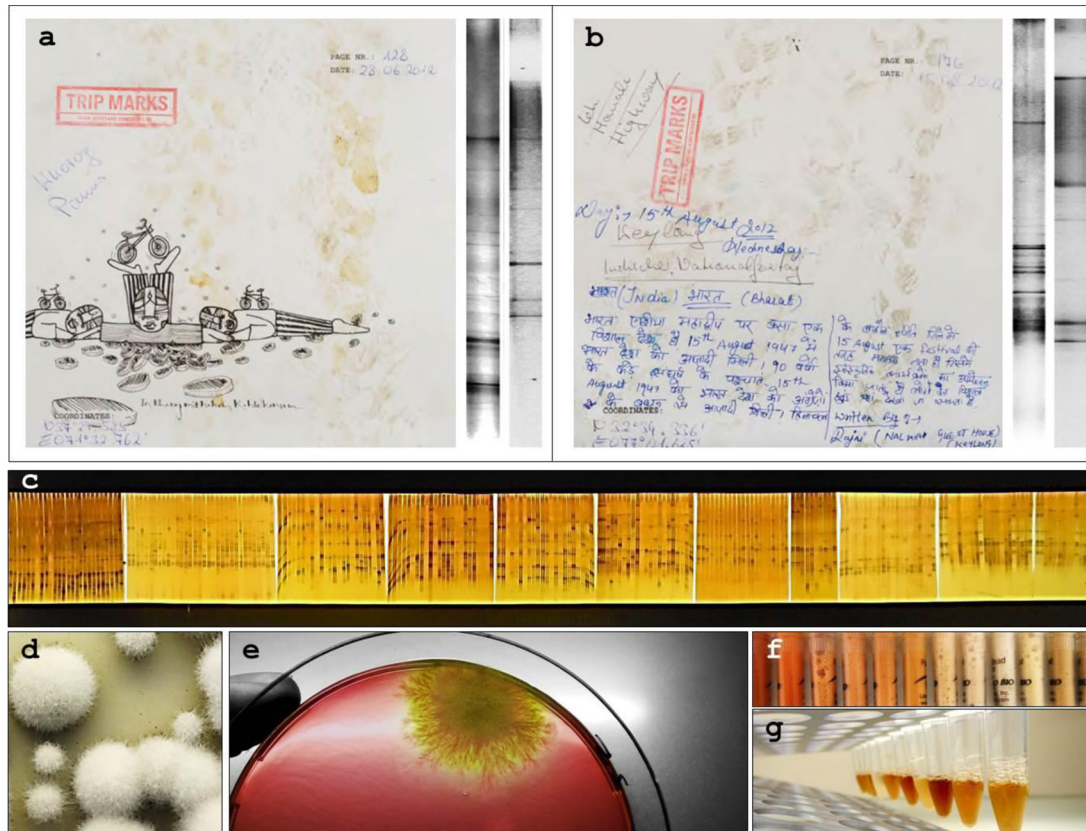
The project *tripmarks* benefited from soil samples achieved by the fusion of art, science, sports and adventure (Burtscher and Nagler, 2014; Fig. 1). We investigated the biodiversity and the spatial distribution of actinobacteria and soil dwelling fungi along a bike route from Austria to Laos to test to what extent spatial and environmental variables are shaping the microbial communities on a continental scale. Bearing in mind the aforementioned dogma we expect that the environmental variables have a larger influence on the communities than the spatial ones, and such patterns will be group-specific. By investigating fungi and actinobacteria, we are able to test this hypothesis for two important soil microbial groups from different domains. While fungi were screened on domain level, actinobacteria were selected as key stone group representing soil bacteria, being one of the dominant bacterial phyla containing one of the largest genera, *Streptomyces* and playing a crucial role in organic matter decomposition (Ascher et al., 2012). In combination with the genetic fingerprinting-DGGE method, the choice of actinobacteria as targets was made because they yield less

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**Fig. 1.** The Adventure—(a) The soil samples after their long journey; (b) Wolfgang Burtscher during the trip; (c) sampling points along the *tripmarks*-route. Symbols represent different transects interrupted by flights or bus rides; colors represent climate zones according to [Kottek et al. \(2006\)](#). Main climates: A=equatorial, B=arid, C=warm temperate, D=snow, E=tundra. Precipitation: W=desert, f=fully humid, s=summer dry, w=winter dry, m=monsoonal. Temperature: k=cold arid, a=hot summer, b=warm summer, c=cool summer, t=tundra.



**Fig. 2.** The Art—(a and b) Two *tripmarks* with their corresponding DGGE lanes for fungi (left) and actinobacteria (right); (c) the DGGE's are arranged on a black light box and used for exhibitions joining art and science; (d and e) various pictures of growing microorganisms have been created and published in an art catalogue ([Burtscher and Nagler, 2014](#)); (e and f) Soil DNA extraction seen from an artistic point of view.

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