The distribution of bacterial operational taxonomic units in European grasslands

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Introduction: Under the auspices of the BiodivERsA project BIOINVENT (www.biodiversa.org/972), this study aimed to determine the distribution of bacterial operational taxonomic units (OTUs) in grasslands along a pan-European transect to help gain insights into the factors driving their colonization patterns.

Materials and methods: Soil samples were taken from three different permanent grassland management types (intensive, low intensive and extensive) in Sweden (SE), Germany (DE), Switzerland (CH), Portugal mainland (PT) and the Azores (AZ) (338 sites in total – 16 cores of 2.5 cm diameter were pooled per site). An amplicon-based Illumina Miseq sequence analysis was conducted on the bacterial 16S rRNA gene and an OTU table constructed. Sample reads were rarefied to the lowest sequencing number and a quintuple Venn diagram was made using the Venn package in R (R core team, 2018).

Results and discussion: A total of 28,174 unique bacterial OTUs were identified (Figure 1); of these 5,901 OTUs (20.9%) were shared among all countries. PT harboured the most unique OTUs (3,534, 12.5%), followed by AZ (2,142, 7.6%), while approx. 3-5% of th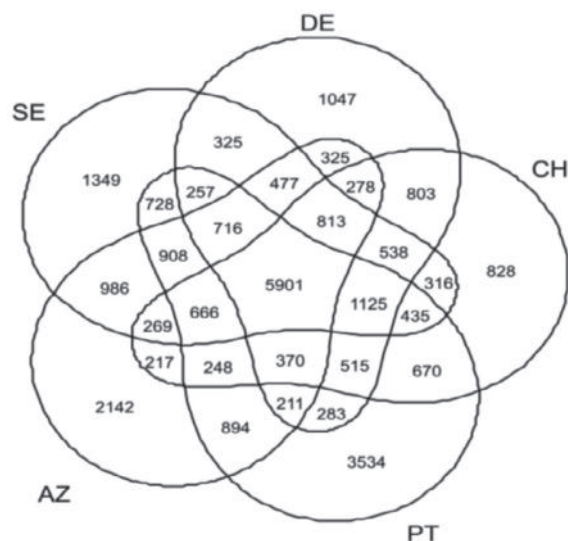e OTUs were unique to CH, DE and SE, respectively. The substantial number of shared bacterial OTUs would suggest a 'core' bacterial community among European grasslands. Country-specific variations in climate, grassland management and soil conditions may explain the relatively high proportion of unique OTUs present in each country.

Conclusion: These results indicate a core grassland microbiome. The large number of country specific OTUs, in spite of the fact that the same management intensity spectrum was sampled in each country, would also suggest that a combination of country-specific climate, soil and management conditions are important determinants of the composition of the soil microbiome.

Figure 1. A quintuple Venn diagram showing the unique and shared bacterial OTUs from the countries of the BIOINVENT transect.

R Development Core Team (2018) R:A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria.