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Spatial patterns of bacteria show that members of higher taxa share ecological characteristics

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INTRODUCTION

The predictability of the physical arrangement of living organisms, at whatever scale it is viewed, is referred to as their spatial pattern (Dale, 1999). Spatial patterns of species diversity are of increasing interest in ecology because they provide information about the underlying processes that shape biodiversity (Levin, 1992).

Whether bacteria display spatial patterns of distribution and at which level of taxonomic organization such patterns can be observed are central questions in microbial ecology. Here we hypothesized that bacterial groups at high taxonomical levels do display spatial patterns of distribution and that these patterns will differ between taxa due to

specific ecological traits.

We investigated how the total and relative abundances of eight bacterial taxa at the phylum or class level were spatially distributed in a field subjected to different cattle grazing regimes by using quantitative PCR and geostatistical modeling. To test whether the spatial distributions of the different taxa were related to soil heterogeneity, we performed exploratory analyses of relationships between abundance of the bacterial taxa and key soil properties

CONCLUSION

Spatial distribution of the abundance of the different taxa

Geostatistical modelling showed strong spatial patterns of the distribution of the abundance of all taxa with autocorrelations ranging between 24.4 and 46.2 m (data not shown).

The distributions of most taxa were similar but without correlation to the soil properties (Fig. 2), which suggest that spatially structured abiotic or biotic factors that were not captured in our study were governing the absolute abundance of the studied bacterial taxa in a similar way.

Therefore, at the absolute abundance level, clear spatial patterns of bacterial taxa were found but there were no significant differences in the spatial distributions of the different taxa.

Spatial distribution of the relative abundance of the different taxa

Geostatistical modelling showed that the relative abundance of all bacterial taxa except the Firmicutes, could be predicted on a field scale with a strong impact of the cattle activity (Fig. 4).

Comparison of the interpolated maps revealed that some of the targeted taxa displayed different or even contrasting spatial patterns, which indicates that they responded differently to spatially structured abiotic or biotic factors (Fig. 4). Positive or negative correlations between relative abundance of bacterial taxa were further confirmed by NMS analysis (Fig. 3) and Pearson's correlations.

In contrast to the absolute abundance data, the relative abundance of several bacterial taxa was found to co-vary with certain soil properties. Links between habitat related properties and spatial differentiation of the targeted taxa supports ecological distinctness between taxa and suggests niche partitioning at the phylum or class level.

These phylum or class-specific bacterial spatial patterns are consistent with the hypothesis that, within a given environment, members of bacterial clades defined at high taxonomical levels share specific ecological characteristics.

Altogether, spatial patterns and ecological relevance of higher taxa provide a conceptual framework as well as operational tools for theory development in bacterial ecology and evolution.

MATERIAL AND METHODS

The experimental site is a grassland field located in South Bohemia, Czech Republic. The field was divided into three areas based on the intensity of cattle impact (Fig. 1). Topsoils (0-20 cm) from 60 sampling points were collected in a 39.6 X 14.4 m grid with a 3.6 m lag distance (Fig. 1).

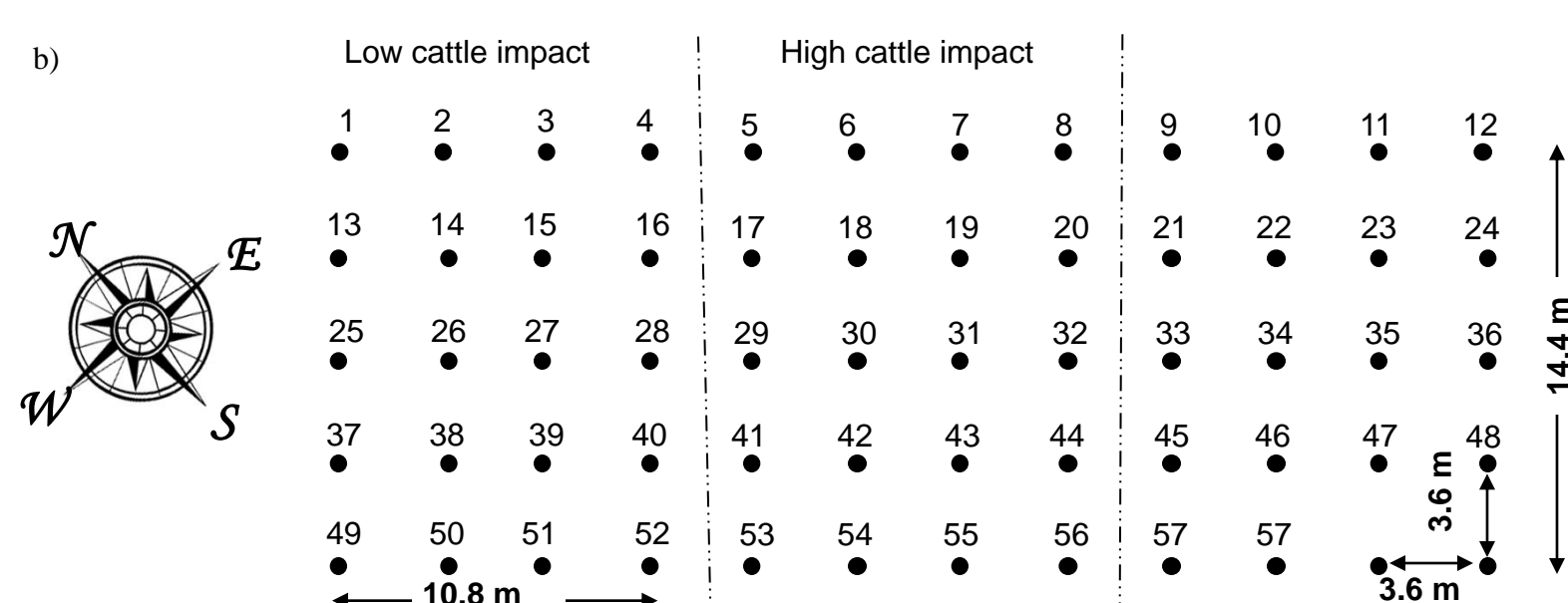


Fig. 1. Distribution of the sampling points at the field site

DNA was extracted from 250 mg of soil according to Martin-Laurent et al. (2001) and abundance of the different taxa was estimated by quantitative PCR using 16S rRNA taxa specific primers and thermal cycling conditions described by Fierer et al. (2005) and Philippot et al.

Geostatistic modeling was performed using the residual maximum likelihood technique (Lark et al. 2006). To assess the spatial variance model α , we calculated the standardized squared deviation, which measures the goodness of theoretical estimates:

$$\theta(\mathbf{x}_0) = \frac{\sum_{k=1}^n \frac{z(\mathbf{x}_k) - \hat{z}(\mathbf{x}_0)}{\sigma^2_K(\mathbf{x}_0)}}{\sigma^2_K(\mathbf{x}_0)}$$

where $z(\mathbf{x}_0)$ is the observed value at location \mathbf{x}_0 , $\hat{z}(\mathbf{x}_0)$ is the kriged estimate and $\sigma^2_K(\mathbf{x}_0)$ the kriging variance.

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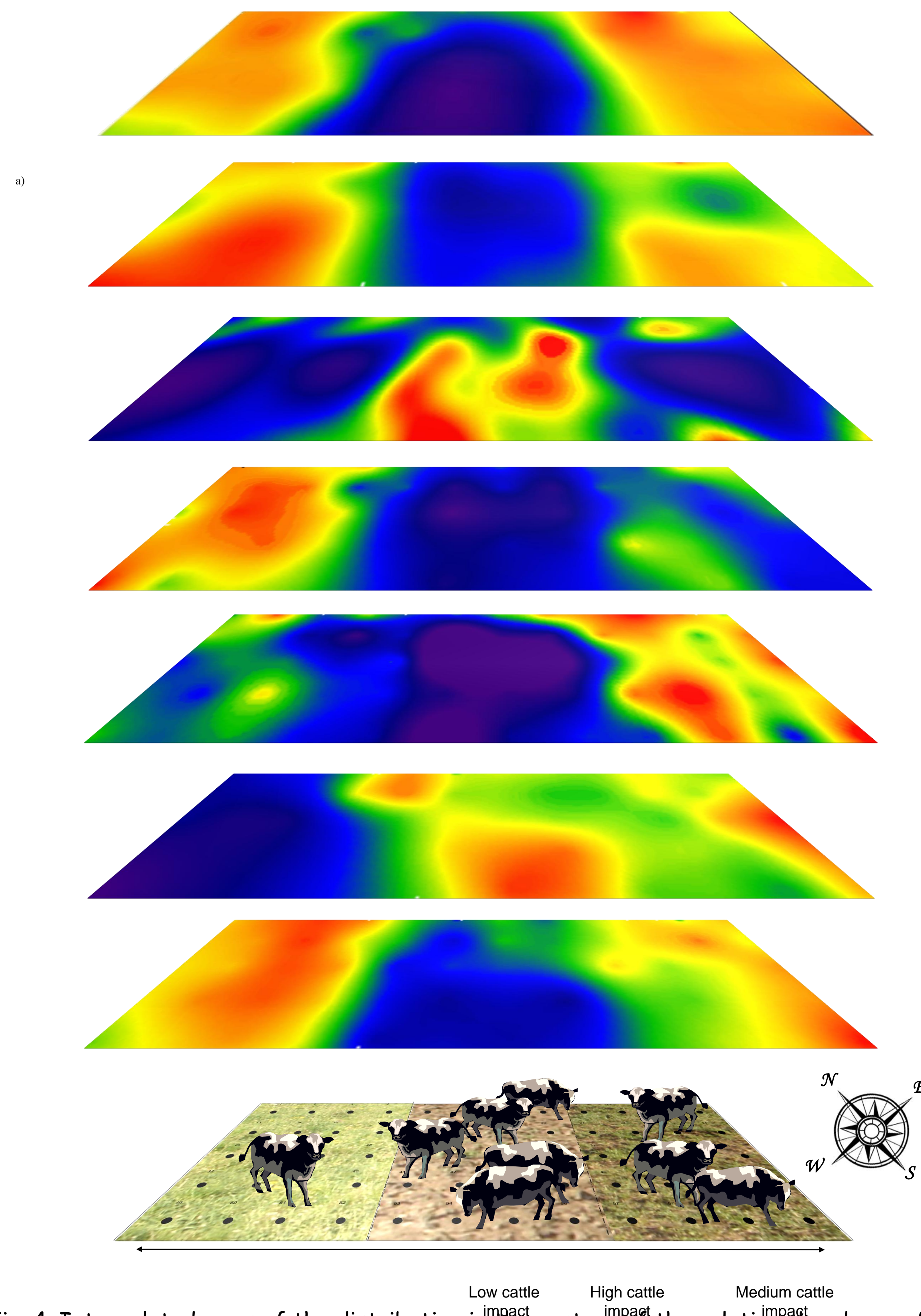


Fig. 4. Interpolated maps of the distribution in the pasture of the relative abundance of the different bacterial taxa within the total bacterial community. The color scale to the right of each map indicates the percentage of the 16S rRNA taxon-specific gene copy number per total bacterial 16S rRNA gene copy number.

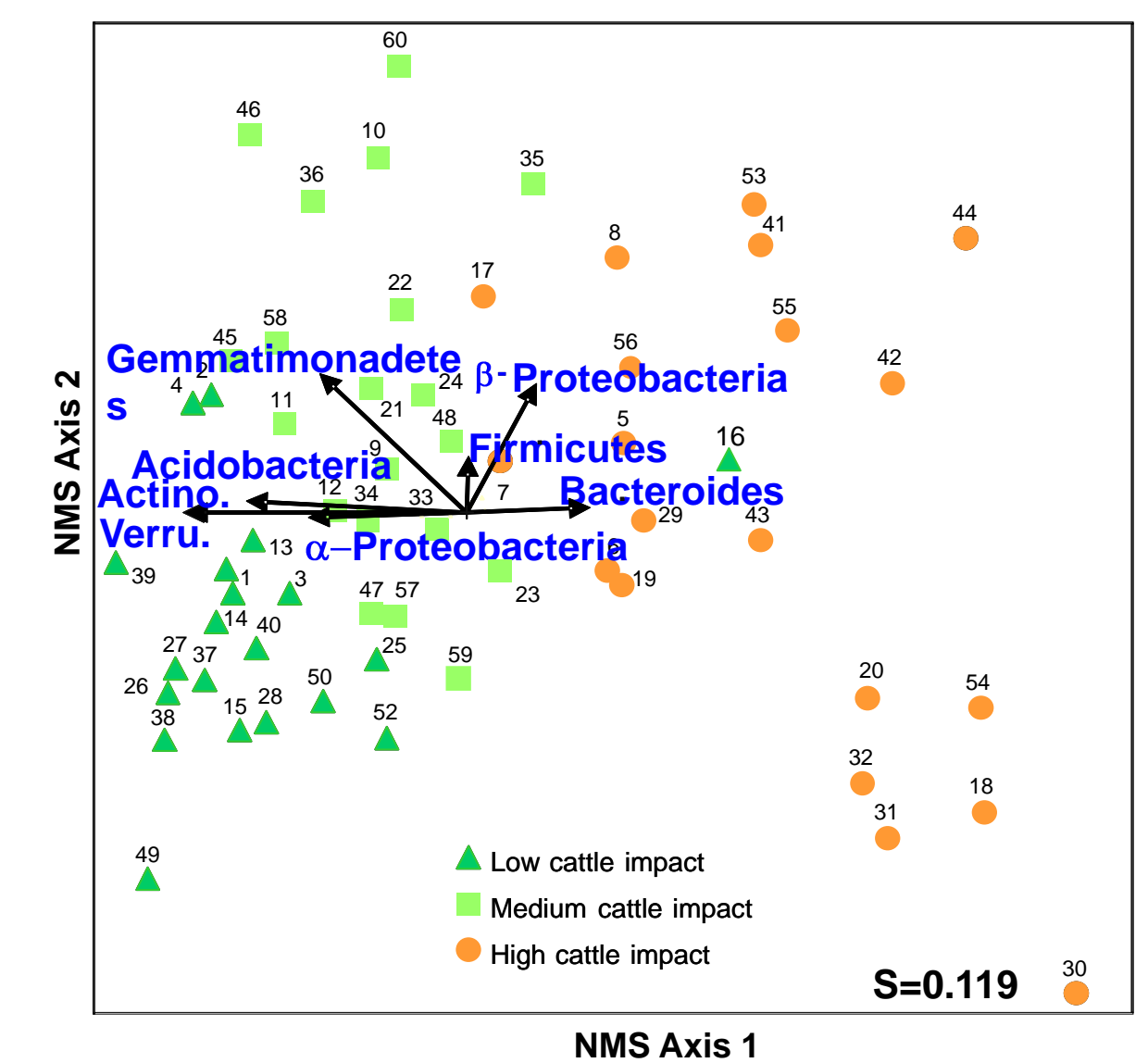


Fig. 3. Non-metric multidimensional scaling analysis of the relative abundance of the different taxa in relation to sampling locations in the field.

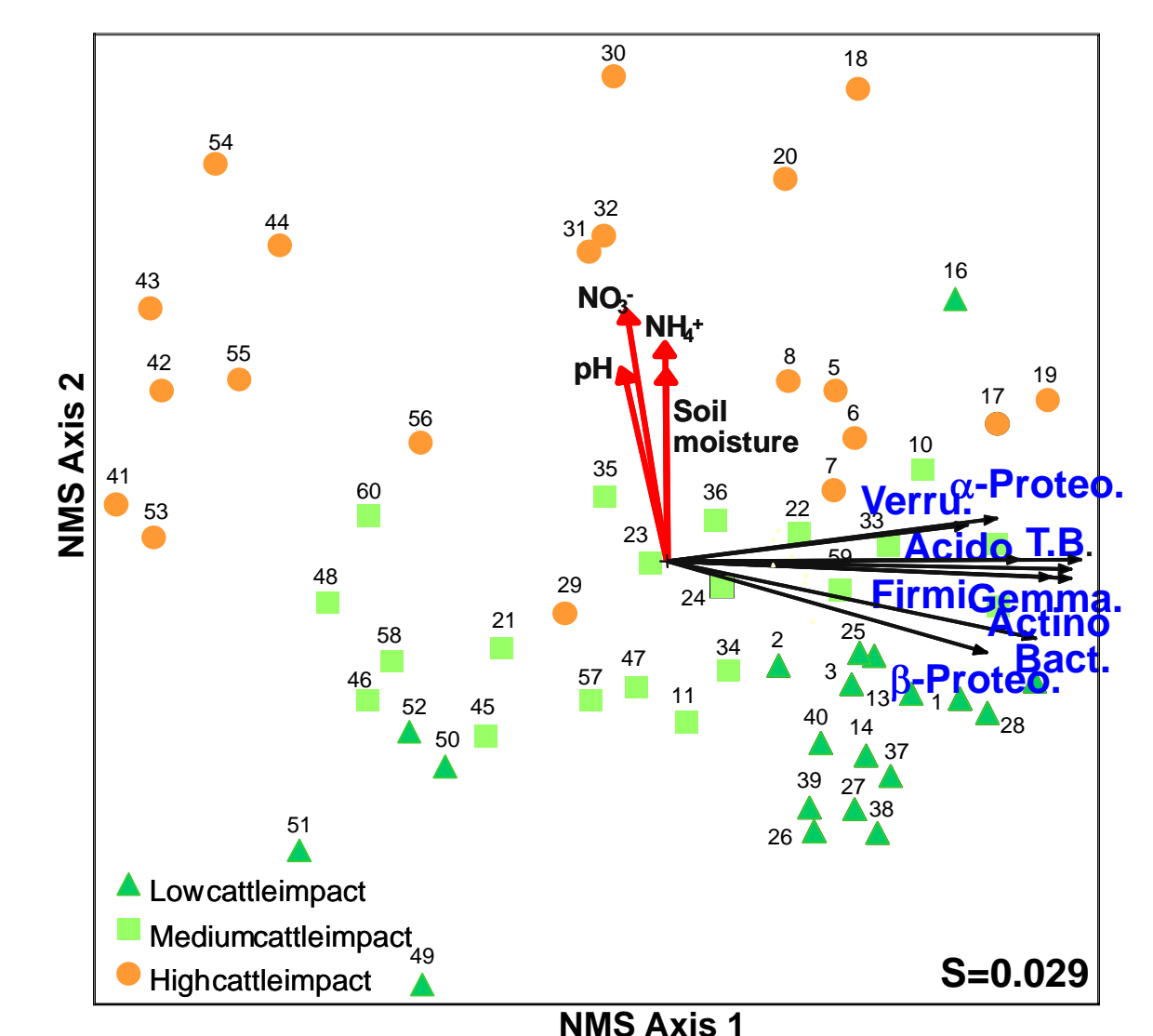


Fig. 2. Non-metric multidimensional scaling analysis of the abundance of the different taxa in relation to sampling locations in the field (T.B.=Total Bacteria).