



while the perennials had NifH sequences most related to *Coralimargarita*, *Novosphingobium* and *Azospirillum*, indicating that the perennials can better select beneficial members. Moreover, higher numbers of genes for nitrogen fixation and lower number of genes for nitrite reduction suggest better nitrogen sustainability of the perennials. Thus our study provides comprehensive evidence showing perennial bioenergy crops have advantages over corn in higher microbial species and functional diversity and in selecting members with beneficial traits, consistent with a higher level of sustainability of perennial biofuel crops.

Core functional microbiome of switchgrass: We used a “multi-omic” approach to establish a minimum core of actively transcribed functions in rhizosphere soils of switchgrass. We used metagenomics and metatranscriptomics to identify shared transcribed functions in samples. The minimum functional core accounts for 99% or 92% of functional annotations depending on annotation database (SEED Subsystems or RefSeq respectively). We then used metaproteomic data to further confirm our minimum functional core. The metaproteome data had 460 unique SEED Subsystem annotations with an abundance of 876,429. All but 12 of the SEED Subsystem annotations were found in the minimum functional core further validating the minimum functional core. The Subsystems with the greatest relative abundance in the metatranscriptome minimum functional core are the Clustering-based subsystem (defined as a cluster of genes known to work together but for which no function has been established), Protein metabolism, Carbohydrates (partly housekeeping functions and partly functions related to sugar utilization), Miscellaneous and RNA metabolism. Obviously the majority of these functions are either “known unknowns” or functions related to housekeeping. These results identify transcripts expressed at high levels and hence targets for further investigation of their function.

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