

Applied Microbiology and Biotechnology

Supplementary Material

Characterization of three plant biomass-degrading microbial consortia by metagenomics- and metasecretomics-based approaches

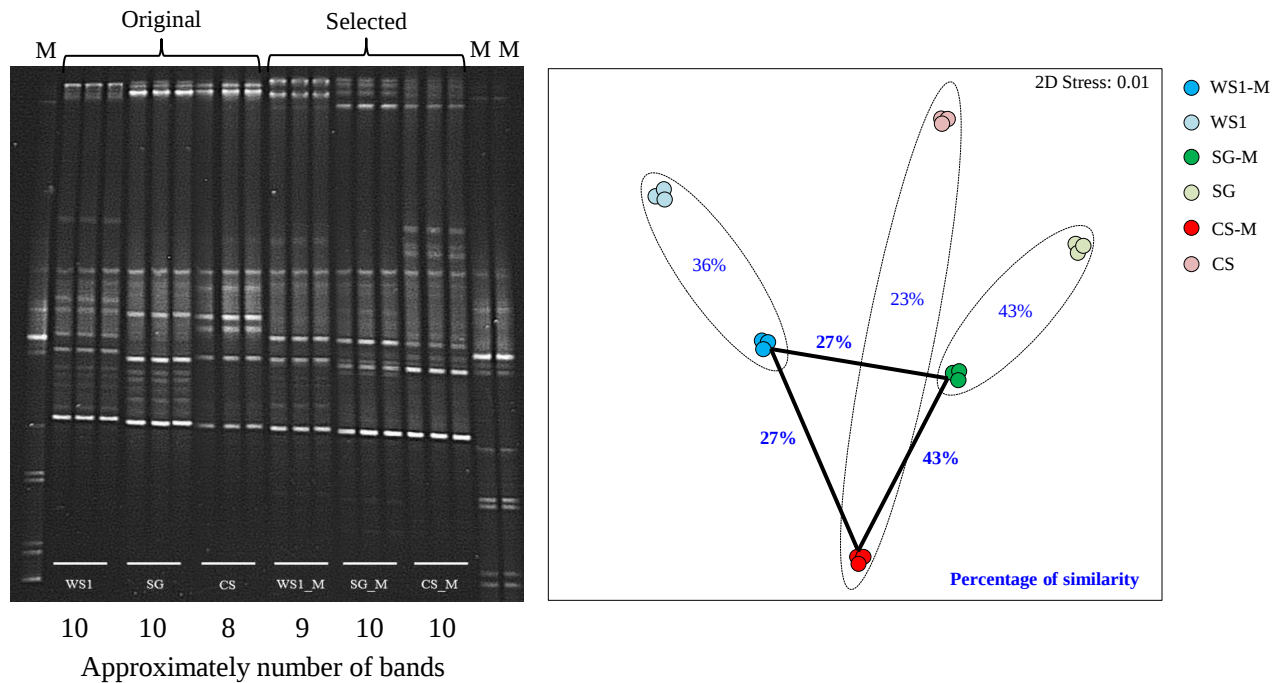
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Affiliations

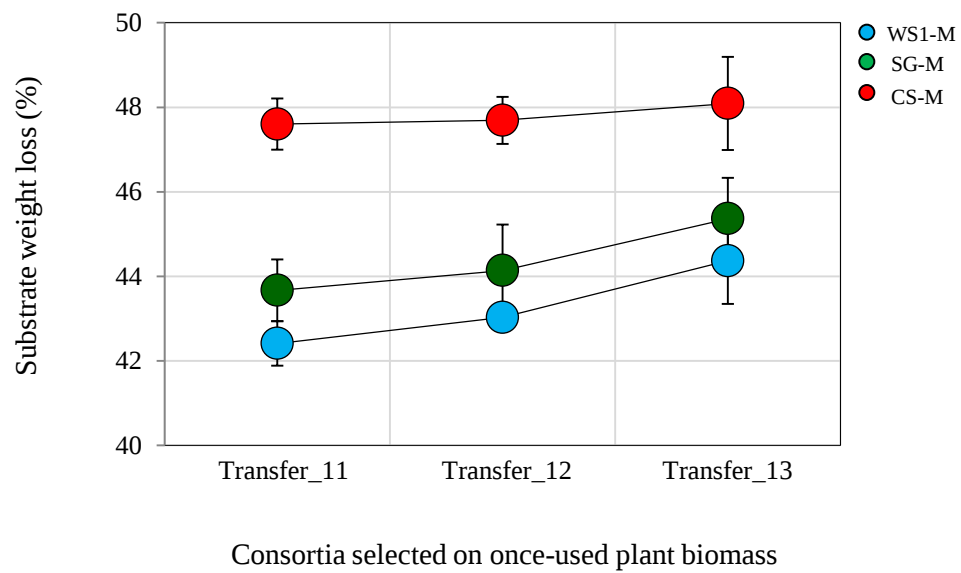
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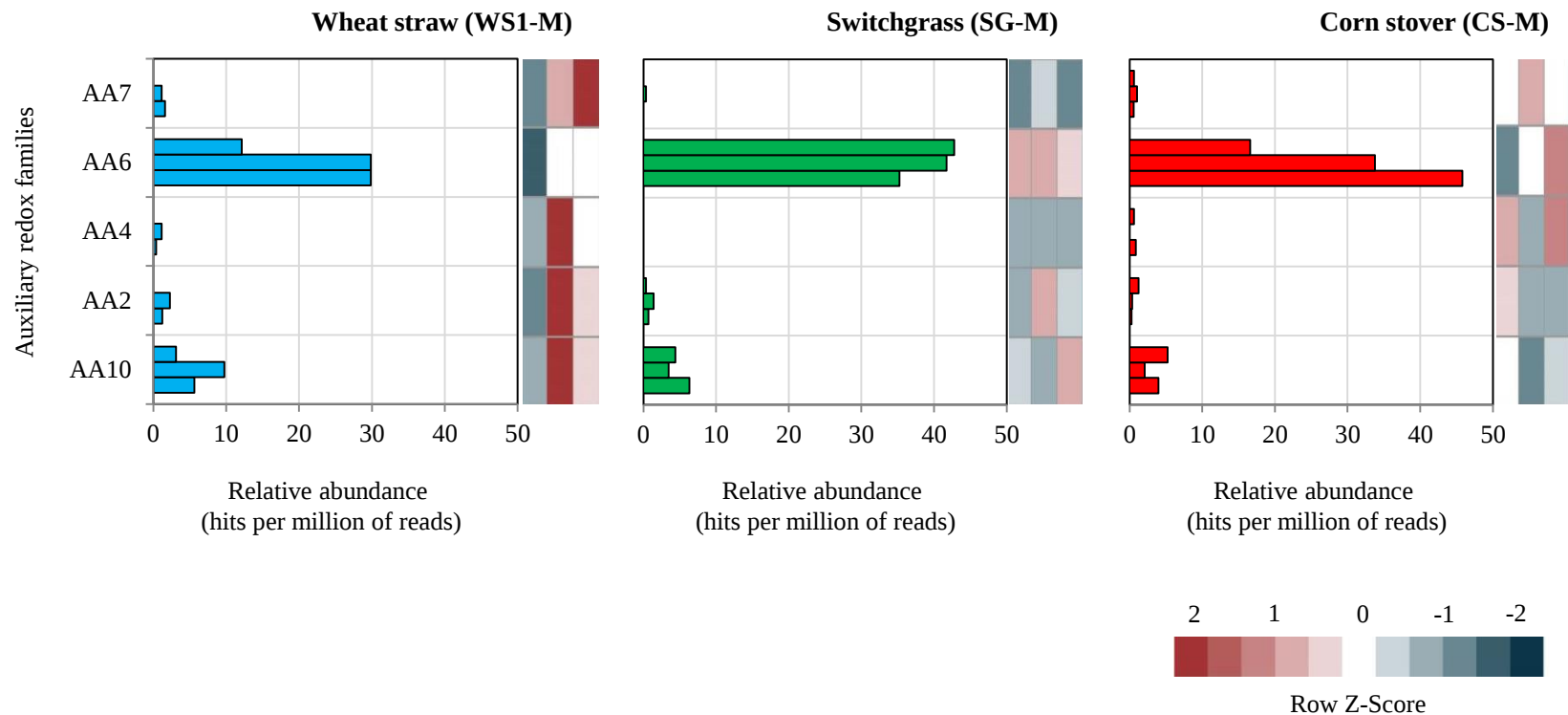
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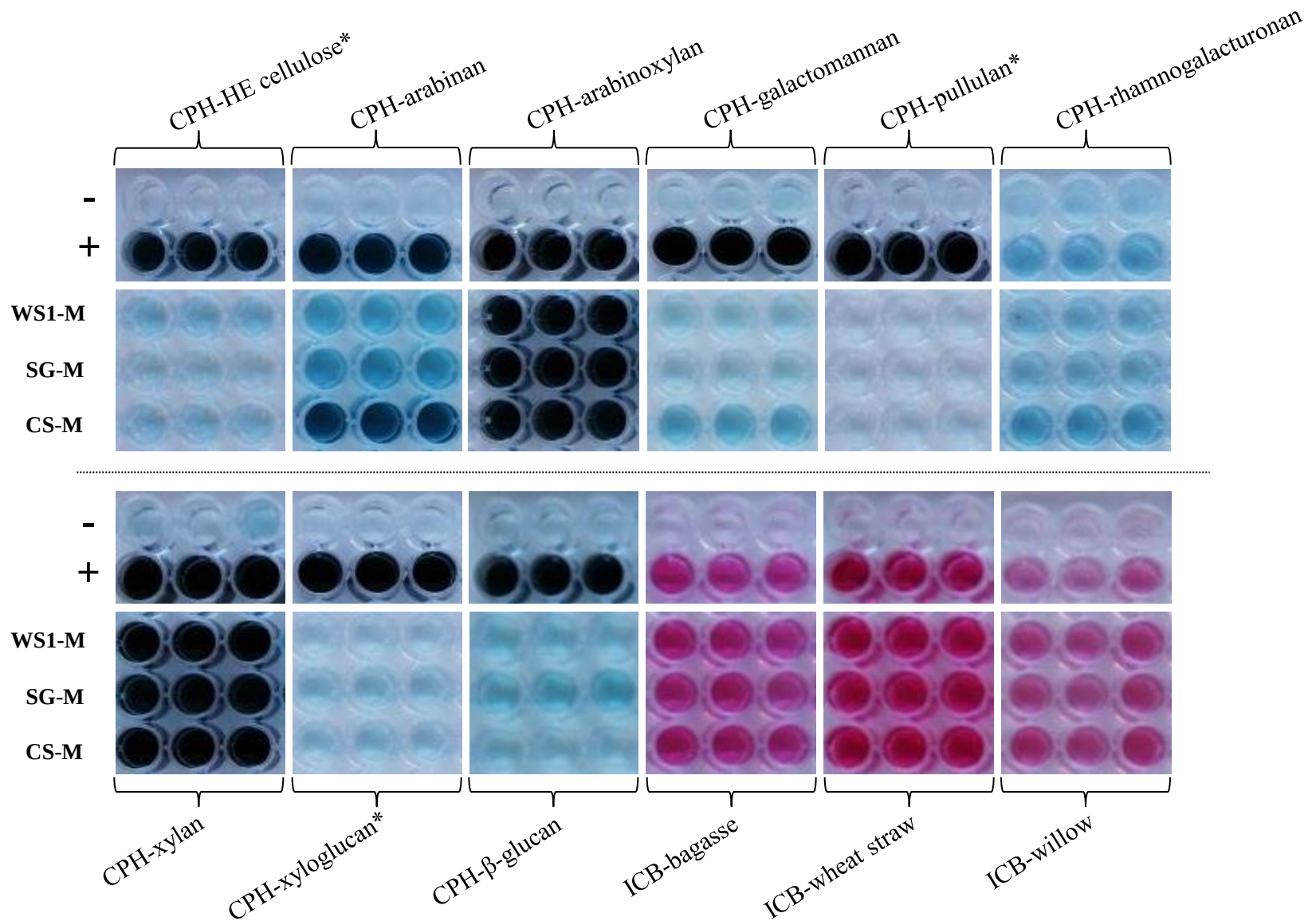
Supplementary Fig S1. 16S rRNA gene bacterial PCR-DGGE cluster analyses comparing soil-derived microbial consortia (original: WS1, SG, CS) with microbial consortia bred on once-used plant biomass (selected: WS1-M, SG-M and CS-M). M means DGGE markers.



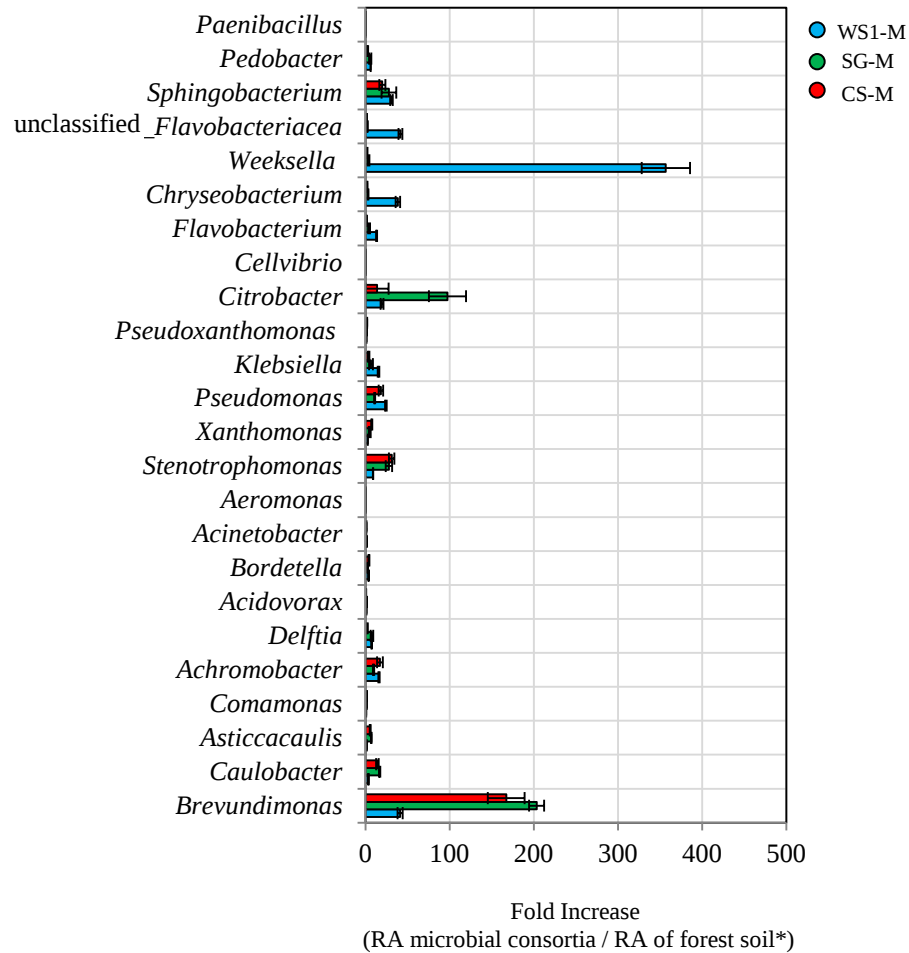
Supplementary Fig S2. Weight loss (%) of different substrates along the transfers 11, 12 and 13



Supplementary Fig S3. Relative abundance (hits per million of reads) of the AA families across the WS1-M, SG-M and CS-M microbial consortia. Data is showed by triplicate flasks. Heat maps were constructed using the row Z-score and comparing the three microbial consortia.



Supplementary Fig S4. Representation of the product plates used to evaluate the secreted enzymatic activity of WS1-M, SG-M and CS-M on nine chromogenic polysaccharides hydrogels (CPH) and three insoluble chromogenic biomass (ICB) substrates. +: positive controls, -: negative control. Asterisks represent substrates in which enzymatic activities were not observed.



Supplementary Fig S5. Fold increase values (relative abundance microbial consortia / relative abundance of forest soil). Asterisk: The relative abundance of each genus was obtained from a forest soil metagenome (Jiménez et al. 2015a) using the same parameters of this study.